Match length	87
% identity	78
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	192537
Contig ID	6712_1.R1039
5'-most EST	LIB3165-021-P1-K1-D5
Method	BLASTX
NCBI GI	g4538959
BLAST score	453
E value	8.0e-45
Match length	123
% identity	72
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	192538
Contig ID	6712_2.R1039
5'-most EST	g5050683
Method	BLASTX
NCBI GI	g1076545
BLAST score	700
E value	8.0e-74
Match length	198
% identity	70
NCBI Description	guanine nucleotide regulatory protein - fava bean >gi|547478|emb|CAA85733| (Z37503) guanine nucleotide regulatory protein [Vicia faba] >gi|1098297|prf||2115367E small GTP-binding protein [Vicia faba]

Seq. No.	192539
Contig ID	6713_1.R1039
5'-most EST	LIB3165-016-P1-K1-F4
Method	BLASTX
NCBI GI	g2633727
BLAST score	260
E value	2.0e-22
Match length	145
% identity	43
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	192540
Contig ID	6715_1.R1039
5'-most EST	LIB3083-053-Q1-L1-A6

Seq. No.	192541
Contig ID	6726_1.R1039
5'-most EST	LIB3145-034-Q1-K1-G4

Seq. No.	192542
Contig ID	6731_1.R1039
5'-most EST	LIB3197-012-P1-M1-G10
Method	BLASTX
NCBI GI	g4204260
BLAST score	196
E value	1.0e-14
Match length	60
% identity	60

NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]
Seq. No.	192543
Contig ID	6736_1.R1039
5'-most EST	uC-gsflmaxxa029g11b1
Method	BLASTX
NCBI GI	g2492504
BLAST score	798
E value	4.0e-85
Match length	331
% identity	41
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi|1669660|emb|CAA70565| (Y09396) protein of AAA family [Capsicum annuum]
Seq. No.	192544
Contig ID	6737_1.R1039
5'-most EST	LIB3083-056-Q1-L1-B8
Method	BLASTX
NCBI GI	g4468990
BLAST score	580
E value	1.0e-59
Match length	183
% identity	67
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	192545
Contig ID	6738_1.R1039
5'-most EST	LIB3083-053-Q1-L1-C9
Method	BLASTX
NCBI GI	g3850587
BLAST score	391
E value	6.0e-38
Match length	99
% identity	79
NCBI Description	(AC005278) Strong similarity to gi|2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb|Z97335. [Arabidopsis thaliana]
Seq. No.	192546
Contig ID	6739_1.R1039
5'-most EST	LIB3083-053-Q1-L1-D10
Method	BLASTX
NCBI GI	g547683
BLAST score	255
E value	5.0e-22
Match length	84
% identity	68
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi|170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi|445601|prf||1909348A heat shock protein hsp80 [Lycopersicon esculentum]
Seq. No.	192547
Contig ID	6741_1.R1039
5'-most EST	LIB3145-029-Q1-K1-A5
Method	BLASTX

NCBI GI g1589778
BLAST score 683
E value 3.0e-72
Match length 134
% identity 93
NCBI Description (U62135) SPINDLY [Arabidopsis thaliana]

Seq. No. 192548
Contig ID 6744_1.R1039
5'-most EST g5049447
Method BLASTX
NCBI GI g3023190
BLAST score 1097
E value 1.0e-120
Match length 259
% identity 84
NCBI Description 14-3-3-LIKE PROTEIN 16R >gi|1888459|emb|CAA72381| (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No. 192549
Contig ID 6744_2.R1039
5'-most EST g5045432
Method BLASTX
NCBI GI g1168195
BLAST score 815
E value 2.0e-87
Match length 197
% identity 82
NCBI Description 14-3-3-LIKE PROTEIN >gi|478595|pir||S20580 protein kinase C inhibitor homolog - Hooker's evening primrose >gi|20062|emb|CAA44642| (X62838) protein kinase C inhibitor homologue [Oenothera elata subsp. hookeri]

Seq. No. 192550
Contig ID 6744_3.R1039
5'-most EST uC-gsflnu33B049d03b1
Method BLASTX
NCBI GI g1168189
BLAST score 743
E value 7.0e-79
Match length 195
% identity 83
NCBI Description 14-3-3-LIKE PROTEIN A (VFA-1433A) >gi|1076542|pir||S52899 14-3-3 brain protein homolog - fava bean >gi|695765|emb|CAA88415| (Z48504) 14-3-3 brain protein homolog [Vicia faba]

Seq. No. 192551
Contig ID 6744_4.R1039
5'-most EST uC-gsflnu33B011h10b1
Method BLASTX
NCBI GI g1168196
BLAST score 260
E value 2.0e-26
Match length 82
% identity 82
NCBI Description 14-3-3-LIKE PROTEIN >gi|555974 (U15036) 14-3-3-like protein

[Pisum sativum]

Seq. No.	192552
Contig ID	6744_6.R1039
5'-most EST	LIB3165-039-Q1-K1-B2
Method	BLASTX
NCBI GI	g1702986
BLAST score	437
E value	3.0e-43
Match length	111
% identity	84
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi|1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi|1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	192553
Contig ID	6744_7.R1039
5'-most EST	LIB3272-021-P1-K1-D5
Method	BLASTX
NCBI GI	g3153902
BLAST score	412
E value	2.0e-40
Match length	109
% identity	78
NCBI Description	(AF066076) 14-3-3-like protein [Helianthus annuus]

Seq. No.	192554
Contig ID	6748_1.R1039
5'-most EST	g5048889
Method	BLASTN
NCBI GI	g3420238
BLAST score	263
E value	1.0e-146
Match length	527
% identity	91
NCBI Description	Gossypium hirsutum actin gene, complete cds

Seq. No.	192555
Contig ID	6750_1.R1039
5'-most EST	LIB3272-045-P1-K1-F7
Method	BLASTX
NCBI GI	g345829
BLAST score	447
E value	4.0e-48
Match length	149
% identity	64
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	192556
Contig ID	6758_1.R1039
5'-most EST	LIB3083-053-Q1-L1-E7
Method	BLASTX
NCBI GI	g1293835
BLAST score	248
E value	4.0e-21
Match length	110
% identity	47

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 192557
Contig ID 6759_1.R1039
5'-most EST LIB3197-046-Q1-M1-E11

Seq. No. 192558
Contig ID 6761_1.R1039
5'-most EST g5044445
Method BLASTX
NCBI GI g3098571
BLAST score 433
E value 4.0e-42
Match length 221
% identity 39
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 192559
Contig ID 6761_2.R1039
5'-most EST LIB3189-032-P1-K1-D2
Method BLASTX
NCBI GI g3098571
BLAST score 230
E value 7.0e-19
Match length 97
% identity 44
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 192560
Contig ID 6763_1.R1039
5'-most EST uC-gsflnu33B072c06b1
Method BLASTX
NCBI GI g2055230
BLAST score 438
E value 3.0e-43
Match length 180
% identity 49
NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 192561
Contig ID 6766_1.R1039
5'-most EST LIB3083-053-Q1-L1-F5
Method BLASTX
NCBI GI g4218121
BLAST score 580
E value 9.0e-60
Match length 191
% identity 58
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 192562
Contig ID 6769_1.R1039
5'-most EST LIB3083-053-Q1-L1-F9

Seq. No. 192563
Contig ID 6771_1.R1039
5'-most EST LIB3083-053-Q1-L1-G12

Seq. No.	192564
Contig ID	6775_1.R1039
5'-most EST	g5046633
Method	BLASTX
NCBI GI	g4263771
BLAST score	345
E value	4.0e-32
Match length	114
% identity	60
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	192565
Contig ID	6775_2.R1039
5'-most EST	LIB3149-018-Q1-K1-B10
Method	BLASTX
NCBI GI	g124226
BLAST score	408
E value	4.0e-79
Match length	159
% identity	89
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi|100278|pir||S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi|19702|emb|CAA45104| (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	192566
Contig ID	6775_3.R1039
5'-most EST	uC-gsronu33B104d08b1
Method	BLASTX
NCBI GI	g1777443
BLAST score	170
E value	8.0e-12
Match length	108
% identity	44
NCBI Description	(U28422) CCA1 [Arabidopsis thaliana] >gi|3510263 (AC005310) DNA-binding protein CCA1 [Arabidopsis thaliana] >gi|4090569 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No.	192567
Contig ID	6775_5.R1039
5'-most EST	g5045445
Method	BLASTX
NCBI GI	g124226
BLAST score	793
E value	1.0e-84
Match length	159
% identity	94
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi|100278|pir||S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi|19702|emb|CAA45104| (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No. 192568

Contig ID	6775_6.R1039
5'-most EST	LIB3146-002-P1-K2-B2
Method	BLASTX
NCBI GI	g124226
BLAST score	786
E value	6.0e-84
Match length	159
% identity	94
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi|100278|pir||S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi|19702|emb|CAA45104| (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	192569
Contig ID	6775_7.R1039
5'-most EST	LIB3146-008-Q1-K1-B4
Method	BLASTN
NCBI GI	g3789947
BLAST score	129
E value	3.0e-66
Match length	353
% identity	84
NCBI Description	Oryza sativa translation initiation factor 5A (eIF-5A) mRNA, complete cds

Seq. No.	192570
Contig ID	6775_9.R1039
5'-most EST	LIB3135-048-Q1-K1-E11
Method	BLASTX
NCBI GI	g124224
BLAST score	620
E value	1.0e-64
Match length	122
% identity	94
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi|100345|pir||S21060 translation initiation factor eIF-5A - common tobacco >gi|19887|emb|CAA45105| (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	192571
Contig ID	6775_12.R1039
5'-most EST	LIB3146-032-Q1-K1-E9
Method	BLASTX
NCBI GI	g124226
BLAST score	424
E value	8.0e-42
Match length	103
% identity	81
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi|100278|pir||S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi|19702|emb|CAA45104| (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	192572
Contig ID	6776_1.R1039

5'-most EST	g5045361
Method	BLASTX
NCBI GI	g4038036
BLAST score	258
E value	7.0e-22
Match length	205
% identity	37
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	192573
Contig ID	6777_1.R1039
5'-most EST	uC-gsflnu33B085h11b1
Method	BLASTX
NCBI GI	g3915089
BLAST score	1382
E value	0.0e+00
Match length	376
% identity	85
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi|2144269|pir||JC5129 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) A - Populus kitakamiensis >gi|1139561|dbj|BAA11579| (D82815) cinnamic acid 4-hydroxylase [Populus kitakamiensis] >gi|1777370|dbj|BAA11576| (D82812) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No.	192574
Contig ID	6778_1.R1039
5'-most EST	uC-gsronu33B124f06b1
Method	BLASTX
NCBI GI	g2982268
BLAST score	677
E value	4.0e-71
Match length	139
% identity	94
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	192575
Contig ID	6778_2.R1039
5'-most EST	uC-gsflnu33B107f10b1
Method	BLASTX
NCBI GI	g730645
BLAST score	640
E value	1.0e-66
Match length	152
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi|629556|pir||S43412 ribosomal protein S15 - Arabidopsis thaliana >gi|313152|emb|CAA80679| (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi|313188|emb|CAA80681| (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi|1903366|gb|AAB70449| (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb|R29788,gb|ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	192576
Contig ID	6778_3.R1039
5'-most EST	LIB3147-039-Q1-K1-G1
Method	BLASTX
NCBI GI	g2982268
BLAST score	581
E value	6.0e-60
Match length	121
% identity	93
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	192577
Contig ID	6778_4.R1039
5'-most EST	LIB3146-023-Q1-K1-C1
Method	BLASTX
NCBI GI	g730645
BLAST score	136
E value	5.0e-11
Match length	117
% identity	41
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi|629556|pir||S43412 ribosomal protein S15 - Arabidopsis thaliana >gi|313152|emb|CAA80679| (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi|313188|emb|CAA80681| (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi|1903366|gb|AAB70449| (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb|R29788,gb|ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	192578
Contig ID	6781_1.R1039
5'-most EST	LIB3189-036-P1-K1-H6
Method	BLASTX
NCBI GI	g2245000
BLAST score	168
E value	2.0e-11
Match length	138
% identity	30
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192579
Contig ID	6783_1.R1039
5'-most EST	LIB3083-053-Q1-L1-H8

Seq. No.	192580
Contig ID	6786_1.R1039
5'-most EST	uC-gsflnu33B084g06b1
Method	BLASTX
NCBI GI	g4218121
BLAST score	523
E value	2.0e-53
Match length	147
% identity	64
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 192581

Contig ID	6787_1.R1039
5'-most EST	LIB3146-007-Q1-K1-E6
Method	BLASTX
NCBI GI	g2864609
BLAST score	262
E value	2.0e-22
Match length	134
% identity	46
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi|4049337|emb|CAA22562| (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	192582
Contig ID	6795_1.R1039
5'-most EST	LIB3083-054-Q1-L1-E11
Method	BLASTX
NCBI GI	g4512673
BLAST score	1073
E value	1.0e-117
Match length	271
% identity	82
NCBI Description	(AC006931) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	192583
Contig ID	6797_1.R1039
5'-most EST	LIB3197-025-Q1-M1-A8

Seq. No.	192584
Contig ID	6801_1.R1039
5'-most EST	LIB3197-025-Q1-M1-A9
Method	BLASTX
NCBI GI	g3283893
BLAST score	408
E value	1.0e-39
Match length	181
% identity	45
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	192585
Contig ID	6807_1.R1039
5'-most EST	LIB3083-108-Q1-L1-F2

Seq. No.	192586
Contig ID	6817_1.R1039
5'-most EST	g5049327
Method	BLASTX
NCBI GI	g2213613
BLAST score	168
E value	2.0e-11
Match length	125
% identity	36
NCBI Description	(AC000103) F21J9.7 [Arabidopsis thaliana]

Seq. No.	192587
Contig ID	6824_1.R1039
5'-most EST	LIB3135-029-Q1-K1-A12

Seq. No.	192588
Contig ID	6829_1.R1039
5'-most EST	LIB3083-055-Q1-L1-C6
Method	BLASTN
NCBI GI	g3327922
BLAST score	33
E value	8.0e-09
Match length	77
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	192589
Contig ID	6831_1.R1039
5'-most EST	uC-gsflnu33B011d03b1
Method	BLASTX
NCBI GI	g3860308
BLAST score	210
E value	2.0e-16
Match length	69
% identity	62
NCBI Description	(AJ012681) hypothetical protein [Cicer arietinum]

Seq. No.	192590
Contig ID	6837_1.R1039
5'-most EST	LIB3272-019-P1-K1-G5

Seq. No.	192591
Contig ID	6857_1.R1039
5'-most EST	uC-gsronu33B002h12b1
Method	BLASTX
NCBI GI	g2879867
BLAST score	412
E value	6.0e-40
Match length	115
% identity	69
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	192592
Contig ID	6864_1.R1039
5'-most EST	LIB3083-055-Q1-L1-G6
Method	BLASTX
NCBI GI	g3834307
BLAST score	259
E value	2.0e-22
Match length	70
% identity	71
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi|2832679 putative protein from Arabidopsis thaliana BAC gb|AL021712. ESTs gb|N65887 and gb|N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	192593
Contig ID	6868_1.R1039
5'-most EST	LIB3120-023-Q1-K1-B3

Seq. No.	192594
Contig ID	6874_1.R1039
5'-most EST	LIB3083-055-Q1-L1-H8

Seq. No.	192595
Contig ID	6877_1.R1039
5'-most EST	uC-gsronu33B038c04b1
Method	BLASTX
NCBI GI	g4049341
BLAST score	374
E value	2.0e-35
Match length	120
% identity	64
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	192596
Contig ID	6885_1.R1039
5'-most EST	uC-gsflmaxxa096h03b1
Method	BLASTX
NCBI GI	g3033381
BLAST score	922
E value	1.0e-99
Match length	216
% identity	84
NCBI Description	(AC004238) putative UDP-galactose-4-epimerase [Arabidopsis thaliana]

Seq. No.	192597
Contig ID	6886_1.R1039
5'-most EST	g5049778
Method	BLASTX
NCBI GI	g2654358
BLAST score	559
E value	3.0e-57
Match length	184
% identity	58
NCBI Description	(Y15522) MNUDC protein [Mus musculus] >gi|2808636|emb|CAA57201| (X81443) Sig 92 [Mus musculus]

Seq. No.	192598
Contig ID	6886_2.R1039
5'-most EST	uC-gsflmaxxa049b09b1
Method	BLASTX
NCBI GI	g2654358
BLAST score	408
E value	2.0e-39
Match length	144
% identity	53
NCBI Description	(Y15522) MNUDC protein [Mus musculus] >gi|2808636|emb|CAA57201| (X81443) Sig 92 [Mus musculus]

Seq. No.	192599
Contig ID	6890_1.R1039
5'-most EST	LIB3145-041-Q1-K1-G1
Method	BLASTX
NCBI GI	g1710780

BLAST score	685
E value	6.0e-72
Match length	186
% identity	70
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi|1321917|emb|CAA65433| (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	192600
Contig ID	6890_2.R1039
5'-most EST	g5044477
Method	BLASTX
NCBI GI	g1710780
BLAST score	444
E value	9.0e-63
Match length	173
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi|1321917|emb|CAA65433| (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	192601
Contig ID	6890_3.R1039
5'-most EST	LIB3135-007-Q1-K1-B8
Method	BLASTX
NCBI GI	g1710780
BLAST score	365
E value	1.0e-34
Match length	97
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi|1321917|emb|CAA65433| (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	192602
Contig ID	6896_1.R1039
5'-most EST	uC-gsflmaxxa064a06b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	238
E value	2.0e-19
Match length	81
% identity	53
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	192603
Contig ID	6908_1.R1039
5'-most EST	LIB3147-029-Q1-K1-E12
Method	BLASTX
NCBI GI	g3341681
BLAST score	382
E value	1.0e-36
Match length	86
% identity	87
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	192604
Contig ID	6918_1.R1039
5'-most EST	LIB3272-033-P1-K1-H4
Method	BLASTX
NCBI GI	g2289002
BLAST score	340
E value	1.0e-31
Match length	148
% identity	52
NCBI Description	(AC002335) unknown protein [Arabidopsis thaliana]

Seq. No.	192605
Contig ID	6926_1.R1039
5'-most EST	g5047023
Method	BLASTX
NCBI GI	g3204134
BLAST score	671
E value	1.0e-70
Match length	176
% identity	67
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	192606
Contig ID	6930_1.R1039
5'-most EST	g3326169
Method	BLASTX
NCBI GI	g2853219
BLAST score	692
E value	7.0e-73
Match length	178
% identity	72
NCBI Description	(AJ000923) glutathione transferase [Carica papaya]

Seq. No.	192607
Contig ID	6930_2.R1039
5'-most EST	uC-gsronu33B117b02b1
Method	BLASTX
NCBI GI	g2341028
BLAST score	666
E value	5.0e-70
Match length	129
% identity	99
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb|X01694). EST gb|AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	192608
Contig ID	6930_3.R1039
5'-most EST	LIB3083-056-Q1-L1-F9
Method	BLASTX
NCBI GI	g2920666
BLAST score	400
E value	7.0e-39
Match length	100
% identity	73
NCBI Description	(AF048978) 2,4-D inducible glutathione S-transferase

[Glycine max]

Seq. No.	192609
Contig ID	6930_4.R1039
5'-most EST	LIB3272-002-P1-K1-A5
Method	BLASTX
NCBI GI	g2052029
BLAST score	451
E value	6.0e-45
Match length	120
% identity	68
NCBI Description	(Y10820) glutathione transferase [Glycine max]

Seq. No.	192610
Contig ID	6930_5.R1039
5'-most EST	uC-gsflnu33B062a08b1
Method	BLASTX
NCBI GI	g2982289
BLAST score	528
E value	4.0e-54
Match length	104
% identity	96
NCBI Description	(AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No.	192611
Contig ID	6931_1.R1039
5'-most EST	LIB3189-034-P1-K1-G12
Method	BLASTX
NCBI GI	g2979555
BLAST score	144
E value	6.0e-09
Match length	70
% identity	36
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	192612
Contig ID	6936_1.R1039
5'-most EST	uC-gsflnu33B027h05b1
Method	BLASTX
NCBI GI	g4193382
BLAST score	386
E value	4.0e-37
Match length	86
% identity	83
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi|4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	192613
Contig ID	6936_2.R1039
5'-most EST	LIB3148-035-Q1-K1-H4
Method	BLASTX
NCBI GI	g4193382
BLAST score	392
E value	6.0e-38
Match length	86
% identity	84

NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi|4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	192614
Contig ID	6936_3.R1039
5'-most EST	LIB3149-046-Q1-K1-B3
Method	BLASTX
NCBI GI	g4097547
BLAST score	282
E value	6.0e-25
Match length	67
% identity	45
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	192615
Contig ID	6937_1.R1039
5'-most EST	LIB3083-056-Q1-L1-G5

Seq. No.	192616
Contig ID	6940_1.R1039
5'-most EST	LIB3083-056-Q1-L1-G9
Method	BLASTX
NCBI GI	g2982783
BLAST score	323
E value	1.0e-29
Match length	228
% identity	32
NCBI Description	(AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex aeolicus]

Seq. No.	192617
Contig ID	6951_1.R1039
5'-most EST	g5050753
Method	BLASTX
NCBI GI	g1171866
BLAST score	825
E value	2.0e-88
Match length	212
% identity	74
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi|629601|pir||S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi|562282|emb|CAA57725| (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	192618
Contig ID	6953_1.R1039
5'-most EST	LIB3083-057-Q1-L1-A10
Method	BLASTN
NCBI GI	g3063438
BLAST score	34
E value	2.0e-09
Match length	74
% identity	86
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	192619
Contig ID	6960_1.R1039
5'-most EST	LIB3189-047-P1-K1-G8

Seq. No.	192620
Contig ID	6965_1.R1039
5'-most EST	LIB3083-057-Q1-L1-D10
Method	BLASTX
NCBI GI	g3927831
BLAST score	1095
E value	1.0e-120
Match length	239
% identity	67
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	192621
Contig ID	6984_1.R1039
5'-most EST	LIB3197-028-Q1-M1-A8
Method	BLASTX
NCBI GI	g135406
BLAST score	671
E value	1.0e-70
Match length	137
% identity	91
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi|99768|pir||A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi|166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi|166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	192622
Contig ID	6993_1.R1039
5'-most EST	g5049634
Method	BLASTX
NCBI GI	g728880
BLAST score	536
E value	1.0e-54
Match length	150
% identity	69
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi|517485|emb|CAA54691| (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi|1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

Seq. No.	192623
Contig ID	6994_1.R1039
5'-most EST	LIB3083-058-Q1-L1-F7
Method	BLASTX
NCBI GI	g2281115
BLAST score	168
E value	9.0e-12
Match length	37
% identity	86
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	192624
Contig ID	7005_1.R1039
5'-most EST	uC-gsronu33B150a01b1
Method	BLASTX
NCBI GI	g3286691
BLAST score	463
E value	6.0e-46
Match length	126
% identity	65
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	192625
Contig ID	7013_1.R1039
5'-most EST	LIB3165-012-P1-K1-D7
Method	BLASTX
NCBI GI	g2388575
BLAST score	325
E value	8.0e-30
Match length	164
% identity	41
NCBI Description	(AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No.	192626
Contig ID	7017_1.R1039
5'-most EST	uC-gsflnu33B142b03b1
Method	BLASTX
NCBI GI	g3005931
BLAST score	774
E value	1.0e-82
Match length	228
% identity	34
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]

Seq. No.	192627
Contig ID	7025_1.R1039
5'-most EST	LIB3083-059-Q1-L1-G9

Seq. No.	192628
Contig ID	7026_1.R1039
5'-most EST	uC-gsronu33B125f04b1
Method	BLASTX
NCBI GI	g3668089
BLAST score	481
E value	8.0e-48
Match length	301
% identity	42
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	192629
Contig ID	7026_2.R1039
5'-most EST	LIB3166-037-P1-K1-E2

Seq. No.	192630
Contig ID	7031_1.R1039
5'-most EST	LIB3083-060-Q1-L1-A11
Method	BLASTX
NCBI GI	g1871185

BLAST score	880
E value	6.0e-95
Match length	199
% identity	79
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	192631
Contig ID	7031_2.R1039
5'-most EST	g5047914
Method	BLASTX
NCBI GI	g3264611
BLAST score	377
E value	5.0e-36
Match length	82
% identity	84
NCBI Description	(AF061511) seven in absentia homolog [Zea mays]

Seq. No.	192632
Contig ID	7036_1.R1039
5'-most EST	g5049144
Method	BLASTX
NCBI GI	g2160182
BLAST score	167
E value	3.0e-11
Match length	59
% identity	51
NCBI Description	(AC000132) ESTs gb|ATTS1236,gb|T43334,gb|N97019,gb|AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	192633
Contig ID	7042_1.R1039
5'-most EST	LIB3165-031-P1-K1-H3
Method	BLASTX
NCBI GI	g1620898
BLAST score	954
E value	1.0e-103
Match length	261
% identity	71
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	192634
Contig ID	7043_1.R1039
5'-most EST	LIB3146-025-Q1-K2-E1
Method	BLASTX
NCBI GI	g2832628
BLAST score	596
E value	2.0e-61
Match length	289
% identity	47
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	192635
Contig ID	7046_1.R1039
5'-most EST	LIB3083-060-Q1-L1-B9
Method	BLASTX
NCBI GI	g1170767

BLAST score	247
E value	5.0e-21
Match length	83
% identity	60
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi|626074|pir||S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi|406051 (U02280) Let1 [Schizosaccharomyces pombe] >gi|4106689|emb|CAA22628| (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No.	192636
Contig ID	7051_1.R1039
5'-most EST	LIB3272-033-P1-K1-G7
Method	BLASTX
NCBI GI	g3834310
BLAST score	712
E value	3.0e-75
Match length	154
% identity	95
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb|D83004 from Homo sapiens. ESTs gb|T88233, gb|Z24464, gb|N37265, gb|H36151, gb|Z34711, gb|AA040983, and gb|T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	192637
Contig ID	7051_2.R1039
5'-most EST	LIB3083-060-Q1-L1-C3
Method	BLASTX
NCBI GI	g1717864
BLAST score	328
E value	3.0e-54
Match length	147
% identity	64
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|2131382|pir||S58092 hypothetical protein YDR092w - yeast (Saccharomyces cerevisiae) >gi|914876|emb|CAA90451| (Z50111) unknown [Saccharomyces cerevisiae] >gi|1480355|emb|CAA67806| (X99443) ubiquitin-conjugating enzyme [Saccharomyces cerevisiae]

Seq. No.	192638
Contig ID	7057_1.R1039
5'-most EST	g5046618
Method	BLASTX
NCBI GI	g3252856
BLAST score	2105
E value	0.0e+00
Match length	446
% identity	89
NCBI Description	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana tabacum]

Seq. No.	192639
Contig ID	7059_1.R1039
5'-most EST	LIB3083-060-Q1-L1-D10

Method	BLASTX
NCBI GI	g1143511
BLAST score	855
E value	4.0e-92
Match length	162
% identity	95
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi|1586034|prf||2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No.	192640
Contig ID	7065_1.R1039
5'-most EST	g5048436

Seq. No.	192641
Contig ID	7073_1.R1039
5'-most EST	g5049795
Method	BLASTX
NCBI GI	g3721864
BLAST score	363
E value	3.0e-34
Match length	212
% identity	40
NCBI Description	(AB016068) Hs Ste24p [Homo sapiens]

Seq. No.	192642
Contig ID	7078_1.R1039
5'-most EST	g5046155
Method	BLASTX
NCBI GI	g3860247
BLAST score	1911
E value	0.0e+00
Match length	385
% identity	91
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	192643
Contig ID	7078_2.R1039
5'-most EST	uC-gsronu33B015g10b1
Method	BLASTX
NCBI GI	g3860247
BLAST score	707
E value	3.0e-76
Match length	159
% identity	87
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	192644
Contig ID	7078_4.R1039
5'-most EST	LIB3148-011-Q1-K1-C7

Seq. No.	192645
Contig ID	7081_1.R1039
5'-most EST	LIB3083-083-Q1-L1-A10
Method	BLASTX
NCBI GI	g1171978
BLAST score	1566

E value	1.0e-175
Match length	501
% identity	31
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi|304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi|2911051|emb|CAA17561| (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	192646
Contig ID	7081_2.R1039
5'-most EST	uC-gsronu33B145b11b1
Method	BLASTX
NCBI GI	g1737492
BLAST score	454
E value	9.0e-45
Match length	181
% identity	58
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	192647
Contig ID	7088_1.R1039
5'-most EST	uC-gsronu33B001g02b1
Method	BLASTX
NCBI GI	g2760317
BLAST score	563
E value	4.0e-58
Match length	138
% identity	81
NCBI Description	(AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No.	192648
Contig ID	7092_1.R1039
5'-most EST	uC-gsronu33B015h05b1
Method	BLASTX
NCBI GI	g3395440
BLAST score	288
E value	1.0e-25
Match length	129
% identity	40
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192649
Contig ID	7093_1.R1039
5'-most EST	LIB3083-060-Q1-L1-G6
Method	BLASTX
NCBI GI	g1420936
BLAST score	418
E value	5.0e-41
Match length	145
% identity	60
NCBI Description	(U61396) Vigna unguiculata aspartic proteinase mRNA, complete cds. [Vigna unguiculata]

Seq. No.	192650
Contig ID	7105_1.R1039
5'-most EST	LIB3197-013-P1-M1-B3
Method	BLASTX

NCBI GI g2384671
BLAST score 711
E value 4.0e-75
Match length 180
% identity 79
NCBI Description (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No. 192651
Contig ID 7118_1.R1039
5'-most EST LIB3083-061-Q1-L1-D12
Method BLASTX
NCBI GI g4454033
BLAST score 584
E value 2.0e-60
Match length 177
% identity 56
NCBI Description (AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No. 192652
Contig ID 7119_1.R1039
5'-most EST g5049823
Method BLASTX
NCBI GI g1107526
BLAST score 151
E value 1.0e-09
Match length 84
% identity 44
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 192653
Contig ID 7126_1.R1039
5'-most EST LIB3083-061-Q1-L1-F12

Seq. No. 192654
Contig ID 7129_1.R1039
5'-most EST LIB3083-061-Q1-L1-G12
Method BLASTX
NCBI GI g2281102
BLAST score 368
E value 6.0e-35
Match length 241
% identity 44
NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No. 192655
Contig ID 7133_1.R1039
5'-most EST g5050294
Method BLASTX
NCBI GI g2959370
BLAST score 284
E value 4.0e-25
Match length 139
% identity 37
NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	192656
Contig ID	7133_2.R1039
5'-most EST	LIB3197-054-Q1-M1-C6
Method	BLASTX
NCBI GI	g2959370
BLAST score	178
E value	9.0e-13
Match length	88
% identity	39
NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	192657
Contig ID	7134_1.R1039
5'-most EST	uC-gsflmaxxa049e03b1

Seq. No.	192658
Contig ID	7146_1.R1039
5'-most EST	LIB3083-062-Q1-L1-D9
Method	BLASTX
NCBI GI	g1181589
BLAST score	348
E value	6.0e-33
Match length	83
% identity	75
NCBI Description	(D83070) high mobility group protein [Canavalia gladiata] >gi|1483173|dbj|BAA13133| (D86594) high mobility group protein [Canavalia gladiata]

Seq. No.	192659
Contig ID	7147_1.R1039
5'-most EST	LIB3146-042-Q1-K1-D1
Method	BLASTX
NCBI GI	g2131352
BLAST score	212
E value	6.0e-17
Match length	120
% identity	38
NCBI Description	hypothetical protein YDL166c - yeast (Saccharomyces cerevisiae) >gi|1061273|emb|CAA91580| (Z67750) putative protein [Saccharomyces cerevisiae] >gi|1431264|emb|CAA98740| (Z74214) ORF YDL166c [Saccharomyces cerevisiae]

Seq. No.	192660
Contig ID	7149_1.R1039
5'-most EST	LIB3083-062-Q1-L1-E12
Method	BLASTX
NCBI GI	g123534
BLAST score	373
E value	8.0e-40
Match length	132
% identity	67
NCBI Description	17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3) >gi|71493|pir||HHSY17 heat shock protein 17 - soybean >gi|18656|emb|CAA25578| (X01104) heat shock protein 6871 (aa 1-153) [Glycine max] >gi|224205|prf||1012218B protein 6871,heat shock [Glycine max]

Seq. No.	192661
Contig ID	7151_1.R1039
5'-most EST	LIB3083-062-Q1-L1-F10
Method	BLASTX
NCBI GI	g2252863
BLAST score	690
E value	8.0e-73
Match length	186
% identity	72
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	192662
Contig ID	7152_1.R1039
5'-most EST	LIB3166-045-P1-K1-E3
Method	BLASTX
NCBI GI	g1815759
BLAST score	290
E value	1.0e-25
Match length	161
% identity	39
NCBI Description	(U85499) pollen-specific protein [Phalaris coerulescens]

Seq. No.	192663
Contig ID	7154_1.R1039
5'-most EST	LIB3149-020-Q1-K1-G10
Method	BLASTX
NCBI GI	g4455365
BLAST score	373
E value	2.0e-35
Match length	76
% identity	84
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	192664
Contig ID	7155_1.R1039
5'-most EST	LIB3197-041-Q1-M1-C10
Method	BLASTX
NCBI GI	g2058456
BLAST score	1277
E value	1.0e-141
Match length	272
% identity	91
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi|2345150|gb|AAB67830| (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	192665
Contig ID	7158_1.R1039
5'-most EST	LIB3166-045-P1-K1-H9
Method	BLASTX
NCBI GI	g3913518
BLAST score	377
E value	3.0e-36
Match length	121
% identity	67

NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi|1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]
Seq. No.	192666
Contig ID	7160_1.R1039
5'-most EST	LIB3120-054-P1-K1-B7
Method	BLASTN
NCBI GI	g2264314
BLAST score	34
E value	2.0e-09
Match length	134
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.	192667
Contig ID	7160_2.R1039
5'-most EST	uC-gsf1nu33B070f02b1
Seq. No.	192668
Contig ID	7160_3.R1039
5'-most EST	uC-gsronu33B041f04b1
Seq. No.	192669
Contig ID	7162_1.R1039
5'-most EST	LIB3189-017-P1-K1-E6
Seq. No.	192670
Contig ID	7165_1.R1039
5'-most EST	LIB3145-041-Q1-K1-H1
Method	BLASTX
NCBI GI	g425194
BLAST score	780
E value	2.0e-83
Match length	155
% identity	97
NCBI Description	(L26243) heat shock protein [Spinacia oleracea] >gi|2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.	192671
Contig ID	7170_1.R1039
5'-most EST	uC-gsronu33B124f11b1
Method	BLASTX
NCBI GI	g4371290
BLAST score	831
E value	6.0e-89
Match length	237
% identity	63
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]
Seq. No.	192672
Contig ID	7172_1.R1039
5'-most EST	LIB3272-046-P1-K1-H11
Method	BLASTX

NCBI GI	g3935152
BLAST score	747
E value	2.0e-79
Match length	198
% identity	72
NCBI Description	(AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No.	192673
Contig ID	7174_1.R1039
5'-most EST	LIB3147-015-Q1-K1-B5
Method	BLASTX
NCBI GI	g3885515
BLAST score	396
E value	3.0e-38
Match length	93
% identity	81
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	192674
Contig ID	7174_2.R1039
5'-most EST	LIB3146-051-Q1-K1-D1
Method	BLASTN
NCBI GI	g3885514
BLAST score	122
E value	7.0e-62
Match length	326
% identity	84
NCBI Description	Medicago sativa clone MS56 unknown mRNA

Seq. No.	192675
Contig ID	7174_3.R1039
5'-most EST	LIB3083-063-Q1-L1-B10
Method	BLASTX
NCBI GI	g3885515
BLAST score	420
E value	4.0e-41
Match length	96
% identity	82
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	192676
Contig ID	7174_5.R1039
5'-most EST	LIB3120-010-Q1-K1-F5
Method	BLASTX
NCBI GI	g3885515
BLAST score	388
E value	1.0e-37
Match length	89
% identity	83
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	192677
Contig ID	7175_1.R1039
5'-most EST	LIB3166-058-P1-K1-F11

Method	BLASTX
NCBI GI	g2576411
BLAST score	171
E value	1.0e-23
Match length	77
% identity	83
NCBI Description	(AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No.	192678
Contig ID	7176_1.R1039
5'-most EST	uC-gsronu33B012a01b1
Method	BLASTX
NCBI GI	g4160280
BLAST score	792
E value	9.0e-85
Match length	170
% identity	81
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	192679
Contig ID	7177_1.R1039
5'-most EST	LIB3135-018-Q1-K1-B5
Method	BLASTX
NCBI GI	g3892051
BLAST score	487
E value	6.0e-49
Match length	110
% identity	81
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	192680
Contig ID	7179_1.R1039
5'-most EST	LIB3272-028-P1-K1-H1
Method	BLASTX
NCBI GI	g2909583
BLAST score	346
E value	2.0e-32
Match length	141
% identity	51
NCBI Description	(AL021926) oxcA [Mycobacterium tuberculosis]

Seq. No.	192681
Contig ID	7196_1.R1039
5'-most EST	LIB3166-006-P1-K1-A5
Method	BLASTN
NCBI GI	g2264306
BLAST score	37
E value	6.0e-11
Match length	161
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	192682
Contig ID	7197_1.R1039

5'-most EST	LIB3083-063-Q1-L1-D1
Method	BLASTX
NCBI GI	g3953478
BLAST score	373
E value	1.0e-35
Match length	187
% identity	47
NCBI Description	(AC002328) F22O2.23 [Arabidopsis thaliana]

Seq. No.	192683
Contig ID	7209_1.R1039
5'-most EST	LIB3083-063-Q1-L1-E10
Method	BLASTX
NCBI GI	g3335335
BLAST score	230
E value	4.0e-37
Match length	161
% identity	59
NCBI Description	(AC004512) ESTs gb|F14113 and gb|T42122 come from this region. [Arabidopsis thaliana]

Seq. No.	192684
Contig ID	7212_1.R1039
5'-most EST	g5045701
Method	BLASTX
NCBI GI	g544358
BLAST score	313
E value	2.0e-31
Match length	216
% identity	42
NCBI Description	FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (FVT-1) >gi|481027|pir||S37652 FVT1 protein - human >gi|296186|emb|CAA45197| (X63657) FVT1 gene is disrupted in a t(2;18) chromosomal translocation involving Ig kappa gene in a follicular lymphoma [Homo sapiens] >gi|4503817|ref|NP_002026.1|pFVT1| follicular lymphoma variant translocation

Seq. No.	192685
Contig ID	7215_1.R1039
5'-most EST	g5046143
Method	BLASTX
NCBI GI	g3142289
BLAST score	1410
E value	1.0e-157
Match length	357
% identity	76
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb|U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	192686
Contig ID	7222_1.R1039
5'-most EST	uC-gsronu33B139h09b1
Method	BLASTX
NCBI GI	g4454464
BLAST score	520
E value	1.0e-105

Match length 293
% identity 66
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 192687
Contig ID 7223_1.R1039
5'-most EST uC-gsflmaxxa090c01b1
Method BLASTX
NCBI GI g3249084
BLAST score 342
E value 3.0e-32
Match length 124
% identity 20
NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene gb|X92750 from Mus musculus. ESTs gb|AA712687 and gb|Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 192688
Contig ID 7226_1.R1039
5'-most EST LIB3083-063-Q1-L1-F7
Method BLASTX
NCBI GI g3646451
BLAST score 254
E value 1.0e-21
Match length 110
% identity 49
NCBI Description (AL031603) mRNA cap methyltransferase [Schizosaccharomyces pombe]

Seq. No. 192689
Contig ID 7227_1.R1039
5'-most EST g5045828
Method BLASTX
NCBI GI g4206787
BLAST score 193
E value 2.0e-14
Match length 130
% identity 37
NCBI Description (AF112863) syntaxin-related protein Nt-syr1 [Nicotiana tabacum]

Seq. No. 192690
Contig ID 7228_1.R1039
5'-most EST uC-gsflnu33B128a08b1
Method BLASTX
NCBI GI g2500345
BLAST score 443
E value 1.0e-43
Match length 128
% identity 70
NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)
>gi|2618578|dbj|BAA23363| (D50420) OTK27 [Homo sapiens]
>gi|3859990 (AF091076) OTK27 [Homo sapiens]
>gi|1589072|prf||2210268A nuclear protein-NHP2-like protein [Homo sapiens]

Seq. No.	192691
Contig ID	7229_1.R1039
5'-most EST	LIB3083-063-Q1-L1-G1

Seq. No.	192692
Contig ID	7230_1.R1039
5'-most EST	LIB3083-063-Q1-L1-G10
Method	BLASTX
NCBI GI	g121631
BLAST score	285
E value	1.0e-25
Match length	73
% identity	73
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi|72323|pir||KNNT2S glycine-rich protein 2 - wood tobacco >gi|19743|emb|CAA42622| (X60007) nsGRP-2 [Nicotiana sylvestris]

Seq. No.	192693
Contig ID	7236_1.R1039
5'-most EST	LIB3189-050-P1-K1-B4
Method	BLASTX
NCBI GI	g2244994
BLAST score	715
E value	3.0e-93
Match length	215
% identity	73
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	192694
Contig ID	7237_1.R1039
5'-most EST	uC-gsronu33B104f07b1

Seq. No.	192695
Contig ID	7239_1.R1039
5'-most EST	LIB3146-008-Q1-K1-D6
Method	BLASTX
NCBI GI	g2497702
BLAST score	201
E value	1.0e-15
Match length	134
% identity	37
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi|2121019|pir||I40710 outer membrane lipoprotein - Citrobacter freundii >gi|717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	192696
Contig ID	7245_1.R1039
5'-most EST	LIB3083-063-Q1-L1-H5
Method	BLASTX
NCBI GI	g4522012
BLAST score	273
E value	5.0e-24
Match length	102
% identity	57

NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192697
Contig ID	7248_1.R1039
5'-most EST	LIB3083-063-Q1-L1-H8
Method	BLASTX
NCBI GI	g114181
BLAST score	295
E value	7.0e-27
Match length	108
% identity	56
NCBI Description	3-DEHYDROQUINATE SYNTHASE >gi|68385|pir||SYECQ 3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli >gi|40968|emb|CAA27495| (X03867) 3-dehydroquinate synthase (aa 1-362) [Escherichia coli] >gi|41225|emb|CAA79666| (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia coli] >gi|606323 (U18997) 3-dehydroquinate synthase [Escherichia coli] >gi|1789791 (AE000414) 3-dehydroquinate synthase [Escherichia coli]

Seq. No.	192698
Contig ID	7249_1.R1039
5'-most EST	LIB3083-063-Q1-L1-H9

Seq. No.	192699
Contig ID	7250_1.R1039
5'-most EST	LIB3083-064-Q1-L1-A1

Seq. No.	192700
Contig ID	7250_3.R1039
5'-most EST	g5046904
Method	BLASTX
NCBI GI	g4455301
BLAST score	805
E value	3.0e-86
Match length	189
% identity	82
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	192701
Contig ID	7251_1.R1039
5'-most EST	LIB3083-103-Q1-L1-A11
Method	BLASTX
NCBI GI	g2154715
BLAST score	1173
E value	1.0e-129
Match length	253
% identity	89
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	192702
Contig ID	7252_1.R1039
5'-most EST	LIB3083-064-Q1-L1-A11
Method	BLASTX
NCBI GI	g3202038
BLAST score	647
E value	1.0e-67

Match length	208
% identity	58
NCBI Description	(AF069322) permease 1 [Mesembryanthemum crystallinum]
Seq. No.	192703
Contig ID	7254_1.R1039
5'-most EST	LIB3146-048-Q1-K1-D9
Seq. No.	192704
Contig ID	7258_1.R1039
5'-most EST	LIB3189-040-P1-K1-E10
Seq. No.	192705
Contig ID	7260_1.R1039
5'-most EST	uC-gsflmaxxa106a08b1
Method	BLASTX
NCBI GI	g3122673
BLAST score	791
E value	2.0e-84
Match length	204
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi|2245027|emb|CAB10447| (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	192706
Contig ID	7260_2.R1039
5'-most EST	uC-gsflnu33B056b10b1
Method	BLASTX
NCBI GI	g2996172
BLAST score	527
E value	1.0e-53
Match length	106
% identity	90
NCBI Description	(AF051760) putative 60S ribosomal protein L15 [Picea mariana]
Seq. No.	192707
Contig ID	7261_1.R1039
5'-most EST	LIB3083-064-Q1-L1-B4
Seq. No.	192708
Contig ID	7263_1.R1039
5'-most EST	LIB3189-008-P1-K1-H1
Method	BLASTX
NCBI GI	g4539417
BLAST score	557
E value	4.0e-57
Match length	122
% identity	82
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]
Seq. No.	192709
Contig ID	7267_2.R1039
5'-most EST	LIB3083-064-Q1-L1-C1
Method	BLASTX
NCBI GI	g2739387
BLAST score	282

E value	5.0e-25
Match length	162
% identity	38
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192710
Contig ID	7267_3.R1039
5'-most EST	LIB3166-051-P1-K1-G6
Method	BLASTX
NCBI GI	g2739387
BLAST score	152
E value	1.0e-09
Match length	101
% identity	43
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192711
Contig ID	7270_1.R1039
5'-most EST	LIB3083-064-Q1-L1-C2
Method	BLASTX
NCBI GI	g2673912
BLAST score	548
E value	7.0e-56
Match length	154
% identity	66
NCBI Description	(AC002561) unknown protein [Arabidopsis thaliana]

Seq. No.	192712
Contig ID	7276_1.R1039
5'-most EST	LIB3145-043-Q1-K1-G10

Seq. No.	192713
Contig ID	7277_1.R1039
5'-most EST	LIB3145-025-Q1-K1-D1
Method	BLASTX
NCBI GI	g1352440
BLAST score	417
E value	6.0e-41
Match length	89
% identity	78
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT) (EIF-4F P26 SUBUNIT) >gi|1002915 (U34597) p26 [Oryza sativa]

Seq. No.	192714
Contig ID	7281_1.R1039
5'-most EST	LIB3189-035-P1-K1-F2

Seq. No.	192715
Contig ID	7293_1.R1039
5'-most EST	LIB3148-036-Q1-K1-G11
Method	BLASTX
NCBI GI	g2129552
BLAST score	503
E value	6.0e-51
Match length	118

% identity	53
NCBI Description	calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)

Seq. No.	192716
Contig ID	7297_1.R1039
5'-most EST	g5045524
Method	BLASTX
NCBI GI	g1771162
BLAST score	1674
E value	0.0e+00
Match length	426
% identity	75
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi|3687307|emb|CAA07000| (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	192717
Contig ID	7303_1.R1039
5'-most EST	uC-gsflnu33B092c03b1
Method	BLASTX
NCBI GI	g4539002
BLAST score	317
E value	3.0e-29
Match length	143
% identity	50
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	192718
Contig ID	7304_1.R1039
5'-most EST	LIB3083-064-Q1-L1-F5
Method	BLASTX
NCBI GI	g3386597
BLAST score	275
E value	4.0e-24
Match length	71
% identity	68
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi|3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No.	192719
Contig ID	7307_1.R1039
5'-most EST	g5044407
Method	BLASTX
NCBI GI	g4510373
BLAST score	644
E value	3.0e-67
Match length	209
% identity	60
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	192720
Contig ID	7309_1.R1039
5'-most EST	LIB3083-064-Q1-L1-G10
Method	BLASTX

NCBI GI	g3885334
BLAST score	1025
E value	1.0e-112
Match length	264
% identity	72
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	192721
Contig ID	7312_1.R1039
5'-most EST	LIB3166-015-P1-K1-A2
Method	BLASTX
NCBI GI	g3885334
BLAST score	518
E value	9.0e-53
Match length	149
% identity	71
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	192722
Contig ID	7312_2.R1039
5'-most EST	LIB3166-016-P1-K1-E1
Method	BLASTN
NCBI GI	g3885325
BLAST score	38
E value	1.0e-11
Match length	70
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	192723
Contig ID	7314_1.R1039
5'-most EST	LIB3083-064-Q1-L1-G5

Seq. No.	192724
Contig ID	7315_1.R1039
5'-most EST	uC-gsflmaxxa097e11b1

Seq. No.	192725
Contig ID	7316_1.R1039
5'-most EST	LIB3149-033-Q1-K1-F1
Method	BLASTX
NCBI GI	g3878134
BLAST score	219
E value	9.0e-18
Match length	75
% identity	49
NCBI Description	(Z68218) K01H12.1 [Caenorhabditis elegans]

Seq. No.	192726
Contig ID	7323_1.R1039
5'-most EST	g5044971
Method	BLASTX
NCBI GI	g4539452
BLAST score	299

E value	5.0e-27
Match length	69
% identity	77
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	192727
Contig ID	7338_1.R1039
5'-most EST	LIB3083-065-Q1-L1-B1
Method	BLASTX
NCBI GI	g4140398
BLAST score	288
E value	8.0e-26
Match length	87
% identity	62
NCBI Description	(AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]

Seq. No.	192728
Contig ID	7339_1.R1039
5'-most EST	g5046648
Method	BLASTX
NCBI GI	g4580471
BLAST score	957
E value	1.0e-104
Match length	274
% identity	66
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	192729
Contig ID	7340_1.R1039
5'-most EST	g3325826

Seq. No.	192730
Contig ID	7343_1.R1039
5'-most EST	LIB3083-065-Q1-L1-B3
Method	BLASTX
NCBI GI	g3142294
BLAST score	1884
E value	0.0e+00
Match length	422
% identity	87
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb|U37354 from S. pombe. ESTs gb|T41979, gb|N37284 and gb|N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	192731
Contig ID	7345_1.R1039
5'-most EST	LIB3135-013-Q1-K1-B11
Method	BLASTX
NCBI GI	g586076
BLAST score	2118
E value	0.0e+00
Match length	420
% identity	95
NCBI Description	TUBULIN BETA-1 CHAIN >gi|486734|pir||S35142 tubulin beta chain - white lupine >gi|402636|emb|CAA49736| (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	192732
Contig ID	7345_2.R1039
5'-most EST	LIB3145-041-Q1-K1-E1

Seq. No.	192733
Contig ID	7345_3.R1039
5'-most EST	LIB3165-052-Q1-K1-H2
Method	BLASTX
NCBI GI	g267082
BLAST score	634
E value	2.0e-66
Match length	122
% identity	95
NCBI Description	TUBULIN BETA-8 CHAIN >gi|320189|pir||JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi|166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	192734
Contig ID	7345_5.R1039
5'-most EST	LIB3148-002-P1-K1-E2
Method	BLASTX
NCBI GI	g1345933
BLAST score	580
E value	1.0e-59
Match length	135
% identity	81
NCBI Description	CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS) >gi|1084323|pir||S53007 citrate synthase - cucurbit >gi|975633|dbj|BAA07328| (D38132) glyoxysomal citrate synthase [Cucurbita sp.]

Seq. No.	192735
Contig ID	7345_10.R1039
5'-most EST	uC-gsronu33B036b11b1
Method	BLASTX
NCBI GI	g135495
BLAST score	187
E value	7.0e-14
Match length	35
% identity	97
NCBI Description	TUBULIN BETA CHAIN >gi|101012|pir||A21649 tubulin beta chain - fission yeast (Schizosaccharomyces pombe) >gi|173523 (M10347) beta-tubulin [Schizosaccharomyces pombe]

Seq. No.	192736
Contig ID	7345_11.R1039
5'-most EST	LIB3147-022-Q1-K1-C3
Method	BLASTX
NCBI GI	g267073
BLAST score	433
E value	1.0e-42
Match length	83
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi|320184|pir||JQ1587 tubulin beta chain - Arabidopsis thaliana >gi|166898 (M84700)

beta-2 tubulin [Arabidopsis thaliana] >gi|166900 (M84701)
beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	192737
Contig ID	7345_12.R1039
5'-most EST	LIB3197-026-Q1-M1-A2
Method	BLASTX
NCBI GI	g267073
BLAST score	561
E value	7.0e-58
Match length	107
% identity	94
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi|320184|pir||JQ1587 tubulin beta chain - Arabidopsis thaliana >gi|166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi|166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	192738
Contig ID	7349_1.R1039
5'-most EST	LIB3083-065-Q1-L1-B9

Seq. No.	192739
Contig ID	7350_1.R1039
5'-most EST	g5048503
Method	BLASTX
NCBI GI	g3250695
BLAST score	194
E value	5.0e-15
Match length	125
% identity	58
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	192740
Contig ID	7352_1.R1039
5'-most EST	LIB3083-065-Q1-L1-C11

Seq. No.	192741
Contig ID	7355_1.R1039
5'-most EST	g5044942
Method	BLASTX
NCBI GI	g4314378
BLAST score	202
E value	2.0e-15
Match length	101
% identity	40
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	192742
Contig ID	7359_1.R1039
5'-most EST	LIB3189-051-P1-K1-D10
Method	BLASTX
NCBI GI	g2879811
BLAST score	542
E value	2.0e-55
Match length	111
% identity	93
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	192743
Contig ID	7359_2.R1039
5'-most EST	uC-gsflnu33B090b04b1
Method	BLASTX
NCBI GI	g2879811
BLAST score	502
E value	9.0e-51
Match length	101
% identity	94
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	192744
Contig ID	7359_3.R1039
5'-most EST	LIB3147-044-Q1-K1-C5
Method	BLASTX
NCBI GI	g2879811
BLAST score	546
E value	5.0e-56
Match length	111
% identity	94
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	192745
Contig ID	7366_1.R1039
5'-most EST	uC-gsflnu33B001c11b1

Seq. No.	192746
Contig ID	7367_1.R1039
5'-most EST	LIB3146-046-Q1-K1-D9
Method	BLASTX
NCBI GI	g3212871
BLAST score	709
E value	7.0e-75
Match length	153
% identity	84
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	192747
Contig ID	7368_1.R1039
5'-most EST	LIB3083-109-Q1-L1-B3
Method	BLASTX
NCBI GI	g2342719
BLAST score	435
E value	1.0e-42
Match length	197
% identity	49
NCBI Description	(AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No.	192748
Contig ID	7372_1.R1039
5'-most EST	LIB3083-065-Q1-L1-E10

Seq. No.	192749
Contig ID	7375_1.R1039
5'-most EST	LIB3147-011-Q1-K1-H6

Method	BLASTX
NCBI GI	g4508079
BLAST score	434
E value	8.0e-43
Match length	98
% identity	79
NCBI Description	(AC005882) 66284 [Arabidopsis thaliana]

Seq. No.	192750
Contig ID	7377_1.R1039
5'-most EST	LIB3083-065-Q1-L1-E4
Method	BLASTX
NCBI GI	g2146739
BLAST score	628
E value	1.0e-65
Match length	152
% identity	79
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi|881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	192751
Contig ID	7380_1.R1039
5'-most EST	uC-gsflnu33B129h06b1

Seq. No.	192752
Contig ID	7388_1.R1039
5'-most EST	LIB3083-065-Q1-L1-F3
Method	BLASTN
NCBI GI	g3510343
BLAST score	40
E value	8.0e-13
Match length	321
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	192753
Contig ID	7393_1.R1039
5'-most EST	LIB3083-073-Q1-L1-E12
Method	BLASTX
NCBI GI	g2827699
BLAST score	149
E value	3.0e-09
Match length	193
% identity	30
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	192754
Contig ID	7399_1.R1039
5'-most EST	g5049621
Method	BLASTX
NCBI GI	g2811025
BLAST score	1700
E value	0.0e+00
Match length	395
% identity	78
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi|1944181|dbj|BAA19607|

(AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	192755
Contig ID	7399_2.R1039
5'-most EST	LIB3147-052-Q1-K1-D11
Method	BLASTX
NCBI GI	g2499819
BLAST score	262
E value	1.0e-22
Match length	56
% identity	84
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi|2130068|pir||S66516 aspartic proteinase 1 precursor - rice >gi|1030715|dbj|BAA06876| (D32165) aspartic protease [Oryza sativa] >gi|1711289|dbj|BAA06875| (D32144) aspartic protease [Oryza sativa]

Seq. No.	192756
Contig ID	7402_1.R1039
5'-most EST	uC-gsflmaxxa058d11b1

Seq. No.	192757
Contig ID	7413_1.R1039
5'-most EST	LIB3083-065-Q1-L1-H5
Method	BLASTX
NCBI GI	g3559805
BLAST score	1120
E value	1.0e-123
Match length	299
% identity	65
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	192758
Contig ID	7414_1.R1039
5'-most EST	LIB3189-050-P1-K1-F2

Seq. No.	192759
Contig ID	7418_1.R1039
5'-most EST	uC-gsflmaxxa095b02b1
Method	BLASTX
NCBI GI	g82263
BLAST score	1185
E value	1.0e-130
Match length	271
% identity	83
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	192760
Contig ID	7423_1.R1039
5'-most EST	uC-gsronu33B160g06b1
Method	BLASTX
NCBI GI	g4115918
BLAST score	482
E value	4.0e-48
Match length	132

% identity	74
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	192761
Contig ID	7424_1.R1039
5'-most EST	LIB3083-071-Q1-L1-A6

Seq. No.	192762
Contig ID	7436_1.R1039
5'-most EST	LIB3197-015-P1-M1-A8

Seq. No.	192763
Contig ID	7436_2.R1039
5'-most EST	LIB3272-006-P1-K1-E7

Seq. No.	192764
Contig ID	7441_1.R1039
5'-most EST	LIB3083-066-Q1-L1-B9
Method	BLASTN
NCBI GI	g18045
BLAST score	99
E value	5.0e-48
Match length	327
% identity	83
NCBI Description	C.lanceolata mRNA for beta-ketoacyl-ACP reductase

Seq. No.	192765
Contig ID	7442_1.R1039
5'-most EST	LIB3189-033-P1-K1-G9
Method	BLASTX
NCBI GI	g2160175
BLAST score	944
E value	1.0e-102
Match length	411
% identity	47
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb|U17135). [Arabidopsis thaliana]

Seq. No.	192766
Contig ID	7445_1.R1039
5'-most EST	LIB3083-066-Q1-L1-C2

Seq. No.	192767
Contig ID	7450_1.R1039
5'-most EST	LIB3197-048-Q1-M1-C11
Method	BLASTX
NCBI GI	g2384671
BLAST score	260
E value	1.0e-24
Match length	114
% identity	62
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	192768
Contig ID	7450_2.R1039

5'-most EST	LIB3145-024-Q1-K1-F11
Method	BLASTX
NCBI GI	g2384671
BLAST score	550
E value	2.0e-56
Match length	194
% identity	61
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	192769
Contig ID	7454_1.R1039
5'-most EST	LIB3083-066-Q1-L1-D10

Seq. No.	192770
Contig ID	7456_1.R1039
5'-most EST	uC-gsronu33B057e06b1

Seq. No.	192771
Contig ID	7458_1.R1039
5'-most EST	LIB3083-066-Q1-L1-D3

Seq. No.	192772
Contig ID	7462_1.R1039
5'-most EST	g5050758
Method	BLASTX
NCBI GI	g4539301
BLAST score	420
E value	7.0e-41
Match length	170
% identity	48
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	192773
Contig ID	7466_1.R1039
5'-most EST	g5046420
Method	BLASTX
NCBI GI	g4006858
BLAST score	661
E value	3.0e-69
Match length	197
% identity	60
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	192774
Contig ID	7474_1.R1039
5'-most EST	LIB3197-055-Q1-M1-D10

Seq. No.	192775
Contig ID	7476_1.R1039
5'-most EST	LIB3120-060-Q1-K1-G9

Seq. No.	192776
Contig ID	7478_1.R1039
5'-most EST	LIB3083-066-Q1-L1-F12

Method	BLASTX
NCBI GI	g3287688
BLAST score	588
E value	8.0e-61
Match length	144
% identity	81
NCBI Description	(AC003979) Contains similarity to ycf37 gene product gb|1001425 from Synechocystis sp. genome gb|D63999. ESTs gb|T43026, gb|R64902, gb|Z18169 and gb|N37374 come from this gene. [Arabidopsis thaliana]

Seq. No.	192777
Contig ID	7484_1.R1039
5'-most EST	LIB3083-066-Q1-L1-F7
Method	BLASTX
NCBI GI	g836950
BLAST score	157
E value	2.0e-10
Match length	158
% identity	12
NCBI Description	(U20810) CIP1 [Arabidopsis thaliana] >gi|1096881|prf||2112355A CIP1 protein [Arabidopsis thaliana]

Seq. No.	192778
Contig ID	7486_1.R1039
5'-most EST	LIB3197-054-Q1-M1-B6
Method	BLASTX
NCBI GI	g3914467
BLAST score	142
E value	1.0e-08
Match length	90
% identity	40
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi|1864003|dbj|BAA19252| (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	192779
Contig ID	7494_1.R1039
5'-most EST	LIB3165-047-Q1-K1-H2
Method	BLASTX
NCBI GI	g4186184
BLAST score	164
E value	5.0e-11
Match length	233
% identity	27
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	192780
Contig ID	7498_1.R1039
5'-most EST	LIB3272-030-P1-K1-E12
Method	BLASTX
NCBI GI	g3763925
BLAST score	404
E value	8.0e-48
Match length	111
% identity	87

NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]
Seq. No.	192781
Contig ID	7501_1.R1039
5'-most EST	g5045963
Method	BLASTX
NCBI GI	g2398807
BLAST score	553
E value	1.0e-56
Match length	166
% identity	64
NCBI Description	(Z99091) succinate dehydrogenase [Schizosaccharomyces pombe]
Seq. No.	192782
Contig ID	7506_1.R1039
5'-most EST	LIB3166-031-P1-K1-F1
Seq. No.	192783
Contig ID	7509_1.R1039
5'-most EST	LIB3083-066-Q1-L1-H8
Method	BLASTX
NCBI GI	g3080390
BLAST score	723
E value	1.0e-76
Match length	182
% identity	74
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]
Seq. No.	192784
Contig ID	7514_1.R1039
5'-most EST	uC-gsronu33b112b01b1
Method	BLASTX
NCBI GI	g475048
BLAST score	1067
E value	1.0e-116
Match length	247
% identity	83
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]
Seq. No.	192785
Contig ID	7516_1.R1039
5'-most EST	LIB3083-119-Q1-L1-B1
Method	BLASTN
NCBI GI	g871769
BLAST score	33
E value	5.0e-09
Match length	266
% identity	15
NCBI Description	V.unguiculata mRNA for glycin-rich protein
Seq. No.	192786
Contig ID	7521_1.R1039
5'-most EST	LIB3166-038-P1-K1-A6
Seq. No.	192787

Contig ID	7527_1.R1039
5'-most EST	LIB3189-012-P1-K1-E5

Seq. No.	192788
Contig ID	7534_1.R1039
5'-most EST	LIB3120-007-Q1-K1-C8
Method	BLASTX
NCBI GI	g3201613
BLAST score	820
E value	9.0e-88
Match length	214
% identity	70
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	192789
Contig ID	7534_2.R1039
5'-most EST	g5046549
Method	BLASTX
NCBI GI	g3201613
BLAST score	285
E value	1.0e-52
Match length	152
% identity	63
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	192790
Contig ID	7535_1.R1039
5'-most EST	g5049416
Method	BLASTX
NCBI GI	g3763926
BLAST score	239
E value	2.0e-23
Match length	98
% identity	62
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	192791
Contig ID	7542_1.R1039
5'-most EST	LIB3083-068-Q1-L1-E9
Method	BLASTX
NCBI GI	g4090884
BLAST score	242
E value	2.0e-20
Match length	72
% identity	68
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	192792
Contig ID	7547_1.R1039
5'-most EST	LIB3145-030-Q1-K1-A5
Method	BLASTX
NCBI GI	g4314390
BLAST score	179
E value	7.0e-13
Match length	91
% identity	45

NCBI Description	(AC006232) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	192793
Contig ID	7549_1.R1039
5'-most EST	LIB3083-068-Q1-L1-G12

Seq. No.	192794
Contig ID	7555_1.R1039
5'-most EST	LIB3083-070-Q1-L1-B10

Seq. No.	192795
Contig ID	7557_1.R1039
5'-most EST	LIB3083-070-Q1-L1-B12
Method	BLASTX
NCBI GI	g3860258
BLAST score	535
E value	2.0e-54
Match length	153
% identity	67
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	192796
Contig ID	7566_1.R1039
5'-most EST	LIB3083-070-Q1-L1-E10
Method	BLASTX
NCBI GI	g2392021
BLAST score	441
E value	9.0e-44
Match length	123
% identity	63
NCBI Description	(D63425) phopholipid hydroperoxide glutathione peroxidase-like protein [Spinacia oleracea]

Seq. No.	192797
Contig ID	7568_1.R1039
5'-most EST	uC-gsflnu33B057b07b1
Method	BLASTX
NCBI GI	g3618343
BLAST score	278
E value	2.0e-24
Match length	191
% identity	34
NCBI Description	(AB009398) 26S proteasome subunit p40.5 [Homo sapiens] >gi|4506223|ref|NP_002808.1|pPSMD13| proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No.	192798
Contig ID	7569_1.R1039
5'-most EST	g5050067
Method	BLASTX
NCBI GI	g1709761
BLAST score	1055
E value	1.0e-115
Match length	250
% identity	82
NCBI Description	PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX 27 KD SUBUNIT) >gi|1262146|emb|CAA65660| (X96974) proteasome subunit [Spinacia oleracea]

Seq. No.	192799
Contig ID	7575_1.R1039
5'-most EST	LIB3083-070-Q1-L1-G11

Seq. No.	192800
Contig ID	7577_1.R1039
5'-most EST	LIB3083-070-Q1-L1-G9
Method	BLASTX
NCBI GI	g1508783
BLAST score	250
E value	3.0e-21
Match length	123
% identity	47
NCBI Description	(Z54351) SecY [Spinacia oleracea]

Seq. No.	192801
Contig ID	7578_1.R1039
5'-most EST	LIB3165-021-P1-K1-A9

Seq. No.	192802
Contig ID	7580_1.R1039
5'-most EST	LIB3197-059-Q1-M1-A1
Method	BLASTX
NCBI GI	g3075394
BLAST score	894
E value	1.0e-107
Match length	256
% identity	73
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi|3559809|emb|CAA09311| (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	192803
Contig ID	7580_2.R1039
5'-most EST	LIB3083-070-Q1-L1-H12

Seq. No.	192804
Contig ID	7582_1.R1039
5'-most EST	LIB3189-036-P1-K1-A11
Method	BLASTX
NCBI GI	g1872521
BLAST score	246
E value	8.0e-21
Match length	99
% identity	32
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi|1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	192805
Contig ID	7586_1.R1039
5'-most EST	LIB3148-053-Q1-K1-G1
Method	BLASTX
NCBI GI	g2262158

BLAST score 310
E value 2.0e-28
Match length 125
% identity 56
NCBI Description (AC002329) putative mitochondrial phosphate translocator protein [Arabidopsis thaliana]

Seq. No. 192806
Contig ID 7591_1.R1039
5'-most EST LIB3083-071-Q1-L1-A9

Seq. No. 192807
Contig ID 7592_1.R1039
5'-most EST LIB3083-071-Q1-L1-B1

Seq. No. 192808
Contig ID 7592_2.R1039
5'-most EST LIB3148-051-Q1-K1-H12

Seq. No. 192809
Contig ID 7594_1.R1039
5'-most EST LIB3166-058-P1-K1-D7

Seq. No. 192810
Contig ID 7597_1.R1039
5'-most EST uC-gsflmaxxa096e09b1
Method BLASTX
NCBI GI g2828147
BLAST score 498
E value 3.0e-50
Match length 151
% identity 63
NCBI Description (AF042384) BC-2 protein [Homo sapiens]

Seq. No. 192811
Contig ID 7598_1.R1039
5'-most EST LIB3083-071-Q1-L1-B4
Method BLASTX
NCBI GI g2864609
BLAST score 129
E value 7.0e-10
Match length 59
% identity 61
NCBI Description (AL021811) putative protein [Arabidopsis thaliana] >gi|4049337|emb|CAA22562| (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 192812
Contig ID 7599_1.R1039
5'-most EST LIB3196-053-P1-M1-H8
Method BLASTX
NCBI GI g4512699
BLAST score 1517
E value 1.0e-169
Match length 390
% identity 75
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase

[Arabidopsis thaliana]

Seq. No.	192813
Contig ID	7602_1.R1039
5'-most EST	uC-gsflnu33B023c02b1
Method	BLASTX
NCBI GI	g3142331
BLAST score	166
E value	2.0e-11
Match length	131
% identity	34
NCBI Description	(U97327) calcyclin binding protein [Mus musculus]

Seq. No.	192814
Contig ID	7604_1.R1039
5'-most EST	uC-gsflnu33B050g05b1
Method	BLASTX
NCBI GI	g3080435
BLAST score	810
E value	6.0e-87
Match length	177
% identity	87
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	192815
Contig ID	7605_1.R1039
5'-most EST	g5046700
Method	BLASTX
NCBI GI	g1524370
BLAST score	557
E value	4.0e-57
Match length	153
% identity	70
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	192816
Contig ID	7607_1.R1039
5'-most EST	LIB3197-056-Q1-M1-F6
Method	BLASTX
NCBI GI	g2583133
BLAST score	158
E value	1.0e-10
Match length	106
% identity	35
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	192817
Contig ID	7611_1.R1039
5'-most EST	g5047880
Method	BLASTX
NCBI GI	g4234941
BLAST score	534
E value	2.0e-54
Match length	160
% identity	76
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	192818
Contig ID	7611_2.R1039
5'-most EST	g5044798
Method	BLASTX
NCBI GI	g2829893
BLAST score	596
E value	1.0e-61
Match length	146
% identity	79
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	192819
Contig ID	7612_1.R1039
5'-most EST	LIB3083-071-Q1-L1-C7
Method	BLASTX
NCBI GI	g1717975
BLAST score	355
E value	2.0e-33
Match length	123
% identity	52
NCBI Description	14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG) >gi|1177435|emb|CAA64670| (X95384) 14.5 kDa translational inhibitor protein, p14.5 [Homo sapiens]

Seq. No.	192820
Contig ID	7620_1.R1039
5'-most EST	uC-gsronu33B126c03b1

Seq. No.	192821
Contig ID	7621_1.R1039
5'-most EST	g5047507
Method	BLASTX
NCBI GI	g3790100
BLAST score	782
E value	2.0e-83
Match length	184
% identity	79
NCBI Description	(AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi]

Seq. No.	192822
Contig ID	7627_1.R1039
5'-most EST	g5048589
Method	BLASTX
NCBI GI	g4427003
BLAST score	700
E value	1.0e-73
Match length	247
% identity	56
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	192823
Contig ID	7628_1.R1039
5'-most EST	LIB3197-039-Q1-M1-B5
Method	BLASTX
NCBI GI	g3360289

BLAST score	612
E value	3.0e-63
Match length	217
% identity	56
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	192824
Contig ID	7634_1.R1039
5'-most EST	LIB3189-044-P1-K1-D10
Method	BLASTX
NCBI GI	g728938
BLAST score	1076
E value	1.0e-118
Match length	231
% identity	92
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi|322841|pir||JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi|285638|dbj|BAA02717| (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare]

Seq. No.	192825
Contig ID	7641_1.R1039
5'-most EST	LIB3148-037-Q1-K1-F11
Method	BLASTX
NCBI GI	g2961377
BLAST score	151
E value	7.0e-10
Match length	62
% identity	17
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	192826
Contig ID	7644_1.R1039
5'-most EST	LIB3083-071-Q1-L1-G3

Seq. No.	192827
Contig ID	7647_1.R1039
5'-most EST	LIB3120-036-Q1-K1-E3

Seq. No.	192828
Contig ID	7648_1.R1039
5'-most EST	LIB3083-114-Q1-L1-D1

Seq. No.	192829
Contig ID	7650_1.R1039
5'-most EST	g5049936
Method	BLASTX
NCBI GI	g3176668
BLAST score	728
E value	5.0e-77
Match length	168
% identity	85
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb|X62724 from Hordeum vulgare. ESTs gb|Z34728, gb|F19974, gb|T75677 and

gb|Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	192830
Contig ID	7650_2.R1039
5'-most EST	uC-gsronu33B087d08b1
Method	BLASTX
NCBI GI	g3176668
BLAST score	732
E value	2.0e-77
Match length	166
% identity	86
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb|X62724 from Hordeum vulgare. ESTs gb|Z34728, gb|F19974, gb|T75677 and gb|Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	192831
Contig ID	7652_1.R1039
5'-most EST	LIB3083-071-Q1-L1-H5
Method	BLASTX
NCBI GI	g2760084
BLAST score	686
E value	9.0e-78
Match length	236
% identity	18
NCBI Description	(Y16045) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	192832
Contig ID	7656_1.R1039
5'-most EST	LIB3196-057-P1-M1-C7
Method	BLASTX
NCBI GI	g2266994
BLAST score	323
E value	7.0e-30
Match length	164
% identity	7
NCBI Description	(U77413) O-linked GlcNAc transferase [Homo sapiens] >gi|4505499|ref|NP_003596.1|pOGT| O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase)

Seq. No.	192833
Contig ID	7657_1.R1039
5'-most EST	LIB3197-007-P1-M1-F6
Method	BLASTX
NCBI GI	g2760830
BLAST score	2022
E value	0.0e+00
Match length	497
% identity	75
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	192834
Contig ID	7661_1.R1039
5'-most EST	uC-gsronu33B149f05b1
Method	BLASTX
NCBI GI	g1351014

BLAST score	205
E value	3.0e-23
Match length	70
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi|968902|dbj|BAA07207| (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	192835
Contig ID	7662_1.R1039
5'-most EST	LIB3135-020-Q1-K1-E11
Method	BLASTN
NCBI GI	g19212
BLAST score	57
E value	5.0e-23
Match length	156
% identity	29
NCBI Description	Tomato extensin mRNA (clone w17-1)

Seq. No.	192836
Contig ID	7663_1.R1039
5'-most EST	LIB3083-072-Q1-L1-A7

Seq. No.	192837
Contig ID	7671_1.R1039
5'-most EST	LIB3165-028-P1-K1-E5
Method	BLASTX
NCBI GI	g2244806
BLAST score	439
E value	1.0e-43
Match length	94
% identity	81
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192838
Contig ID	7672_1.R1039
5'-most EST	LIB3083-072-Q1-L1-B6
Method	BLASTX
NCBI GI	g457517
BLAST score	241
E value	4.0e-20
Match length	120
% identity	42
NCBI Description	(L12579) alternatively spliced [Homo sapiens] >gi|4503169|ref|NP_001904.1|pCUTL1| cut (Drosophila)-like 1 (CCAAT displacement protein)

Seq. No.	192839
Contig ID	7675_1.R1039
5'-most EST	LIB3083-092-Q1-L1-F9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	192840
Contig ID	7678_1.R1039
5'-most EST	g2604018
Method	BLASTX
NCBI GI	g2435522
BLAST score	320
E value	2.0e-29
Match length	124
% identity	52
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	192841
Contig ID	7680_1.R1039
5'-most EST	g5049558
Method	BLASTX
NCBI GI	g1172977
BLAST score	808
E value	2.0e-86
Match length	182
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi|606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	192842
Contig ID	7682_1.R1039
5'-most EST	LIB3083-104-Q1-L1-E5

Seq. No.	192843
Contig ID	7684_1.R1039
5'-most EST	g5047415
Method	BLASTX
NCBI GI	g4567262
BLAST score	941
E value	1.0e-102
Match length	192
% identity	90
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No.	192844
Contig ID	7687_1.R1039
5'-most EST	LIB3196-016-P1-M1-D10
Method	BLASTN
NCBI GI	g969118
BLAST score	141
E value	3.0e-73
Match length	502
% identity	98
NCBI Description	Gossypium herbaceum 5S ribosomal RNA gene and non-transcribed spacer, clone

Seq. No.	192845
Contig ID	7687_2.R1039
5'-most EST	g5047481
Method	BLASTX
NCBI GI	g1076738
BLAST score	649

E value 6.0e-68
Match length 127
% identity 93
NCBI Description beta-tubulin R2242 - rice

Seq. No. 192846
Contig ID 7687_3.R1039
5'-most EST LIB3197-022-Q1-M1-G2
Method BLASTX
NCBI GI g1174600
BLAST score 2192
E value 0.0e+00
Match length 438
% identity 94
NCBI Description TUBULIN BETA CHAIN >gi|493710|dbj|BAA06382| (D30717) beta-tubulin [Oryza sativa]

Seq. No. 192847
Contig ID 7687_4.R1039
5'-most EST uC-gsflnu33B133g02b1
Method BLASTN
NCBI GI g969118
BLAST score 136
E value 3.0e-70
Match length 477
% identity 95
NCBI Description Gossypium herbaceum 5S ribosomal RNA gene and non-transcribed spacer, clone

Seq. No. 192848
Contig ID 7687_5.R1039
5'-most EST LIB3149-025-Q1-K1-F9
Method BLASTX
NCBI GI g1174600
BLAST score 699
E value 9.0e-74
Match length 142
% identity 90
NCBI Description TUBULIN BETA CHAIN >gi|493710|dbj|BAA06382| (D30717) beta-tubulin [Oryza sativa]

Seq. No. 192849
Contig ID 7688_1.R1039
5'-most EST LIB3189-006-P1-K1-H1
Method BLASTX
NCBI GI g3283409
BLAST score 155
E value 4.0e-10
Match length 73
% identity 48
NCBI Description (AF068754) heat shock factor binding protein 1 HSBP1 [Homo sapiens] >gi|4557647|ref|NP_001528.1|pHSBP1| heat shock factor binding protein

Seq. No. 192850
Contig ID 7688_2.R1039
5'-most EST LIB3189-006-P1-K1-G9

Seq. No.	192851
Contig ID	7697_1.R1039
5'-most EST	LIB3145-042-Q1-K1-B7
Method	BLASTX
NCBI GI	g1223579
BLAST score	214
E value	8.0e-26
Match length	136
% identity	46
NCBI Description	(X96481) cDNA101 [Arabidopsis thaliana]

Seq. No.	192852
Contig ID	7698_3.R1039
5'-most EST	LIB3196-019-P1-M1-A6

Seq. No.	192853
Contig ID	7704_1.R1039
5'-most EST	LIB3135-053-Q1-K1-F5
Method	BLASTX
NCBI GI	g2281115
BLAST score	1009
E value	1.0e-110
Match length	222
% identity	86
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	192854
Contig ID	7714_1.R1039
5'-most EST	uC-gsflnu33B071e11b1

Seq. No.	192855
Contig ID	7715_1.R1039
5'-most EST	LIB3149-004-P1-K1-H8
Method	BLASTX
NCBI GI	g3033384
BLAST score	672
E value	2.0e-70
Match length	170
% identity	74
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	192856
Contig ID	7721_1.R1039
5'-most EST	LIB3165-051-Q1-K1-B4
Method	BLASTX
NCBI GI	g166878
BLAST score	567
E value	3.0e-58
Match length	202
% identity	59
NCBI Description	(M95796) St12p protein [Arabidopsis thaliana]

Seq. No.	192857
Contig ID	7725_1.R1039
5'-most EST	LIB3083-073-Q1-L1-A9

Method	BLASTX
NCBI GI	g4539369
BLAST score	244
E value	1.0e-20
Match length	78
% identity	63
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	192858
Contig ID	7728_1.R1039
5'-most EST	uC-gsflmaxxa064c01b1

Seq. No.	192859
Contig ID	7730_1.R1039
5'-most EST	LIB3083-073-Q1-L1-B2

Seq. No.	192860
Contig ID	7733_1.R1039
5'-most EST	LIB3120-045-P1-K1-F10

Seq. No.	192861
Contig ID	7735_1.R1039
5'-most EST	LIB3083-073-Q1-L1-B7

Seq. No.	192862
Contig ID	7736_1.R1039
5'-most EST	uC-gsronu33B103d01b1

Seq. No.	192863
Contig ID	7738_1.R1039
5'-most EST	g5044230
Method	BLASTX
NCBI GI	g1800147
BLAST score	586
E value	2.0e-60
Match length	227
% identity	56
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	192864
Contig ID	7741_1.R1039
5'-most EST	LIB3145-011-Q1-K1-B10

Seq. No.	192865
Contig ID	7744_1.R1039
5'-most EST	LIB3083-073-Q1-L1-C5
Method	BLASTX
NCBI GI	g3355470
BLAST score	255
E value	1.0e-34
Match length	98
% identity	73
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	192866
Contig ID	7745_1.R1039

5'-most EST	LIB3083-073-Q1-L1-C7
Method	BLASTX
NCBI GI	g4056481
BLAST score	530
E value	7.0e-54
Match length	232
% identity	37
NCBI Description	(AC005896) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	192867
Contig ID	7753_1.R1039
5'-most EST	g5046713
Method	BLASTX
NCBI GI	g1706695
BLAST score	163
E value	7.0e-11
Match length	210
% identity	29
NCBI Description	PHOSPHOMEVALONATE KINASE >gi|1362436|pir||S57588 phosphomevalonate kinase (EC 2.7.4.2) - yeast (Saccharomyces cerevisiae) >gi|887601|emb|CAA90191| (Z49939) Erg8p [Saccharomyces cerevisiae]

Seq. No.	192868
Contig ID	7757_1.R1039
5'-most EST	LIB3189-017-P1-K1-C7
Method	BLASTX
NCBI GI	g730512
BLAST score	504
E value	3.0e-51
Match length	117
% identity	88
NCBI Description	RAS-RELATED PROTEIN RIC2 >gi|481506|pir||S38741 GTP-binding protein ric2 - rice >gi|218228|dbj|BAA02904| (D13758) ras-related GTP binding protein [Oryza sativa]

Seq. No.	192869
Contig ID	7760_2.R1039
5'-most EST	LIB3166-042-P1-K1-F9
Method	BLASTX
NCBI GI	g627469
BLAST score	310
E value	3.0e-28
Match length	169
% identity	16
NCBI Description	hypothetical protein 2 - human (fragment)

Seq. No.	192870
Contig ID	7765_1.R1039
5'-most EST	g3325714
Method	BLASTX
NCBI GI	g3850816
BLAST score	799
E value	2.0e-85
Match length	188
% identity	74

NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	192871
Contig ID	7776_1.R1039
5'-most EST	LIB3083-073-Q1-L1-G11
Method	BLASTX
NCBI GI	g3335337
BLAST score	430
E value	4.0e-42
Match length	132
% identity	70
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb|L23574 from A. thaliana. ESTs gb|Z30712, gb|Z30713, gb|Z26204, gb|N37975 and gb|N96330 come from this gene

Seq. No.	192872
Contig ID	7776_2.R1039
5'-most EST	LIB3146-033-Q1-K1-F3
Method	BLASTX
NCBI GI	g3335337
BLAST score	378
E value	2.0e-36
Match length	114
% identity	68
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb|L23574 from A. thaliana. ESTs gb|Z30712, gb|Z30713, gb|Z26204, gb|N37975 and gb|N96330 come from this gene

Seq. No.	192873
Contig ID	7779_1.R1039
5'-most EST	LIB3083-073-Q1-L1-G3

Seq. No.	192874
Contig ID	7791_1.R1039
5'-most EST	LIB3083-073-Q1-L1-H4

Seq. No.	192875
Contig ID	7799_1.R1039
5'-most EST	LIB3189-037-P1-K1-D12

Seq. No.	192876
Contig ID	7800_1.R1039
5'-most EST	LIB3083-074-Q1-L1-A6
Method	BLASTX
NCBI GI	g425194
BLAST score	862
E value	7.0e-93
Match length	190
% identity	87
NCBI Description	(L26243) heat shock protein [Spinacia oleracea] >gi|2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	192877
Contig ID	7802_1.R1039
5'-most EST	LIB3166-031-P1-K1-F10
Method	BLASTX
NCBI GI	g4206765
BLAST score	357
E value	1.0e-33
Match length	166
% identity	46
NCBI Description	(AF104329) putative type 1 membrane protein [Arabidopsis thaliana]

Seq. No.	192878
Contig ID	7807_1.R1039
5'-most EST	LIB3083-094-Q1-L1-B12
Method	BLASTX
NCBI GI	g3482967
BLAST score	290
E value	3.0e-26
Match length	59
% identity	92
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|4559345|gb|AAD23006.1|AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	192879
Contig ID	7808_1.R1039
5'-most EST	LIB3272-043-P1-K1-F6

Seq. No.	192880
Contig ID	7815_1.R1039
5'-most EST	LIB3083-074-Q1-L1-C6
Method	BLASTX
NCBI GI	g4262241
BLAST score	372
E value	2.0e-35
Match length	179
% identity	50
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	192881
Contig ID	7819_1.R1039
5'-most EST	LIB3189-040-P1-K1-A3
Method	BLASTX
NCBI GI	g1077345
BLAST score	154
E value	6.0e-10
Match length	73
% identity	44
NCBI Description	hypothetical protein YLR290c - yeast (Saccharomyces cerevisiae) >gi|596046 (U17243) L8003.16 gene product [Saccharomyces cerevisiae]

Seq. No.	192882
Contig ID	7827_1.R1039
5'-most EST	LIB3083-099-Q1-L1-F10

Method	BLASTX
NCBI GI	g1778051
BLAST score	210
E value	2.0e-16
Match length	107
% identity	39
NCBI Description	(U62583) Prt1 homolog [Homo sapiens] >gi|4503527|ref|NP_003742.1|pEIF3S9| UNKNOWN

Seq. No.	192883
Contig ID	7832_1.R1039
5'-most EST	LIB3083-074-Q1-L1-E8
Method	BLASTX
NCBI GI	g3367568
BLAST score	778
E value	5.0e-83
Match length	172
% identity	84
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	192884
Contig ID	7837_1.R1039
5'-most EST	LIB3083-074-Q1-L1-F4
Method	BLASTN
NCBI GI	g3449327
BLAST score	58
E value	8.0e-24
Match length	146
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	192885
Contig ID	7842_1.R1039
5'-most EST	LIB3272-039-P1-K1-A10
Method	BLASTX
NCBI GI	g2498490
BLAST score	490
E value	5.0e-77
Match length	286
% identity	55
NCBI Description	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi|1854579 (L35556) Int-6 [Mus musculus] >gi|2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi|2351382 (U54562) eIF3-p48 [Homo sapiens] >gi|2688818 (U85947) Int-6 [Homo sapiens] >gi|2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi|4503521|ref|NP_001559.1|pEIF3S6| murine mammary tumor integration site 6 (oncogene homolog)

Seq. No.	192886
Contig ID	7846_1.R1039
5'-most EST	LIB3272-013-P1-K1-H9
Method	BLASTX
NCBI GI	g2244810
BLAST score	291
E value	3.0e-26

Match length	67
% identity	87
NCBI Description	(Z97336) CCAAT-binding transcription factor subunit A(CBF-A) [Arabidopsis thaliana]

Seq. No.	192887
Contig ID	7849_1.R1039
5'-most EST	LIB3083-074-Q1-L1-G7
Method	BLASTX
NCBI GI	g4512667
BLAST score	487
E value	7.0e-49
Match length	224
% identity	46
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	192888
Contig ID	7860_1.R1039
5'-most EST	uC-gsronu33B090c11b1

Seq. No.	192889
Contig ID	7861_1.R1039
5'-most EST	g5047737
Method	BLASTX
NCBI GI	g3043428
BLAST score	903
E value	2.0e-97
Match length	191
% identity	92
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	192890
Contig ID	7861_2.R1039
5'-most EST	LIB3149-018-Q1-K1-E11
Method	BLASTX
NCBI GI	g3043428
BLAST score	910
E value	3.0e-98
Match length	197
% identity	91
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	192891
Contig ID	7861_3.R1039
5'-most EST	uC-gsflnu33B136b12b1
Method	BLASTX
NCBI GI	g3043428
BLAST score	707
E value	3.0e-91
Match length	197
% identity	87
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	192892
Contig ID	7877_1.R1039
5'-most EST	LIB3197-058-Q1-M1-H1
Method	BLASTX

NCBI GI	g116229
BLAST score	1015
E value	1.0e-117
Match length	280
% identity	78
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR >gi|99676|pir||S20876 chaperonin hsp60 precursor - Arabidopsis thaliana >gi|16221|emb|CAA77646| (Z11547) chaperonin hsp60 [Arabidopsis thaliana]

Seq. No.	192893
Contig ID	7877_2.R1039
5'-most EST	LIB3197-059-Q1-M1-A6
Method	BLASTX
NCBI GI	g461735
BLAST score	1094
E value	1.0e-120
Match length	242
% identity	90
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR >gi|478785|pir||S29315 chaperonin 60 - cucurbit >gi|12544|emb|CAA50217| (X70867) chaperonin 60 [Cucurbita sp.]

Seq. No.	192894
Contig ID	7881_1.R1039
5'-most EST	LIB3149-046-Q1-K1-A9
Method	BLASTX
NCBI GI	g2119045
BLAST score	713
E value	2.0e-75
Match length	178
% identity	54
NCBI Description	small nuclear ribonucleoprotein U1A - potato >gi|1050840|emb|CAA90282| (Z49990) U1snRNP-specific protein, U1A [Solanum tuberosum]

Seq. No.	192895
Contig ID	7884_1.R1039
5'-most EST	uC-gsflnu33B126f11b1

Seq. No.	192896
Contig ID	7886_1.R1039
5'-most EST	uC-gsflnu33B064c08b1
Method	BLASTX
NCBI GI	g3928099
BLAST score	474
E value	3.0e-47
Match length	260
% identity	20
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	192897
Contig ID	7892_1.R1039
5'-most EST	LIB3146-034-Q1-K1-G8
Method	BLASTX
NCBI GI	g3759184

BLAST score	625
E value	2.0e-65
Match length	127
% identity	87
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	192898
Contig ID	7894_1.R1039
5'-most EST	LIB3145-040-Q1-K1-F6
Method	BLASTX
NCBI GI	g2618688
BLAST score	828
E value	7.0e-89
Match length	197
% identity	77
NCBI Description	(AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No.	192899
Contig ID	7899_1.R1039
5'-most EST	LIB3272-041-P1-K1-H1
Method	BLASTX
NCBI GI	g3024583
BLAST score	184
E value	7.0e-14
Match length	96
% identity	48
NCBI Description	RT14 PROTEIN HOMOLOG >gi|2347196 (AC002338) RT14 protein isolog [Arabidopsis thaliana]

Seq. No.	192900
Contig ID	7901_1.R1039
5'-most EST	LIB3197-034-Q1-M1-D9
Method	BLASTX
NCBI GI	g2894592
BLAST score	560
E value	2.0e-57
Match length	139
% identity	76
NCBI Description	(AL021889) predicted protein [Arabidopsis thaliana]

Seq. No.	192901
Contig ID	7901_2.R1039
5'-most EST	LIB3149-032-Q1-K1-C3
Method	BLASTX
NCBI GI	g2894592
BLAST score	378
E value	2.0e-36
Match length	92
% identity	74
NCBI Description	(AL021889) predicted protein [Arabidopsis thaliana]

Seq. No.	192902
Contig ID	7902_1.R1039
5'-most EST	LIB3083-076-Q1-L1-E1
Method	BLASTX
NCBI GI	g3695059
BLAST score	447

E value 1.0e-44
Match length 114
% identity 82
NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No. 192903
Contig ID 7903_1.R1039
5'-most EST LIB3147-003-Q1-K1-C2
Method BLASTX
NCBI GI g4490705
BLAST score 575
E value 2.0e-59
Match length 131
% identity 89
NCBI Description (AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No. 192904
Contig ID 7904_1.R1039
5'-most EST LIB3083-076-Q1-L1-E2
Method BLASTX
NCBI GI g1223922
BLAST score 595
E value 8.0e-62
Match length 138
% identity 78
NCBI Description (U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No. 192905
Contig ID 7906_1.R1039
5'-most EST LIB3145-038-Q1-K1-A5

Seq. No. 192906
Contig ID 7909_1.R1039
5'-most EST g5049666
Method BLASTX
NCBI GI g3790548
BLAST score 1177
E value 1.0e-129
Match length 254
% identity 86
NCBI Description (AF064064) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No. 192907
Contig ID 7909_2.R1039
5'-most EST LIB3189-001-P1-K1-C11
Method BLASTX
NCBI GI g4126401
BLAST score 527
E value 1.0e-53
Match length 127
% identity 80
NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 192908

Contig ID	7911_1.R1039
5'-most EST	uC-gsflmaxxa003e09b1
Method	BLASTX
NCBI GI	g2492952
BLAST score	1079
E value	1.0e-118
Match length	277
% identity	75
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi|542026|pir||S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi|410482|emb|CAA79859| (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	192909
Contig ID	7911_2.R1039
5'-most EST	g5046831
Method	BLASTX
NCBI GI	g2492952
BLAST score	734
E value	1.0e-142
Match length	301
% identity	83
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi|542026|pir||S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi|410482|emb|CAA79859| (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	192910
Contig ID	7911_4.R1039
5'-most EST	LIB3148-048-Q1-K1-H4
Method	BLASTX
NCBI GI	g2492952
BLAST score	316
E value	6.0e-29
Match length	77
% identity	78
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi|542026|pir||S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi|410482|emb|CAA79859| (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	192911
Contig ID	7917_1.R1039
5'-most EST	LIB3083-076-Q1-L1-F3
Method	BLASTX
NCBI GI	g484656
BLAST score	603
E value	6.0e-71
Match length	175
% identity	75
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi|452165|dbj|BAA05408| (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	192912
Contig ID	7922_1.R1039
5'-most EST	LIB3197-031-Q1-M1-B12
Method	BLASTX
NCBI GI	g3377843
BLAST score	643
E value	4.0e-67
Match length	168
% identity	77
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	192913
Contig ID	7924_1.R1039
5'-most EST	LIB3083-076-Q1-L1-G10
Method	BLASTX
NCBI GI	g2832649
BLAST score	629
E value	9.0e-66
Match length	162
% identity	72
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]

Seq. No.	192914
Contig ID	7925_1.R1039
5'-most EST	g5045275
Method	BLASTX
NCBI GI	g2244993
BLAST score	245
E value	1.0e-20
Match length	96
% identity	49
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	192915
Contig ID	7926_1.R1039
5'-most EST	uC-gsronu33B044c07b1
Method	BLASTX
NCBI GI	g464980
BLAST score	805
E value	4.0e-86
Match length	152
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|166422 (L06967) ubiquitin carrier protein [Medicago sativa]

Seq. No.	192916
Contig ID	7926_2.R1039
5'-most EST	LIB3145-018-Q1-K1-F6
Method	BLASTN
NCBI GI	g166421
BLAST score	101
E value	2.0e-49
Match length	293

% identity	84
NCBI Description	Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No.	192917
Contig ID	7940_1.R1039
5'-most EST	LIB3083-112-Q1-L1-H3
Method	BLASTN
NCBI GI	g4159706
BLAST score	38
E value	7.0e-12
Match length	74
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]

Seq. No.	192918
Contig ID	7943_1.R1039
5'-most EST	LIB3147-037-Q1-K1-D4

Seq. No.	192919
Contig ID	7943_2.R1039
5'-most EST	LIB3147-022-Q1-K1-C4

Seq. No.	192920
Contig ID	7944_1.R1039
5'-most EST	g5050519
Method	BLASTX
NCBI GI	g3281853
BLAST score	842
E value	1.0e-90
Match length	201
% identity	89
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	192921
Contig ID	7946_1.R1039
5'-most EST	uC-gsflmaxxa028h12b1
Method	BLASTX
NCBI GI	g4539545
BLAST score	1200
E value	1.0e-132
Match length	246
% identity	94
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]

Seq. No.	192922
Contig ID	7946_4.R1039
5'-most EST	uC-gsflmaxxa061f10b1
Method	BLASTX
NCBI GI	g4539545
BLAST score	384
E value	3.0e-37
Match length	97
% identity	78
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]

Seq. No.	192923
Contig ID	7947_1.R1039
5'-most EST	LIB3166-040-P1-K1-H3
Method	BLASTX
NCBI GI	g730165
BLAST score	208
E value	3.0e-16
Match length	80
% identity	54
NCBI Description	EARLY NODULIN 93 (N-93) >gi|486679|pir||S34801 nodulin (clone GmN93) - soybean >gi|218262|dbj|BAA02724| (D13506) early nodulin [Glycine max] >gi|3763851|dbj|BAA33816| (AB018378) early nodulin [Glycine max] >gi|447138|prf||1913422D nodulin [Glycine max]

Seq. No.	192924
Contig ID	7951_1.R1039
5'-most EST	g5044273
Method	BLASTX
NCBI GI	g1752734
BLAST score	665
E value	1.0e-69
Match length	213
% identity	62
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	192925
Contig ID	7952_1.R1039
5'-most EST	LIB3083-077-Q1-L1-A8
Method	BLASTX
NCBI GI	g4105772
BLAST score	387
E value	3.0e-37
Match length	85
% identity	43
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	192926
Contig ID	7953_1.R1039
5'-most EST	g5045380
Method	BLASTX
NCBI GI	g967125
BLAST score	721
E value	3.0e-76
Match length	150
% identity	92
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	192927
Contig ID	7956_1.R1039
5'-most EST	LIB3196-010-P1-M1-A3
Method	BLASTX
NCBI GI	g3551523
BLAST score	201
E value	1.0e-15
Match length	119
% identity	34

NCBI Description	(AB017026) oxysterol-binding protein [Mus musculus]
Seq. No.	192928
Contig ID	7960_1.R1039
5'-most EST	LIB3147-027-Q1-K1-H4
Method	BLASTX
NCBI GI	g3287690
BLAST score	145
E value	3.0e-10
Match length	113
% identity	42
NCBI Description	(AC003979) T22J18.15 [Arabidopsis thaliana]
Seq. No.	192929
Contig ID	7964_1.R1039
5'-most EST	LIB3272-005-P1-K1-F10
Method	BLASTX
NCBI GI	g1174583
BLAST score	215
E value	5.0e-17
Match length	142
% identity	33
NCBI Description	TRANSALDOLASE >gi|1074653|pir||D64167 hypothetical protein HI1125 - Haemophilus influenzae (strain Rd KW20) >gi|1574680 (U32792) transaldolase B (talB) [Haemophilus influenzae Rd]
Seq. No.	192930
Contig ID	7971_1.R1039
5'-most EST	LIB3197-037-Q1-M1-D3
Seq. No.	192931
Contig ID	7976_1.R1039
5'-most EST	LIB3147-019-Q1-K1-H6
Method	BLASTX
NCBI GI	g3892058
BLAST score	489
E value	7.0e-49
Match length	227
% identity	46
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]
Seq. No.	192932
Contig ID	7979_1.R1039
5'-most EST	LIB3083-077-Q1-L1-D3
Method	BLASTX
NCBI GI	g4432837
BLAST score	253
E value	1.0e-21
Match length	161
% identity	40
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.	192933
Contig ID	7982_1.R1039
5'-most EST	LIB3145-043-Q1-K1-A1

Seq. No.	192934
Contig ID	7985_1.R1039
5'-most EST	LIB3197-022-Q1-M1-D1
Method	BLASTX
NCBI GI	g4335763
BLAST score	430
E value	5.0e-42
Match length	161
% identity	50
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	192935
Contig ID	8000_1.R1039
5'-most EST	LIB3083-077-Q1-L1-F3
Method	BLASTX
NCBI GI	g1514639
BLAST score	829
E value	4.0e-89
Match length	187
% identity	83
NCBI Description	(X85181) alpha-glucan phosphorylase [Spinacia oleracea]

Seq. No.	192936
Contig ID	8002_1.R1039
5'-most EST	uC-gsronu33B162f07b2
Method	BLASTX
NCBI GI	g3876473
BLAST score	172
E value	6.0e-12
Match length	138
% identity	28
NCBI Description	(Z72508) F28H7.4 [Caenorhabditis elegans]

Seq. No.	192937
Contig ID	8003_1.R1039
5'-most EST	LIB3166-039-P1-K1-F5

Seq. No.	192938
Contig ID	8004_1.R1039
5'-most EST	LIB3272-041-P1-K1-F8
Method	BLASTX
NCBI GI	g3023841
BLAST score	354
E value	2.0e-33
Match length	89
% identity	75
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi|1695179|emb|CAA70704| (Y09513) G protein beta subunit [Nicotiana plumbaginifolia]

Seq. No.	192939
Contig ID	8011_1.R1039
5'-most EST	g5047575
Method	BLASTX
NCBI GI	g1209020
BLAST score	297

E value 3.0e-26
Match length 246
% identity 34
NCBI Description (U09584) PL6 protein [Homo sapiens]

Seq. No. 192940
Contig ID 8011_2.R1039
5'-most EST g5047582
Method BLASTX
NCBI GI g1209020
BLAST score 145
E value 6.0e-09
Match length 128
% identity 34
NCBI Description (U09584) PL6 protein [Homo sapiens]

Seq. No. 192941
Contig ID 8018_1.R1039
5'-most EST uC-gsflmaxxa026a09b1

Seq. No. 192942
Contig ID 8023_1.R1039
5'-most EST LIB3166-008-P1-K1-H1
Method BLASTX
NCBI GI g4580460
BLAST score 618
E value 2.0e-64
Match length 152
% identity 84
NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No. 192943
Contig ID 8024_1.R1039
5'-most EST LIB3083-077-Q1-L1-H6
Method BLASTX
NCBI GI g2911148
BLAST score 649
E value 4.0e-68
Match length 157
% identity 81
NCBI Description (AB005808) NADP-malic enzyme [Aloe arborescens]

Seq. No. 192944
Contig ID 8026_1.R1039
5'-most EST uC-gsflnu33B015a06b1

Seq. No. 192945
Contig ID 8027_1.R1039
5'-most EST g5047193
Method BLASTX
NCBI GI g3924823
BLAST score 275
E value 4.0e-24
Match length 137
% identity 43
NCBI Description (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST

yk491a11.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	192946
Contig ID	8032_1.R1039
5'-most EST	LIB3120-017-Q1-K1-G11
Method	BLASTX
NCBI GI	g3927831
BLAST score	625
E value	2.0e-65
Match length	141
% identity	81
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	192947
Contig ID	8035_1.R1039
5'-most EST	LIB3165-016-P1-K1-G1
Method	BLASTX
NCBI GI	g548847
BLAST score	165
E value	3.0e-12
Match length	45
% identity	98
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi|1086182|pir||S39501 ribosomal protein S12 - curled-leaved tobacco >gi|225248|prf||1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	192948
Contig ID	8035_2.R1039
5'-most EST	LIB3083-078-Q1-L1-A8

Seq. No.	192949
Contig ID	8035_3.R1039
5'-most EST	LIB3148-029-Q1-K1-A9
Method	BLASTN
NCBI GI	g12292
BLAST score	312
E value	1.0e-175
Match length	514
% identity	91
NCBI Description	Spinach chloroplast DNA homologous to ARS and ARC elements upstream of rDNA operon

Seq. No.	192950
Contig ID	8039_1.R1039
5'-most EST	LIB3146-047-Q1-K1-H5
Method	BLASTX
NCBI GI	g1350720
BLAST score	455
E value	3.0e-45
Match length	111
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	192951
Contig ID	8039_3.R1039

5'-most EST	uC-gsronu33B080g02b1
Method	BLASTX
NCBI GI	g1350720
BLAST score	455
E value	2.0e-45
Match length	111
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	192952
Contig ID	8039_5.R1039
5'-most EST	LIB3135-035-Q1-K1-D6
Method	BLASTX
NCBI GI	g1350720
BLAST score	376
E value	4.0e-36
Match length	110
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	192953
Contig ID	8043_1.R1039
5'-most EST	LIB3197-042-Q1-M1-B9
Method	BLASTX
NCBI GI	g2194118
BLAST score	196
E value	5.0e-15
Match length	69
% identity	54
NCBI Description	(AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No.	192954
Contig ID	8046_1.R1039
5'-most EST	LIB3165-051-Q1-K1-A2
Method	BLASTX
NCBI GI	g4531440
BLAST score	190
E value	5.0e-14
Match length	149
% identity	39
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	192955
Contig ID	8056_1.R1039
5'-most EST	LIB3148-042-Q1-K1-C12

Seq. No.	192956
Contig ID	8070_1.R1039
5'-most EST	LIB3083-078-Q1-L1-D7
Method	BLASTX
NCBI GI	g3395431
BLAST score	254
E value	2.0e-21
Match length	148
% identity	41
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	192957
Contig ID	8071_1.R1039
5'-most EST	LIB3083-078-Q1-L1-D8
Method	BLASTX
NCBI GI	g2673910
BLAST score	190
E value	3.0e-14
Match length	94
% identity	48
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192958
Contig ID	8072_1.R1039
5'-most EST	uC-gsflnu33B064e12b1
Method	BLASTX
NCBI GI	g4510383
BLAST score	991
E value	1.0e-107
Match length	318
% identity	65
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	192959
Contig ID	8076_1.R1039
5'-most EST	LIB3272-014-P1-K1-G5

Seq. No.	192960
Contig ID	8085_1.R1039
5'-most EST	LIB3083-082-Q1-L1-G6
Method	BLASTX
NCBI GI	g1082054
BLAST score	146
E value	3.0e-09
Match length	129
% identity	27
NCBI Description	(Z49859) copper transporter protein [Arabidopsis thaliana]

Seq. No.	192961
Contig ID	8086_1.R1039
5'-most EST	g5048507
Method	BLASTX
NCBI GI	g1518540
BLAST score	1137
E value	0.0e+00
Match length	480
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	192962
Contig ID	8087_1.R1039
5'-most EST	LIB3083-078-Q1-L1-F2
Method	BLASTX
NCBI GI	g4220521
BLAST score	383
E value	1.0e-36
Match length	143
% identity	59

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 192963
Contig ID 8099_1.R1039
5'-most EST LIB3083-078-Q1-L1-G3
Method BLASTX
NCBI GI g3608154
BLAST score 460
E value 5.0e-46
Match length 140
% identity 67
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 192964
Contig ID 8100_1.R1039
5'-most EST LIB3083-078-Q1-L1-G4

Seq. No. 192965
Contig ID 8102_1.R1039
5'-most EST uC-gsflnu33B012g09b1
Method BLASTX
NCBI GI g1771780
BLAST score 677
E value 4.0e-71
Match length 156
% identity 85
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 192966
Contig ID 8102_2.R1039
5'-most EST uC-gsflnu33B109f05b1
Method BLASTX
NCBI GI g1771780
BLAST score 677
E value 4.0e-71
Match length 156
% identity 85
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 192967
Contig ID 8102_3.R1039
5'-most EST LIB3147-001-Q1-K2-D5
Method BLASTX
NCBI GI g1771780
BLAST score 660
E value 3.0e-69
Match length 156
% identity 84
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 192968
Contig ID 8103_1.R1039
5'-most EST LIB3083-078-Q1-L1-G8
Method BLASTX
NCBI GI g1552169
BLAST score 300
E value 7.0e-27

Match length	193
% identity	38
NCBI Description	(D42138) PIG-B [Homo sapiens]

Seq. No.	192969
Contig ID	8108_1.R1039
5'-most EST	LIB3083-078-Q1-L1-H12
Method	BLASTN
NCBI GI	g3241920
BLAST score	38
E value	7.0e-12
Match length	139
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	192970
Contig ID	8111_1.R1039
5'-most EST	LIB3272-009-P1-K1-H7

Seq. No.	192971
Contig ID	8113_1.R1039
5'-most EST	LIB3149-040-Q1-K1-A5
Method	BLASTX
NCBI GI	g4544432
BLAST score	786
E value	5.0e-84
Match length	218
% identity	71
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]

Seq. No.	192972
Contig ID	8117_1.R1039
5'-most EST	LIB3197-040-Q1-M1-D12
Method	BLASTX
NCBI GI	g4469023
BLAST score	558
E value	2.0e-57
Match length	124
% identity	85
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	192973
Contig ID	8119_1.R1039
5'-most EST	LIB3197-012-P1-M1-B12

Seq. No.	192974
Contig ID	8119_2.R1039
5'-most EST	LIB3147-022-Q1-K1-B2

Seq. No.	192975
Contig ID	8119_4.R1039
5'-most EST	LIB3083-079-Q1-L1-A12
Method	BLASTX
NCBI GI	g2465008
BLAST score	160

E value	1.0e-21
Match length	213
% identity	37
NCBI Description	(AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No.	192976
Contig ID	8120_1.R1039
5'-most EST	LIB3120-036-Q1-K1-A8
Method	BLASTX
NCBI GI	g1085922
BLAST score	440
E value	2.0e-43
Match length	178
% identity	56
NCBI Description	hypothetical protein 224 - evening primrose mitochondrion >gi|459533|emb|CAA54968| (X78038) orf224; homology to ribosomal protein S1 of E. coli [Oenothera berteriana]

Seq. No.	192977
Contig ID	8132_1.R1039
5'-most EST	uC-gsronu33B106b10b2
Method	BLASTX
NCBI GI	g606942
BLAST score	546
E value	9.0e-56
Match length	187
% identity	58
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	192978
Contig ID	8133_1.R1039
5'-most EST	LIB3165-024-P1-K1-F7
Method	BLASTX
NCBI GI	g2245378
BLAST score	160
E value	1.0e-10
Match length	36
% identity	75
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	192979
Contig ID	8137_1.R1039
5'-most EST	uC-gsflnu33B026b12b1
Method	BLASTX
NCBI GI	g2738998
BLAST score	628
E value	1.0e-65
Match length	135
% identity	86
NCBI Description	(AF022458) CYP98A2p [Glycine max]

Seq. No.	192980
Contig ID	8139_1.R1039
5'-most EST	LIB3149-062-Q1-K1-G8
Method	BLASTX
NCBI GI	g2245091
BLAST score	190

E value 5.0e-14
Match length 117
% identity 42
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 192981
Contig ID 8146_1.R1039
5'-most EST uC-gsflmaxxa014b08b1

Seq. No. 192982
Contig ID 8151_1.R1039
5'-most EST LIB3120-026-Q1-K1-E8
Method BLASTX
NCBI GI g3212871
BLAST score 324
E value 6.0e-30
Match length 124
% identity 57
NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 192983
Contig ID 8152_1.R1039
5'-most EST LIB3083-113-Q1-L1-G12
Method BLASTX
NCBI GI g3582002
BLAST score 201
E value 2.0e-15
Match length 148
% identity 34
NCBI Description (AJ010943) tomato invertase inhibitor [Lycopersicon esculentum]

Seq. No. 192984
Contig ID 8153_1.R1039
5'-most EST uC-gsronu33B153d12b2

Seq. No. 192985
Contig ID 8157_1.R1039
5'-most EST LIB3147-017-Q1-K1-B8
Method BLASTX
NCBI GI g2500345
BLAST score 269
E value 8.0e-24
Match length 78
% identity 72
NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)
>gi|2618578|dbj|BAA23363| (D50420) OTK27 [Homo sapiens]
>gi|3859990 (AF091076) OTK27 [Homo sapiens]
>gi|1589072|prf||2210268A nuclear protein-NHP2-like protein [Homo sapiens]

Seq. No. 192986
Contig ID 8167_1.R1039
5'-most EST uC-gsflnu33B062a02b1
Method BLASTX

NCBI GI	g4204765
BLAST score	393
E value	9.0e-57
Match length	142
% identity	81
NCBI Description	(U51194) peroxidase [Glycine max]

Seq. No.	192987
Contig ID	8168_1.R1039
5'-most EST	LIB3146-028-Q1-K1-D9
Method	BLASTX
NCBI GI	g4102839
BLAST score	1126
E value	1.0e-123
Match length	273
% identity	78
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	192988
Contig ID	8170_1.R1039
5'-most EST	LIB3083-080-Q1-L1-C10

Seq. No.	192989
Contig ID	8171_1.R1039
5'-most EST	LIB3083-083-Q1-L1-D5
Method	BLASTX
NCBI GI	g3342552
BLAST score	253
E value	9.0e-22
Match length	101
% identity	48
NCBI Description	(AF076979) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	192990
Contig ID	8175_1.R1039
5'-most EST	LIB3083-080-Q1-L1-C4
Method	BLASTX
NCBI GI	g4490715
BLAST score	286
E value	2.0e-25
Match length	179
% identity	35
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	192991
Contig ID	8177_1.R1039
5'-most EST	LIB3147-059-Q1-K1-E11
Method	BLASTX
NCBI GI	g2262173
BLAST score	911
E value	2.0e-98
Match length	197
% identity	89
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	192992
Contig ID	8179_1.R1039
5'-most EST	LIB3197-060-Q1-M1-F6

Seq. No.	192993
Contig ID	8182_1.R1039
5'-most EST	g5046109
Method	BLASTX
NCBI GI	g1082054
BLAST score	352
E value	4.0e-33
Match length	124
% identity	55
NCBI Description	(Z49859) copper transporter protein [Arabidopsis thaliana]

Seq. No.	192994
Contig ID	8190_1.R1039
5'-most EST	LIB3272-006-P1-K1-F5
Method	BLASTX
NCBI GI	g3769472
BLAST score	310
E value	4.0e-37
Match length	105
% identity	68
NCBI Description	(AF064732) putative phospholipase A2 [Dianthus caryophyllus]

Seq. No.	192995
Contig ID	8195_1.R1039
5'-most EST	LIB3083-080-Q1-L1-E2

Seq. No.	192996
Contig ID	8197_1.R1039
5'-most EST	LIB3197-030-Q1-M1-E4
Method	BLASTX
NCBI GI	g461812
BLAST score	363
E value	2.0e-34
Match length	195
% identity	41
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi|167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi|445604|prf||1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	192997
Contig ID	8197_2.R1039
5'-most EST	LIB3149-019-Q1-K1-A9
Method	BLASTX
NCBI GI	g3522945
BLAST score	263
E value	1.0e-22
Match length	114
% identity	44
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	192998
Contig ID	8205_1.R1039
5'-most EST	LIB3166-033-P1-K1-F2
Method	BLASTX
NCBI GI	g3252813
BLAST score	1263
E value	1.0e-139
Match length	266
% identity	87
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi|3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	192999
Contig ID	8206_1.R1039
5'-most EST	LIB3083-080-Q1-L1-F12
Method	BLASTX
NCBI GI	g2245108
BLAST score	156
E value	2.0e-10
Match length	46
% identity	63
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	193000
Contig ID	8212_1.R1039
5'-most EST	LIB3272-015-P1-K1-E6

Seq. No.	193001
Contig ID	8215_1.R1039
5'-most EST	LIB3083-080-Q1-L1-G10
Method	BLASTX
NCBI GI	g3522956
BLAST score	509
E value	1.0e-51
Match length	154
% identity	64
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	193002
Contig ID	8216_1.R1039
5'-most EST	LIB3083-080-Q1-L1-G12
Method	BLASTX
NCBI GI	g3482933
BLAST score	579
E value	4.0e-61
Match length	151
% identity	73
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	193003
Contig ID	8217_1.R1039
5'-most EST	LIB3083-080-Q1-L1-G2
Method	BLASTX
NCBI GI	g2347199

BLAST score	1294
E value	1.0e-143
Match length	406
% identity	63
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	193004
Contig ID	8218_1.R1039
5'-most EST	g5045343
Method	BLASTN
NCBI GI	g3395421
BLAST score	34
E value	7.0e-09
Match length	77
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	193005
Contig ID	8219_1.R1039
5'-most EST	LIB3120-028-Q1-K1-C8
Method	BLASTX
NCBI GI	g4432855
BLAST score	418
E value	4.0e-41
Match length	131
% identity	68
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	193006
Contig ID	8221_1.R1039
5'-most EST	uC-gsronu33B163c02b2
Method	BLASTX
NCBI GI	g2828296
BLAST score	1864
E value	0.0e+00
Match length	437
% identity	58
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	193007
Contig ID	8221_2.R1039
5'-most EST	LIB3135-028-Q1-K1-D10
Method	BLASTX
NCBI GI	g2828296
BLAST score	430
E value	3.0e-42
Match length	93
% identity	59
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	193008
Contig ID	8224_1.R1039
5'-most EST	uC-gsflnu33B092d08b1
Method	BLASTX
NCBI GI	g3360289
BLAST score	1315

E value	1.0e-145
Match length	380
% identity	66
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	193009
Contig ID	8225_1.R1039
5'-most EST	LIB3166-043-P1-K1-H1
Method	BLASTX
NCBI GI	g4415942
BLAST score	453
E value	7.0e-49
Match length	171
% identity	63
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193010
Contig ID	8226_1.R1039
5'-most EST	LIB3166-052-P1-K1-C6

Seq. No.	193011
Contig ID	8228_1.R1039
5'-most EST	uC-gsflnu33B114e08b1
Method	BLASTX
NCBI GI	g629692
BLAST score	456
E value	2.0e-45
Match length	127
% identity	71
NCBI Description	hypothetical protein - common tobacco >gi|506471|emb|CAA56189| (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No.	193012
Contig ID	8231_1.R1039
5'-most EST	g5049878
Method	BLASTX
NCBI GI	g3868853
BLAST score	439
E value	5.0e-43
Match length	113
% identity	72
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	193013
Contig ID	8232_1.R1039
5'-most EST	uC-gsronu33B150g06b1

Seq. No.	193014
Contig ID	8237_1.R1039
5'-most EST	LIB3083-081-Q1-L1-A1
Method	BLASTX
NCBI GI	g2829894
BLAST score	604
E value	1.0e-62
Match length	181

% identity	65
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	193015
Contig ID	8238_1.R1039
5'-most EST	g5050529
Method	BLASTX
NCBI GI	g4220527
BLAST score	903
E value	3.0e-97
Match length	333
% identity	53
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	193016
Contig ID	8238_2.R1039
5'-most EST	LIB3197-002-P1-M1-D10
Method	BLASTX
NCBI GI	g4220527
BLAST score	185
E value	1.0e-13
Match length	54
% identity	67
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	193017
Contig ID	8239_1.R1039
5'-most EST	LIB3083-081-Q1-L1-A11
Method	BLASTX
NCBI GI	g3355470
BLAST score	431
E value	2.0e-42
Match length	124
% identity	68
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	193018
Contig ID	8241_1.R1039
5'-most EST	uC-gsflnu33B031f05b1
Method	BLASTX
NCBI GI	g4097569
BLAST score	148
E value	2.0e-09
Match length	36
% identity	78
NCBI Description	(U64915) GMFP4 [Glycine max]

Seq. No.	193019
Contig ID	8242_1.R1039
5'-most EST	uC-gsronu33B019a06b1
Method	BLASTX
NCBI GI	g4454026
BLAST score	399
E value	3.0e-44
Match length	151
% identity	68

NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	193020
Contig ID	8244_1.R1039
5'-most EST	LIB3165-002-Q1-K1-B11
Method	BLASTX
NCBI GI	g4510345
BLAST score	333
E value	1.0e-30
Match length	168
% identity	43
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	193021
Contig ID	8248_1.R1039
5'-most EST	g5044700
Method	BLASTX
NCBI GI	g2384956
BLAST score	203
E value	2.0e-15
Match length	127
% identity	40
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	193022
Contig ID	8248_2.R1039
5'-most EST	LIB3120-045-P1-K1-B8
Method	BLASTX
NCBI GI	g2384956
BLAST score	146
E value	3.0e-09
Match length	112
% identity	35
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	193023
Contig ID	8251_1.R1039
5'-most EST	LIB3083-081-Q1-L1-B11
Method	BLASTX
NCBI GI	g3402722
BLAST score	488
E value	4.0e-49
Match length	122
% identity	76
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	193024
Contig ID	8254_1.R1039
5'-most EST	g5047675
Method	BLASTX
NCBI GI	g4510345
BLAST score	269
E value	2.0e-23
Match length	130
% identity	43

NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.	193025
Contig ID	8255_1.R1039
5'-most EST	LIB3165-034-P1-K3-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	731
E value	2.0e-77
Match length	212
% identity	52
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]
Seq. No.	193026
Contig ID	8262_1.R1039
5'-most EST	uC-gsflnu33B109a05b1
Method	BLASTX
NCBI GI	g4056420
BLAST score	497
E value	7.0e-50
Match length	176
% identity	57
NCBI Description	(AC005322) ESTs gb|T144077 and gb|T43352 come from this gene. [Arabidopsis thaliana]
Seq. No.	193027
Contig ID	8265_1.R1039
5'-most EST	LIB3272-028-P1-K1-B5
Method	BLASTX
NCBI GI	g2370312
BLAST score	1459
E value	1.0e-162
Match length	422
% identity	67
NCBI Description	(AJ000995) DnaJ-like protein [Medicago sativa] >gi|3202020 (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
Seq. No.	193028
Contig ID	8265_2.R1039
5'-most EST	uC-gsflnu33B009d02b1
Method	BLASTX
NCBI GI	g2984709
BLAST score	168
E value	1.0e-11
Match length	71
% identity	46
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	193029
Contig ID	8266_1.R1039
5'-most EST	LIB3197-022-Q1-M1-F10
Seq. No.	193030
Contig ID	8267_1.R1039
5'-most EST	LIB3197-004-P1-M1-A3
Method	BLASTX
NCBI GI	g1665817

BLAST score	164
E value	7.0e-11
Match length	96
% identity	35
NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	193031
Contig ID	8267_2.R1039
5'-most EST	LIB3166-028-P1-K1-A4

Seq. No.	193032
Contig ID	8268_1.R1039
5'-most EST	LIB3083-081-Q1-L1-C5

Seq. No.	193033
Contig ID	8269_1.R1039
5'-most EST	uC-gsronu33B129c06b1
Method	BLASTX
NCBI GI	g4545262
BLAST score	159
E value	1.0e-10
Match length	44
% identity	64
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	193034
Contig ID	8269_2.R1039
5'-most EST	LIB3166-047-P1-K1-H9
Method	BLASTX
NCBI GI	g4545262
BLAST score	165
E value	2.0e-11
Match length	44
% identity	66
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	193035
Contig ID	8269_3.R1039
5'-most EST	LIB3148-059-Q1-K1-C2
Method	BLASTX
NCBI GI	g4545262
BLAST score	163
E value	4.0e-11
Match length	43
% identity	67
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	193036
Contig ID	8281_1.R1039
5'-most EST	LIB3272-007-P1-K1-F12
Method	BLASTX
NCBI GI	g4510363
BLAST score	703

E value	4.0e-74
Match length	146
% identity	89
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	193037
Contig ID	8281_2.R1039
5'-most EST	uC-gsronu33B037a04b1
Method	BLASTX
NCBI GI	g4510363
BLAST score	672
E value	1.0e-70
Match length	137
% identity	89
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	193038
Contig ID	8282_1.R1039
5'-most EST	LIB3197-013-P1-M1-A4
Method	BLASTX
NCBI GI	g3582436
BLAST score	1182
E value	1.0e-130
Match length	315
% identity	70
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	193039
Contig ID	8283_1.R1039
5'-most EST	uC-gsronu33B018d05b1
Method	BLASTX
NCBI GI	g4098129
BLAST score	1340
E value	1.0e-148
Match length	318
% identity	79
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	193040
Contig ID	8285_1.R1039
5'-most EST	uC-gsflmaxxa040d08b1
Method	BLASTX
NCBI GI	g3983665
BLAST score	501
E value	8.0e-51
Match length	127
% identity	77
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	193041
Contig ID	8286_1.R1039
5'-most EST	LIB3149-046-Q1-K1-G10
Method	BLASTX
NCBI GI	g2832623
BLAST score	388

E value	4.0e-37
Match length	111
% identity	65
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	193042
Contig ID	8288_1.R1039
5'-most EST	LIB3145-038-Q1-K1-G6
Method	BLASTX
NCBI GI	g4406763
BLAST score	202
E value	2.0e-15
Match length	150
% identity	37
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	193043
Contig ID	8294_1.R1039
5'-most EST	LIB3083-081-Q1-L1-E7
Method	BLASTX
NCBI GI	g1946355
BLAST score	280
E value	1.0e-24
Match length	193
% identity	35
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi|2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	193044
Contig ID	8297_1.R1039
5'-most EST	uC-gsronu33B011a10b1
Method	BLASTX
NCBI GI	g3927830
BLAST score	629
E value	1.0e-65
Match length	230
% identity	45
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193045
Contig ID	8299_1.R1039
5'-most EST	LIB3083-081-Q1-L1-F11

Seq. No.	193046
Contig ID	8300_1.R1039
5'-most EST	LIB3272-020-P1-K1-C1
Method	BLASTN
NCBI GI	g3033373
BLAST score	45
E value	1.0e-15
Match length	363
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	193047
Contig ID	8306_1.R1039
5'-most EST	LIB3135-011-Q1-K1-D5
Method	BLASTX
NCBI GI	g3335350
BLAST score	313
E value	3.0e-28
Match length	242
% identity	33
NCBI Description	(AC004512) Similar to gb|Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	193048
Contig ID	8312_1.R1039
5'-most EST	uC-gsronu33B037a06b1
Method	BLASTX
NCBI GI	g2144270
BLAST score	248
E value	1.0e-21
Match length	81
% identity	68
NCBI Description	trans-cinnamate 4-monooxygenase (EC 1.14.13.11) B - Populus kitakamiensis (fragment) >gi|1777371|dbj|BAA11577| (D82813) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No.	193049
Contig ID	8314_1.R1039
5'-most EST	LIB3147-057-Q1-K1-D2
Method	BLASTX
NCBI GI	g2605932
BLAST score	596
E value	1.0e-61
Match length	145
% identity	81
NCBI Description	(AF029898) aspartate aminotransferase [Lotus corniculatus]

Seq. No.	193050
Contig ID	8315_1.R1039
5'-most EST	LIB3083-081-Q1-L1-G5
Method	BLASTX
NCBI GI	g2950210
BLAST score	324
E value	4.0e-30
Match length	87
% identity	76
NCBI Description	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	193051
Contig ID	8324_1.R1039
5'-most EST	g5046588
Method	BLASTX
NCBI GI	g2213628
BLAST score	281
E value	3.0e-26
Match length	269
% identity	35

NCBI Description	(AC000103) F21J9.20 [Arabidopsis thaliana]

Seq. No.	193052
Contig ID	8336_1.R1039
5'-most EST	LIB3165-018-P1-K1-F8
Method	BLASTX
NCBI GI	g3176072
BLAST score	1377
E value	1.0e-153
Match length	277
% identity	91
NCBI Description	(AJ002485) protein phosphatase 1, catalytic beta subunit [Medicago sativa]

Seq. No.	193053
Contig ID	8339_1.R1039
5'-most EST	g5045771
Method	BLASTX
NCBI GI	g2880042
BLAST score	354
E value	2.0e-33
Match length	168
% identity	46
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	193054
Contig ID	8340_1.R1039
5'-most EST	g5045156
Method	BLASTX
NCBI GI	g2494320
BLAST score	414
E value	2.0e-40
Match length	92
% identity	88
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi|1806575|emb|CAA67868| (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	193055
Contig ID	8340_2.R1039
5'-most EST	g5047453
Method	BLASTX
NCBI GI	g4160402
BLAST score	1027
E value	1.0e-112
Match length	352
% identity	63
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No.	193056
Contig ID	8344_1.R1039
5'-most EST	LIB3083-082-Q1-L1-B3
Method	BLASTX
NCBI GI	g4490737
BLAST score	430

E value 2.0e-42
Match length 166
% identity 30
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 193057
Contig ID 8344_2.R1039
5'-most EST uC-gsronu33B139e07b1
Method BLASTX
NCBI GI g4490737
BLAST score 341
E value 7.0e-32
Match length 122
% identity 60
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 193058
Contig ID 8344_3.R1039
5'-most EST LIB3145-045-Q1-K1-G1
Method BLASTX
NCBI GI g4490737
BLAST score 310
E value 2.0e-28
Match length 87
% identity 72
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 193059
Contig ID 8346_1.R1039
5'-most EST uC-gsronu33B062e11b1

Seq. No. 193060
Contig ID 8353_1.R1039
5'-most EST LIB3083-082-Q1-L1-C12
Method BLASTX
NCBI GI g3367571
BLAST score 242
E value 2.0e-20
Match length 62
% identity 69
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 193061
Contig ID 8355_1.R1039
5'-most EST g5044930
Method BLASTX
NCBI GI g2467274
BLAST score 266
E value 6.0e-23
Match length 116
% identity 52
NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 193062
Contig ID 8361_1.R1039
5'-most EST LIB3083-082-Q1-L1-D1
Method BLASTX

NCBI GI	g1351595
BLAST score	157
E value	2.0e-10
Match length	70
% identity	27
NCBI Description	HYPOTHETICAL 88.2 KD PROTEIN C4G8.03C IN CHROMOSOME I >gi|2130430|pir||S62480 hypothetical protein SPAC4G8.03c - fission yeast (Schizosaccharomyces pombe) >gi|1022348|emb|CAA91204| (Z56276) unknown [Schizosaccharomyces pombe]

Seq. No.	193063
Contig ID	8365_1.R1039
5'-most EST	uC-gsflmaxxa038g11b1

Seq. No.	193064
Contig ID	8367_1.R1039
5'-most EST	LIB3083-082-Q1-L1-D5
Method	BLASTX
NCBI GI	g3860255
BLAST score	193
E value	1.0e-14
Match length	73
% identity	62
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193065
Contig ID	8368_1.R1039
5'-most EST	g5049415
Method	BLASTX
NCBI GI	g120669
BLAST score	857
E value	4.0e-92
Match length	198
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|66014|pir||DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi|19566|emb|CAA42905| (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	193066
Contig ID	8368_2.R1039
5'-most EST	g5045768
Method	BLASTX
NCBI GI	g120669
BLAST score	895
E value	1.0e-161
Match length	331
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|66014|pir||DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi|19566|emb|CAA42905| (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 193067

Contig ID	8369_1.R1039
5'-most EST	LIB3166-033-P1-K1-G1
Method	BLASTX
NCBI GI	g3461817
BLAST score	288
E value	1.0e-25
Match length	65
% identity	82
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	193068
Contig ID	8370_1.R1039
5'-most EST	g5047566
Method	BLASTX
NCBI GI	g4006914
BLAST score	1576
E value	1.0e-176
Match length	423
% identity	71
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No.	193069
Contig ID	8372_1.R1039
5'-most EST	g5048498
Method	BLASTX
NCBI GI	g3142290
BLAST score	814
E value	3.0e-87
Match length	207
% identity	80
NCBI Description	(AC002411) Contains similarity to gb|Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	193070
Contig ID	8373_1.R1039
5'-most EST	LIB3083-082-Q1-L1-E10
Method	BLASTX
NCBI GI	g4455275
BLAST score	184
E value	3.0e-13
Match length	223
% identity	21
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	193071
Contig ID	8377_1.R1039
5'-most EST	LIB3196-028-P1-M1-F3
Method	BLASTX
NCBI GI	g2852449
BLAST score	765
E value	2.0e-81
Match length	202
% identity	77
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi|2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	193072
Contig ID	8380_1.R1039
5'-most EST	LIB3148-012-Q1-K1-C12

Seq. No.	193073
Contig ID	8381_1.R1039
5'-most EST	LIB3083-082-Q1-L1-E7
Method	BLASTX
NCBI GI	g3212865
BLAST score	677
E value	2.0e-71
Match length	160
% identity	84
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	193074
Contig ID	8382_1.R1039
5'-most EST	LIB3083-082-Q1-L1-E8
Method	BLASTX
NCBI GI	g2914700
BLAST score	1170
E value	1.0e-129
Match length	240
% identity	55
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	193075
Contig ID	8383_1.R1039
5'-most EST	uC-gsronu33B099a02b1

Seq. No.	193076
Contig ID	8388_1.R1039
5'-most EST	LIB3165-038-Q1-K1-E4

Seq. No.	193077
Contig ID	8389_1.R1039
5'-most EST	LIB3083-082-Q1-L1-F3
Method	BLASTX
NCBI GI	g2435518
BLAST score	321
E value	2.0e-40
Match length	119
% identity	77
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	193078
Contig ID	8394_1.R1039
5'-most EST	LIB3083-082-Q1-L1-F8

Seq. No.	193079
Contig ID	8397_1.R1039
5'-most EST	LIB3145-024-Q1-K1-C1
Method	BLASTX
NCBI GI	g4262140
BLAST score	298

E value 9.0e-27
Match length 111
% identity 57
NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No. 193080
Contig ID 8399_1.R1039
5'-most EST g5050403
Method BLASTX
NCBI GI g1871192
BLAST score 746
E value 4.0e-79
Match length 288
% identity 62
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 193081
Contig ID 8400_1.R1039
5'-most EST LIB3083-082-Q1-L1-G2
Method BLASTX
NCBI GI g2281115
BLAST score 405
E value 2.0e-39
Match length 175
% identity 54
NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No. 193082
Contig ID 8406_1.R1039
5'-most EST LIB3166-010-P1-K1-H7
Method BLASTX
NCBI GI g116923
BLAST score 317
E value 4.0e-29
Match length 187
% identity 39
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi|111414|pir||S13520 beta-COP protein - rat >gi|55819|emb|CAA40505| (X57228) beta COP [Rattus norvegicus]

Seq. No. 193083
Contig ID 8407_1.R1039
5'-most EST g5047501
Method BLASTX
NCBI GI g2959324
BLAST score 549
E value 4.0e-56
Match length 128
% identity 81
NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No. 193084
Contig ID 8427_1.R1039
5'-most EST LIB3083-083-Q1-L1-A5

Method	BLASTX
NCBI GI	g464987
BLAST score	779
E value	5.0e-83
Match length	148
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi|421858|pir||S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi|297878|emb|CAA78715| (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi|349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	193085
Contig ID	8429_1.R1039
5'-most EST	g5047240
Method	BLASTX
NCBI GI	g441457
BLAST score	787
E value	5.0e-84
Match length	148
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	193086
Contig ID	8429_2.R1039
5'-most EST	LIB3146-041-Q1-K1-D4
Method	BLASTX
NCBI GI	g464987
BLAST score	788
E value	4.0e-84
Match length	148
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi|421858|pir||S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi|297878|emb|CAA78715| (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi|349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	193087
Contig ID	8429_3.R1039
5'-most EST	LIB3083-083-Q1-L1-A8
Method	BLASTN
NCBI GI	g297877
BLAST score	187
E value	1.0e-100
Match length	447
% identity	85
NCBI Description	A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog >gi|349212|gb|L00640|ATHUBCC Arabidopsis thaliana ubiquitin conjugating enzyme mRNA, complete cds

Seq. No.	193088

Contig ID	8433_1.R1039
5'-most EST	LIB3197-054-Q1-M1-C5
Method	BLASTX
NCBI GI	g4406372
BLAST score	1052
E value	1.0e-115
Match length	259
% identity	76
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	193089
Contig ID	8435_1.R1039
5'-most EST	LIB3083-083-Q1-L1-B2
Method	BLASTX
NCBI GI	g1839578
BLAST score	2148
E value	0.0e+00
Match length	635
% identity	64
NCBI Description	vacuolar invertase 1, GIN1 [Vitis vinifera=grape berries, Sultana, berries, Peptide, 642 aa]

Seq. No.	193090
Contig ID	8439_1.R1039
5'-most EST	g5044979

Seq. No.	193091
Contig ID	8439_2.R1039
5'-most EST	LIB3189-044-P1-K1-A3

Seq. No.	193092
Contig ID	8447_1.R1039
5'-most EST	uC-gsflmaxxa098f12b1
Method	BLASTX
NCBI GI	g4006868
BLAST score	278
E value	2.0e-24
Match length	166
% identity	40
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	193093
Contig ID	8449_1.R1039
5'-most EST	g5049149
Method	BLASTX
NCBI GI	g2498982
BLAST score	330
E value	2.0e-30
Match length	129
% identity	50
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT (TAFII-31) (TAFII-32) (TAFII32) (NEURONAL CELL DEATH RELATED GENE IN NEURON -7) (DN-7) >gi|1103900 (U40188) induced upon programmed cell death in neuronally differentiated PC12 cells [Rattus norvegicus]

Seq. No.	193094
Contig ID	8454_1.R1039
5'-most EST	LIB3083-083-Q1-L1-D12
Method	BLASTX
NCBI GI	g3687389
BLAST score	854
E value	5.0e-92
Match length	189
% identity	88
NCBI Description	(Y16124) putative cullin protein [Lycopersicon esculentum]

Seq. No.	193095
Contig ID	8463_1.R1039
5'-most EST	LIB3083-109-Q1-L1-D2

Seq. No.	193096
Contig ID	8465_1.R1039
5'-most EST	LIB3147-036-Q1-K1-D11
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	2.0e-20
Match length	61
% identity	80
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	193097
Contig ID	8465_2.R1039
5'-most EST	LIB3083-100-Q1-L1-A12
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	9.0e-21
Match length	61
% identity	80
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	193098
Contig ID	8468_1.R1039
5'-most EST	LIB3135-014-Q1-K1-E6
Method	BLASTX
NCBI GI	g3193287
BLAST score	604
E value	1.0e-62
Match length	150
% identity	69
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	193099
Contig ID	8472_1.R1039
5'-most EST	g3326550

Seq. No.	193100
Contig ID	8479_1.R1039

5'-most EST	LIB3083-083-Q1-L1-F4
Method	BLASTX
NCBI GI	g3158474
BLAST score	1323
E value	1.0e-146
Match length	282
% identity	90
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	193101
Contig ID	8479_2.R1039
5'-most EST	LIB3135-028-Q1-K1-G6
Method	BLASTX
NCBI GI	g401189
BLAST score	469
E value	4.0e-47
Match length	111
% identity	83
NCBI Description	WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi|485511|pir||S33617 trg-31 protein - garden pea >gi|20426|emb|CAA79159| (Z18288) trg-31 [Pisum sativum]

Seq. No.	193102
Contig ID	8479_4.R1039
5'-most EST	uC-gsronu33B037g11b1
Method	BLASTX
NCBI GI	g3183640
BLAST score	268
E value	3.0e-23
Match length	52
% identity	96
NCBI Description	(AJ005869) transmembrane channel protein [Cicer arietinum]

Seq. No.	193103
Contig ID	8479_5.R1039
5'-most EST	LIB3149-063-Q1-K1-A2
Method	BLASTX
NCBI GI	g2149955
BLAST score	423
E value	2.0e-49
Match length	139
% identity	77
NCBI Description	(U97023) putative aquaporin-1 [Phaseolus vulgaris]

Seq. No.	193104
Contig ID	8482_1.R1039
5'-most EST	LIB3196-049-P1-M1-A4
Method	BLASTX
NCBI GI	g2493852
BLAST score	291
E value	6.0e-26
Match length	63
% identity	84
NCBI Description	CYTOCHROME C OXIDASE POLYPEPTIDE VC >gi|1070356|emb|CAA92107| (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare]

Seq. No. 193105
Contig ID 8486_1.R1039
5'-most EST g5050102
Method BLASTX
NCBI GI g4371295
BLAST score 502
E value 2.0e-50
Match length 127
% identity 79
NCBI Description (AC006260) putative CCAAT-binding transcription factor [Arabidopsis thaliana]

Seq. No. 193106
Contig ID 8487_1.R1039
5'-most EST LIB3166-050-P1-K1-E11

Seq. No. 193107
Contig ID 8489_1.R1039
5'-most EST uC-gsflnu33B071g02b1

Seq. No. 193108
Contig ID 8491_1.R1039
5'-most EST g5047125
Method BLASTX
NCBI GI g98837
BLAST score 200
E value 4.0e-15
Match length 123
% identity 37
NCBI Description enantiomer-selective amidase - Rhodococcus sp >gi|152052 (M74531) enantiomerase-selective amidase [Rhodococcus sp.]

Seq. No. 193109
Contig ID 8502_1.R1039
5'-most EST g3326588
Method BLASTX
NCBI GI g3928084
BLAST score 1125
E value 1.0e-123
Match length 390
% identity 58
NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 193110
Contig ID 8506_1.R1039
5'-most EST LIB3189-007-P1-K1-D1
Method BLASTX
NCBI GI g2702272
BLAST score 693
E value 1.0e-94
Match length 333
% identity 23
NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No. 193111

Contig ID 8521_1.R1039
5'-most EST LIB3083-087-Q1-L1-A6
Method BLASTX
NCBI GI g2388689
BLAST score 701
E value 3.0e-74
Match length 154
% identity 86
NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 193112
Contig ID 8527_1.R1039
5'-most EST LIB3197-012-P1-M1-E12

Seq. No. 193113
Contig ID 8533_1.R1039
5'-most EST uC-gsronu33B134h10b1

Seq. No. 193114
Contig ID 8552_1.R1039
5'-most EST LIB3083-087-Q1-L1-E9
Method BLASTX
NCBI GI g2564112
BLAST score 537
E value 1.0e-54
Match length 231
% identity 46
NCBI Description (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No. 193115
Contig ID 8555_1.R1039
5'-most EST LIB3083-087-Q1-L1-F4
Method BLASTX
NCBI GI g3367523
BLAST score 405
E value 1.0e-39
Match length 117
% identity 64
NCBI Description (AC004392) ESTs gb|AA728658 and gb|N95943 come from this gene. [Arabidopsis thaliana]

Seq. No. 193116
Contig ID 8556_1.R1039
5'-most EST LIB3166-014-P1-K1-G8
Method BLASTX
NCBI GI g3193316
BLAST score 306
E value 1.0e-27
Match length 139
% identity 53
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 193117
Contig ID 8557_1.R1039
5'-most EST g5049736

Method	BLASTX
NCBI GI	g4325367
BLAST score	201
E value	3.0e-15
Match length	101
% identity	49
NCBI Description	(AF128396) contains similarity to Nicotiana tabacum B-type cyclin (GB:D50737) [Arabidopsis thaliana]

Seq. No.	193118
Contig ID	8559_1.R1039
5'-most EST	LIB3083-090-Q1-L1-A3
Method	BLASTX
NCBI GI	g2160156
BLAST score	581
E value	4.0e-60
Match length	156
% identity	67
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb|Z73100). [Arabidopsis thaliana]

Seq. No.	193119
Contig ID	8575_1.R1039
5'-most EST	LIB3196-029-P1-M1-B6
Method	BLASTX
NCBI GI	g4530585
BLAST score	357
E value	1.0e-33
Match length	85
% identity	74
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	193120
Contig ID	8575_2.R1039
5'-most EST	LIB3147-009-Q1-K1-G1

Seq. No.	193121
Contig ID	8575_3.R1039
5'-most EST	LIB3148-055-Q1-K1-B8
Method	BLASTX
NCBI GI	g4530585
BLAST score	109
E value	5.0e-11
Match length	86
% identity	47
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	193122
Contig ID	8578_1.R1039
5'-most EST	uC-gsronu33B167e04b1
Method	BLASTX
NCBI GI	g1172872
BLAST score	1400
E value	1.0e-155
Match length	331
% identity	79
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi|541856|pir||JN0718

drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi|435618|dbj|BAA02373| (D13042) thiol protease [Arabidopsis thaliana] >gi|4539328|emb|CAB38829.1| (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	193123
Contig ID	8578_2.R1039
5'-most EST	LIB3165-048-Q1-K1-H2
Method	BLASTX
NCBI GI	g1172872
BLAST score	310
E value	2.0e-28
Match length	132
% identity	56
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi|541856|pir||JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi|435618|dbj|BAA02373| (D13042) thiol protease [Arabidopsis thaliana] >gi|4539328|emb|CAB38829.1| (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	193124
Contig ID	8588_1.R1039
5'-most EST	g5048493
Method	BLASTX
NCBI GI	g3172538
BLAST score	820
E value	6.0e-88
Match length	225
% identity	74
NCBI Description	(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No.	193125
Contig ID	8588_2.R1039
5'-most EST	uC-gsflnu33B090c03b1
Method	BLASTX
NCBI GI	g3172538
BLAST score	436
E value	7.0e-43
Match length	108
% identity	78
NCBI Description	(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No.	193126
Contig ID	8593_1.R1039
5'-most EST	LIB3147-050-Q1-K1-F4
Method	BLASTX
NCBI GI	g1871195
BLAST score	601
E value	1.0e-109
Match length	306
% identity	61
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi|2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	193127
Contig ID	8600_1.R1039
5'-most EST	LIB3083-088-Q1-L1-D6
Method	BLASTX
NCBI GI	g3367522
BLAST score	538
E value	8.0e-55
Match length	200
% identity	54
NCBI Description	(AC004392) EST gb|T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	193128
Contig ID	8607_1.R1039
5'-most EST	LIB3197-026-Q1-M1-B7
Method	BLASTX
NCBI GI	g4150963
BLAST score	280
E value	1.0e-24
Match length	171
% identity	39
NCBI Description	(Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No.	193129
Contig ID	8608_1.R1039
5'-most EST	LIB3147-011-Q1-K1-E6
Method	BLASTX
NCBI GI	g3309243
BLAST score	745
E value	4.0e-79
Match length	169
% identity	84
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	193130
Contig ID	8608_2.R1039
5'-most EST	g5048653
Method	BLASTX
NCBI GI	g3309243
BLAST score	935
E value	1.0e-101
Match length	193
% identity	91
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	193131
Contig ID	8619_1.R1039
5'-most EST	uC-gsflnu33B143b03b1
Method	BLASTX
NCBI GI	g2506496
BLAST score	691
E value	1.0e-72
Match length	210
% identity	64
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)

>gi|1890156|emb|CAA72413| (Y11727) gluthatione S-transferase [Arabidopsis thaliana]

Seq. No.	193132
Contig ID	8620_1.R1039
5'-most EST	LIB3135-044-Q1-K1-F3
Method	BLASTX
NCBI GI	g1710807
BLAST score	1707
E value	0.0e+00
Match length	414
% identity	84
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi|1185390 (U21105) alphacpn60 [Pisum sativum]

Seq. No.	193133
Contig ID	8623_1.R1039
5'-most EST	LIB3197-027-Q1-M1-E11
Method	BLASTX
NCBI GI	g3551954
BLAST score	204
E value	9.0e-16
Match length	95
% identity	41
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	193134
Contig ID	8626_1.R1039
5'-most EST	LIB3083-091-Q1-L1-G10
Method	BLASTX
NCBI GI	g418904
BLAST score	635
E value	3.0e-66
Match length	199
% identity	69
NCBI Description	heat shock protein 83 - Arabidopsis thaliana >gi|166770 (M62984) heat shock protein 83 [Arabidopsis thaliana]

Seq. No.	193135
Contig ID	8627_1.R1039
5'-most EST	uC-gsronu33B141e01b1
Method	BLASTX
NCBI GI	g2879811
BLAST score	519
E value	1.0e-52
Match length	101
% identity	95
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	193136
Contig ID	8627_2.R1039
5'-most EST	LIB3165-058-P1-K1-F3
Method	BLASTX
NCBI GI	g2879811
BLAST score	516

E value	2.0e-52
Match length	101
% identity	94
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	193137
Contig ID	8627_4.R1039
5'-most EST	LIB3196-020-P1-M1-C4
Method	BLASTX
NCBI GI	g4115933
BLAST score	381
E value	1.0e-36
Match length	122
% identity	71
NCBI Description	(AF118223) contains similarity to human RNA polymerase II complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No.	193138
Contig ID	8636_1.R1039
5'-most EST	LIB3272-009-P1-K1-G1
Method	BLASTX
NCBI GI	g4220518
BLAST score	483
E value	3.0e-48
Match length	203
% identity	48
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193139
Contig ID	8636_2.R1039
5'-most EST	LIB3145-023-Q1-K1-G5
Method	BLASTX
NCBI GI	g1350956
BLAST score	550
E value	4.0e-56
Match length	117
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	193140
Contig ID	8636_3.R1039
5'-most EST	uC-gsflnu33B115b10b1
Method	BLASTX
NCBI GI	g1350956
BLAST score	550
E value	3.0e-56
Match length	117
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	193141
Contig ID	8636_5.R1039
5'-most EST	LIB3189-023-P1-K1-E2
Method	BLASTX
NCBI GI	g1350956
BLAST score	483
E value	1.0e-48

Match length	100
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	193142
Contig ID	8637_1.R1039
5'-most EST	LIB3197-054-Q1-M1-E12
Method	BLASTX
NCBI GI	g1345965
BLAST score	1018
E value	1.0e-111
Match length	246
% identity	84
NCBI Description	FLORAL HOMEOTIC PROTEIN FBP2 (FLORAL BINDING PROTEIN 2) >gi|1181186 (M91666) transcription factor [Petunia hybrida]

Seq. No.	193143
Contig ID	8640_1.R1039
5'-most EST	g5046350
Method	BLASTX
NCBI GI	g3023751
BLAST score	194
E value	2.0e-14
Match length	121
% identity	36
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi|1076772|pir||S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi|854626|emb|CAA60505| (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	193144
Contig ID	8640_2.R1039
5'-most EST	LIB3166-040-P1-K1-D8

Seq. No.	193145
Contig ID	8643_1.R1039
5'-most EST	uC-gsronu33B110d11b1
Method	BLASTX
NCBI GI	g3668086
BLAST score	638
E value	2.0e-66
Match length	216
% identity	60
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	193146
Contig ID	8643_2.R1039
5'-most EST	LIB3145-002-P1-K1-A11
Method	BLASTX
NCBI GI	g3668086
BLAST score	353
E value	6.0e-35
Match length	125
% identity	64
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	193147
Contig ID	8649_1.R1039
5'-most EST	g5046825
Method	BLASTX
NCBI GI	g3582436
BLAST score	826
E value	1.0e-88
Match length	203
% identity	78
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	193148
Contig ID	8656_1.R1039
5'-most EST	LIB3083-089-Q1-L1-D8

Seq. No.	193149
Contig ID	8665_1.R1039
5'-most EST	LIB3083-089-Q1-L1-F11

Seq. No.	193150
Contig ID	8691_1.R1039
5'-most EST	g5045992
Method	BLASTX
NCBI GI	g1408471
BLAST score	630
E value	2.0e-65
Match length	139
% identity	84
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	193151
Contig ID	8691_2.R1039
5'-most EST	LIB3083-101-Q1-L1-E4
Method	BLASTX
NCBI GI	g1408471
BLAST score	633
E value	5.0e-66
Match length	139
% identity	86
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	193152
Contig ID	8700_1.R1039
5'-most EST	g5048857
Method	BLASTX
NCBI GI	g3953458
BLAST score	1020
E value	1.0e-111
Match length	237
% identity	88
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 193153

Contig ID	8701_1.R1039
5'-most EST	LIB3189-052-P1-K1-C12
Method	BLASTX
NCBI GI	g3193303
BLAST score	417
E value	7.0e-41
Match length	124
% identity	61
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	193154
Contig ID	8702_1.R1039
5'-most EST	LIB3083-090-Q1-L1-B8

Seq. No.	193155
Contig ID	8704_1.R1039
5'-most EST	LIB3166-045-P1-K1-H8
Method	BLASTX
NCBI GI	g4193388
BLAST score	743
E value	8.0e-79
Match length	168
% identity	85
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	193156
Contig ID	8713_2.R1039
5'-most EST	LIB3197-037-Q1-M1-A9
Method	BLASTX
NCBI GI	g4006848
BLAST score	347
E value	8.0e-33
Match length	89
% identity	76
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	193157
Contig ID	8718_1.R1039
5'-most EST	g5048264
Method	BLASTX
NCBI GI	g2244816
BLAST score	254
E value	1.0e-21
Match length	91
% identity	67
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193158
Contig ID	8719_1.R1039
5'-most EST	LIB3147-027-Q1-K1-B6
Method	BLASTX
NCBI GI	g4539327

BLAST score	392
E value	5.0e-38
Match length	130
% identity	63
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	193159
Contig ID	8720_1.R1039
5'-most EST	g3326558
Method	BLASTX
NCBI GI	g2149640
BLAST score	1396
E value	1.0e-155
Match length	317
% identity	84
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	193160
Contig ID	8731_1.R1039
5'-most EST	g3326294
Method	BLASTX
NCBI GI	g1707017
BLAST score	639
E value	4.0e-85
Match length	173
% identity	90
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	193161
Contig ID	8731_2.R1039
5'-most EST	LIB3197-045-Q1-M1-H7
Method	BLASTX
NCBI GI	g1707017
BLAST score	551
E value	5.0e-71
Match length	153
% identity	87
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	193162
Contig ID	8748_1.R1039
5'-most EST	LIB3083-090-Q1-L1-H1
Method	BLASTN
NCBI GI	g4159700
BLAST score	50
E value	9.0e-19
Match length	421
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence [Arabidopsis thaliana]

Seq. No.	193163
Contig ID	8750_1.R1039
5'-most EST	LIB3083-090-Q1-L1-H12
Method	BLASTX
NCBI GI	g4455174
BLAST score	323

E value	1.0e-32
Match length	128
% identity	66
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	193164
Contig ID	8750_2.R1039
5'-most EST	uC-gsronu33B159e08b1
Method	BLASTX
NCBI GI	g3650030
BLAST score	275
E value	8.0e-25
Match length	112
% identity	59
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	193165
Contig ID	8768_1.R1039
5'-most EST	LIB3083-091-Q1-L1-B5

Seq. No.	193166
Contig ID	8776_1.R1039
5'-most EST	uC-gsflmaxxa045h12b1

Seq. No.	193167
Contig ID	8778_1.R1039
5'-most EST	LIB3083-091-Q1-L1-E1
Method	BLASTX
NCBI GI	g4567251
BLAST score	546
E value	1.0e-55
Match length	129
% identity	73
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	193168
Contig ID	8783_1.R1039
5'-most EST	LIB3135-053-Q1-K1-G2
Method	BLASTX
NCBI GI	g2853081
BLAST score	424
E value	1.0e-41
Match length	115
% identity	69
NCBI Description	(AL021768) ATP binding protein - like [Arabidopsis thaliana]

Seq. No.	193169
Contig ID	8790_1.R1039
5'-most EST	uC-gsflmaxxa098c04b1
Method	BLASTX
NCBI GI	g2351378
BLAST score	328
E value	8.0e-38
Match length	327
% identity	37
NCBI Description	(U54558) translation initiation factor eIF3 p66 subunit

[Homo sapiens] >gi|4200328|emb|CAA18440| (AL022313) EIF3-P66 [Homo sapiens] >gi|4503523|ref|NP_003744.1|pEIF3S7| UNKNOWN

Seq. No.	193170
Contig ID	8791_1.R1039
5'-most EST	g5049018
Method	BLASTX
NCBI GI	g4008006
BLAST score	569
E value	1.0e-58
Match length	176
% identity	65
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	193171
Contig ID	8792_1.R1039
5'-most EST	LIB3145-035-Q1-K1-B7
Method	BLASTX
NCBI GI	g2244970
BLAST score	1387
E value	1.0e-154
Match length	332
% identity	74
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi|2326365|emb|CAA74765| (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	193172
Contig ID	8795_1.R1039
5'-most EST	LIB3197-026-Q1-M1-B12
Method	BLASTX
NCBI GI	g485742
BLAST score	523
E value	2.0e-53
Match length	110
% identity	93
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	193173
Contig ID	8804_1.R1039
5'-most EST	LIB3083-092-Q1-L1-A12

Seq. No.	193174
Contig ID	8806_1.R1039
5'-most EST	uC-gsflnu33B141d01b1
Method	BLASTX
NCBI GI	g123544
BLAST score	507
E value	2.0e-51
Match length	144
% identity	67
NCBI Description	18.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.5) >gi|81788|pir||S00646 heat shock protein 18.5-C - soybean >gi|18654|emb|CAA30154| (X07160) hsp18.5-C protein (AA 1 - 161) [Glycine max]

Seq. No.	193175
Contig ID	8810_1.R1039
5'-most EST	g5049313
Method	BLASTX
NCBI GI	g3882183
BLAST score	266
E value	2.0e-46
Match length	186
% identity	38
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]

Seq. No.	193176
Contig ID	8815_1.R1039
5'-most EST	uC-gsflnu33B135c03b1
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	4.0e-30
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi|481909|pir||S40089 ribosomal protein S25 - tomato >gi|435679|emb|CAA54132| (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi|1584836|prf||2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	193177
Contig ID	8832_1.R1039
5'-most EST	LIB3083-092-Q1-L1-F7
Method	BLASTX
NCBI GI	g3925363
BLAST score	522
E value	1.0e-54
Match length	152
% identity	81
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	193178
Contig ID	8839_1.R1039
5'-most EST	uC-gsflmaxxa057g05b1
Method	BLASTX
NCBI GI	g2982243
BLAST score	406
E value	2.0e-39
Match length	155
% identity	52
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	193179
Contig ID	8843_1.R1039
5'-most EST	LIB3189-028-P1-K1-G9
Method	BLASTX
NCBI GI	g2431771
BLAST score	251
E value	3.0e-21
Match length	113

% identity	48
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	193180
Contig ID	8843_2.R1039
5'-most EST	LIB3148-030-Q1-K1-H7

Seq. No.	193181
Contig ID	8843_3.R1039
5'-most EST	LIB3189-013-P1-K1-E8
Method	BLASTX
NCBI GI	g2431771
BLAST score	246
E value	7.0e-21
Match length	112
% identity	48
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	193182
Contig ID	8844_1.R1039
5'-most EST	LIB3146-022-Q1-K1-F3
Method	BLASTX
NCBI GI	g2335096
BLAST score	199
E value	5.0e-15
Match length	209
% identity	28
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193183
Contig ID	8848_1.R1039
5'-most EST	LIB3083-114-Q1-L1-F10
Method	BLASTX
NCBI GI	g4567304
BLAST score	399
E value	1.0e-38
Match length	181
% identity	45
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	193184
Contig ID	8853_1.R1039
5'-most EST	uC-gsflmaxxa090g03b1
Method	BLASTX
NCBI GI	g1172977
BLAST score	862
E value	8.0e-93
Match length	187
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi|606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	193185
Contig ID	8853_2.R1039
5'-most EST	uC-gsflnu33B026f10b1
Method	BLASTX
NCBI GI	g1172977

BLAST score	561
E value	1.0e-57
Match length	139
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi|606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	193186
Contig ID	8854_1.R1039
5'-most EST	uC-gsronu33B031a12b1
Method	BLASTX
NCBI GI	g4006876
BLAST score	342
E value	1.0e-31
Match length	272
% identity	38
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193187
Contig ID	8859_1.R1039
5'-most EST	uC-gsflmaxxa039d12b1
Method	BLASTX
NCBI GI	g730456
BLAST score	577
E value	2.0e-59
Match length	140
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	193188
Contig ID	8859_2.R1039
5'-most EST	g5045481
Method	BLASTX
NCBI GI	g730456
BLAST score	595
E value	1.0e-61
Match length	140
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	193189
Contig ID	8859_3.R1039
5'-most EST	g5048642
Method	BLASTX
NCBI GI	g730456
BLAST score	593
E value	3.0e-61
Match length	140
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	193190
Contig ID	8859_4.R1039
5'-most EST	LIB3146-028-Q1-K1-A7
Method	BLASTX
NCBI GI	g730456
BLAST score	593

E value	3.0e-61
Match length	140
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	193191
Contig ID	8861_1.R1039
5'-most EST	LIB3149-057-Q1-K1-C7

Seq. No.	193192
Contig ID	8862_1.R1039
5'-most EST	g3326817

Seq. No.	193193
Contig ID	8866_1.R1039
5'-most EST	LIB3083-120-Q1-L1-F1
Method	BLASTX
NCBI GI	g3953463
BLAST score	262
E value	9.0e-23
Match length	99
% identity	48
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	193194
Contig ID	8867_1.R1039
5'-most EST	LIB3197-027-Q1-M1-C2
Method	BLASTX
NCBI GI	g3036816
BLAST score	216
E value	6.0e-17
Match length	152
% identity	40
NCBI Description	(AL022373) myosin-like protein [Arabidopsis thaliana]

Seq. No.	193195
Contig ID	8869_1.R1039
5'-most EST	uC-gsflmaxxa048e08b1
Method	BLASTX
NCBI GI	g3702332
BLAST score	904
E value	2.0e-97
Match length	253
% identity	69
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	193196
Contig ID	8871_1.R1039
5'-most EST	LIB3083-094-Q1-L1-D2
Method	BLASTN
NCBI GI	g20419
BLAST score	44
E value	1.0e-15
Match length	272
% identity	15
NCBI Description	P.amygdalus mRNA for extensin

Seq. No.	193197
Contig ID	8878_1.R1039
5'-most EST	LIB3083-094-Q1-L1-D6
Method	BLASTX
NCBI GI	g3860008
BLAST score	427
E value	8.0e-42
Match length	138
% identity	61
NCBI Description	(AF091085) unknown [Homo sapiens]

Seq. No.	193198
Contig ID	8879_1.R1039
5'-most EST	LIB3272-041-P1-K1-E3
Method	BLASTX
NCBI GI	g4510345
BLAST score	482
E value	3.0e-48
Match length	158
% identity	58
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	193199
Contig ID	8888_1.R1039
5'-most EST	uC-gsronu33B109g10b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	51
E value	1.0e-19
Match length	95
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	193200
Contig ID	8890_1.R1039
5'-most EST	LIB3083-094-Q1-L1-E8
Method	BLASTX
NCBI GI	g3924848
BLAST score	193
E value	2.0e-14
Match length	161
% identity	32
NCBI Description	(Z81586) cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	193201
Contig ID	8890_2.R1039
5'-most EST	uC-gsflnu33B079g05b1

Seq. No.	193202
Contig ID	8892_1.R1039
5'-most EST	uC-gsflnu33B005a08b1
Method	BLASTX
NCBI GI	g3128176
BLAST score	341
E value	5.0e-32

Match length	115
% identity	56
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	193203
Contig ID	8895_1.R1039
5'-most EST	LIB3272-032-P1-K1-H7
Method	BLASTX
NCBI GI	g3264767
BLAST score	835
E value	3.0e-89
Match length	272
% identity	58
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	193204
Contig ID	8895_4.R1039
5'-most EST	LIB3146-002-P1-K2-A11
Method	BLASTX
NCBI GI	g3264767
BLAST score	417
E value	7.0e-41
Match length	151
% identity	54
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	193205
Contig ID	8906_1.R1039
5'-most EST	uC-gsflnu33B023b06b1
Method	BLASTX
NCBI GI	g3860250
BLAST score	1528
E value	1.0e-170
Match length	382
% identity	78
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	193206
Contig ID	8906_2.R1039
5'-most EST	LIB3166-026-P1-K1-D11
Method	BLASTX
NCBI GI	g1076501
BLAST score	288
E value	4.0e-25
Match length	82
% identity	66
NCBI Description	cell wall protein - alfalfa >gi|3818416 (AF028841) proline-rich cell wall protein [Medicago sativa]

Seq. No.	193207
Contig ID	8906_3.R1039
5'-most EST	uC-gsflnu33B085e09b1
Method	BLASTX
NCBI GI	g1076501
BLAST score	214
E value	4.0e-17

Match length	46
% identity	85
NCBI Description	cell wall protein - alfalfa >gi|3818416 (AF028841) proline-rich cell wall protein [Medicago sativa]

Seq. No.	193208
Contig ID	8906_4.R1039
5'-most EST	LIB3166-028-P1-K1-C4
Method	BLASTX
NCBI GI	g1076501
BLAST score	257
E value	1.0e-21
Match length	82
% identity	61
NCBI Description	cell wall protein - alfalfa >gi|3818416 (AF028841) proline-rich cell wall protein [Medicago sativa]

Seq. No.	193209
Contig ID	8916_1.R1039
5'-most EST	LIB3145-026-Q1-K1-D4
Method	BLASTX
NCBI GI	g4263787
BLAST score	560
E value	2.0e-57
Match length	186
% identity	67
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	193210
Contig ID	8917_1.R1039
5'-most EST	LIB3189-034-P1-K1-F11
Method	BLASTX
NCBI GI	g3983663
BLAST score	412
E value	2.0e-40
Match length	136
% identity	62
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]

Seq. No.	193211
Contig ID	8921_1.R1039
5'-most EST	LIB3083-095-Q1-L1-A12
Method	BLASTX
NCBI GI	g3142294
BLAST score	382
E value	9.0e-37
Match length	83
% identity	88
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb|U37354 from S. pombe. ESTs gb|T41979, gb|N37284 and gb|N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	193212
Contig ID	8923_1.R1039
5'-most EST	LIB3120-015-Q1-K1-G7

Seq. No.	193213

Contig ID	8926_1.R1039
5'-most EST	LIB3120-013-Q1-K1-F10
Method	BLASTX
NCBI GI	g1942360
BLAST score	340
E value	6.0e-32
Match length	121
% identity	49
NCBI Description	Actin-Binding Protein

Seq. No.	193214
Contig ID	8928_1.R1039
5'-most EST	g5050090
Method	BLASTX
NCBI GI	g2829865
BLAST score	601
E value	2.0e-62
Match length	137
% identity	88
NCBI Description	(AC002396) N-terminal region similar to DNA-J proteins [Arabidopsis thaliana]

Seq. No.	193215
Contig ID	8936_1.R1039
5'-most EST	g5046798
Method	BLASTX
NCBI GI	g1352660
BLAST score	227
E value	2.0e-18
Match length	137
% identity	36
NCBI Description	COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR >gi|924850 (U26264) CHOp24 [Cricetulus griseus]

Seq. No.	193216
Contig ID	8937_1.R1039
5'-most EST	uC-gsronu33B166b07b2
Method	BLASTX
NCBI GI	g3482933
BLAST score	592
E value	2.0e-61
Match length	151
% identity	72
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	193217
Contig ID	8946_1.R1039
5'-most EST	LIB3083-095-Q1-L1-C3

Seq. No.	193218
Contig ID	8953_1.R1039
5'-most EST	LIB3083-095-Q1-L1-D2
Method	BLASTX
NCBI GI	g3377820
BLAST score	387
E value	4.0e-37

Match length	123
% identity	64
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	193219
Contig ID	8956_1.R1039
5'-most EST	g5048016
Method	BLASTX
NCBI GI	g2194142
BLAST score	761
E value	6.0e-81
Match length	153
% identity	84
NCBI Description	(AC002062) ESTs gb|N38288,gb|T43486,gb|AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	193220
Contig ID	8965_1.R1039
5'-most EST	uC-gsflmaxxa061c01b1
Method	BLASTX
NCBI GI	g3914002
BLAST score	1611
E value	1.0e-180
Match length	393
% identity	80
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi|2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	193221
Contig ID	8966_1.R1039
5'-most EST	LIB3165-037-P1-K1-D3
Method	BLASTX
NCBI GI	g4204261
BLAST score	242
E value	7.0e-20
Match length	301
% identity	30
NCBI Description	(AC005223) 27887 [Arabidopsis thaliana]

Seq. No.	193222
Contig ID	8971_1.R1039
5'-most EST	LIB3083-097-Q1-L1-A5
Method	BLASTX
NCBI GI	g1657382
BLAST score	795
E value	4.0e-85
Match length	158
% identity	91
NCBI Description	(Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No.	193223
Contig ID	8972_1.R1039
5'-most EST	g3326528
Method	BLASTX
NCBI GI	g2204234

BLAST score	415
E value	2.0e-40
Match length	150
% identity	60
NCBI Description	(Y13862) enoyl-ACP reductase [Nicotiana tabacum]

Seq. No.	193224
Contig ID	8974_1.R1039
5'-most EST	uC-gsronu33B031g11b1

Seq. No.	193225
Contig ID	8976_1.R1039
5'-most EST	LIB3083-095-Q1-L1-F6
Method	BLASTX
NCBI GI	g3402713
BLAST score	571
E value	7.0e-59
Match length	170
% identity	66
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193226
Contig ID	8979_1.R1039
5'-most EST	LIB3146-010-Q1-K1-E11

Seq. No.	193227
Contig ID	8981_1.R1039
5'-most EST	LIB3165-006-P1-K3-B1
Method	BLASTX
NCBI GI	g2559012
BLAST score	1484
E value	1.0e-165
Match length	412
% identity	70
NCBI Description	(AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi|4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No.	193228
Contig ID	8981_2.R1039
5'-most EST	LIB3146-001-P1-K2-H5
Method	BLASTX
NCBI GI	g549056
BLAST score	1121
E value	1.0e-123
Match length	303
% identity	72
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi|631651|pir||S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi|468546|emb|CAA83428| (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	193229
Contig ID	8994_1.R1039
5'-most EST	LIB3083-095-Q1-L1-H4
Method	BLASTX

NCBI GI	g2065531
BLAST score	276
E value	2.0e-32
Match length	172
% identity	49
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	193230
Contig ID	8997_1.R1039
5'-most EST	uC-gsronu33B124h09b1
Method	BLASTX
NCBI GI	g1408471
BLAST score	547
E value	7.0e-56
Match length	139
% identity	76
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	193231
Contig ID	8997_2.R1039
5'-most EST	g5050291
Method	BLASTX
NCBI GI	g478673
BLAST score	383
E value	2.0e-36
Match length	126
% identity	60
NCBI Description	proline-rich protein precursor - kidney bean >gi|21046|emb|CAA42942| (X60391) proline-rich protein [Phaseolus vulgaris]

Seq. No.	193232
Contig ID	9006_1.R1039
5'-most EST	LIB3147-011-Q1-K1-G4
Method	BLASTX
NCBI GI	g418507
BLAST score	327
E value	4.0e-30
Match length	161
% identity	41
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi|541097|pir||S40872 hypothetical protein f161 - Escherichia coli >gi|305032 (L19201) ORF_f161 [Escherichia coli] >gi|1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi|1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	193233
Contig ID	9009_1.R1039
5'-most EST	LIB3148-058-Q1-K1-G10
Method	BLASTX
NCBI GI	g2668505
BLAST score	175
E value	1.0e-12

Match length	87
% identity	46
NCBI Description	(U61837) putative cyclin G1 interacting protein [Homo sapiens]

Seq. No.	193234
Contig ID	9011_1.R1039
5'-most EST	LIB3147-038-Q1-K2-C5
Method	BLASTX
NCBI GI	g231660
BLAST score	624
E value	8.0e-65
Match length	279
% identity	49
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	193235
Contig ID	9018_1.R1039
5'-most EST	LIB3272-049-P1-K1-E11
Method	BLASTX
NCBI GI	g3169182
BLAST score	313
E value	9.0e-29
Match length	78
% identity	76
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	193236
Contig ID	9020_1.R1039
5'-most EST	LIB3189-001-P1-K1-F2
Method	BLASTX
NCBI GI	g131773
BLAST score	542
E value	3.0e-55
Match length	137
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi|82724|pir||B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	193237
Contig ID	9021_1.R1039
5'-most EST	LIB3145-025-Q1-K1-B6
Method	BLASTX
NCBI GI	g3928083
BLAST score	789
E value	2.0e-84
Match length	188
% identity	76
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	193238
Contig ID	9023_2.R1039
5'-most EST	LIB3083-097-Q1-L1-D1
Method	BLASTX
NCBI GI	g2129703
BLAST score	208

E value	1.0e-16
Match length	93
% identity	46
NCBI Description	receptor kinase - Arabidopsis thaliana >gi|2129704|pir||S71184 receptor kinase - Arabidopsis thaliana >gi|166692 (M80238) receptor kinase [Arabidopsis thaliana] >gi|445123|prf||1908429A receptor kinase [Arabidopsis thaliana]

Seq. No.	193239
Contig ID	9027_1.R1039
5'-most EST	LIB3197-058-Q1-M1-B1
Method	BLASTX
NCBI GI	g1663706
BLAST score	189
E value	4.0e-14
Match length	80
% identity	49
NCBI Description	(D87685) similar to human transcription factor TFIIS (S34159). [Homo sapiens]

Seq. No.	193240
Contig ID	9029_1.R1039
5'-most EST	LIB3165-033-P1-K1-D1

Seq. No.	193241
Contig ID	9031_1.R1039
5'-most EST	LIB3145-020-Q1-K1-E12
Method	BLASTX
NCBI GI	g1351365
BLAST score	185
E value	1.0e-13
Match length	56
% identity	62
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN (CR6) >gi|2130002|pir||S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi|633683|emb|CAA57768| (X82325) cytochrome c reductase subunit [Solanum tuberosum]

Seq. No.	193242
Contig ID	9033_1.R1039
5'-most EST	LIB3166-051-P1-K1-C6
Method	BLASTX
NCBI GI	g1755178
BLAST score	576
E value	2.0e-59
Match length	159
% identity	69
NCBI Description	(U75200) germin-like protein [Arabidopsis thaliana]

Seq. No.	193243
Contig ID	9038_1.R1039
5'-most EST	uC-gsronu33B036a05b1
Method	BLASTX
NCBI GI	g1531758
BLAST score	607
E value	5.0e-78

Match length	161
% identity	82
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi|3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	193244
Contig ID	9043_1.R1039
5'-most EST	LIB3197-021-Q1-M1-B3

Seq. No.	193245
Contig ID	9047_1.R1039
5'-most EST	g5049888
Method	BLASTX
NCBI GI	g2623296
BLAST score	375
E value	9.0e-36
Match length	123
% identity	65
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193246
Contig ID	9048_1.R1039
5'-most EST	LIB3083-097-Q1-L1-G3
Method	BLASTX
NCBI GI	g1488647
BLAST score	204
E value	1.0e-15
Match length	67
% identity	63
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]

Seq. No.	193247
Contig ID	9058_1.R1039
5'-most EST	g5050528
Method	BLASTX
NCBI GI	g2252842
BLAST score	158
E value	4.0e-11
Match length	138
% identity	39
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	193248
Contig ID	9068_1.R1039
5'-most EST	g5047116

Seq. No.	193249
Contig ID	9073_1.R1039
5'-most EST	LIB3272-055-P1-K1-G11

Seq. No.	193250
Contig ID	9075_1.R1039
5'-most EST	LIB3083-099-Q1-L1-B9
Method	BLASTN
NCBI GI	g4567193
BLAST score	71
E value	8.0e-32

Match length	223
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	193251
Contig ID	9077_1.R1039
5'-most EST	uC-gsflmaxxa094h12b1

Seq. No.	193252
Contig ID	9078_1.R1039
5'-most EST	LIB3149-027-Q1-K1-A2
Method	BLASTX
NCBI GI	g1172873
BLAST score	423
E value	2.0e-41
Match length	85
% identity	74
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi|541857|pir||JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi|435619|dbj|BAA02374| (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	193253
Contig ID	9089_1.R1039
5'-most EST	uC-gsronu33B104c12b1
Method	BLASTX
NCBI GI	g4006881
BLAST score	663
E value	2.0e-69
Match length	204
% identity	55
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	193254
Contig ID	9105_1.R1039
5'-most EST	LIB3149-064-Q1-K1-E6
Method	BLASTX
NCBI GI	g3377820
BLAST score	393
E value	4.0e-38
Match length	98
% identity	77
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	193255
Contig ID	9106_1.R1039
5'-most EST	uC-gsflnu33B061g02b1

Seq. No.	193256
Contig ID	9117_1.R1039
5'-most EST	LIB3083-114-Q1-L1-H5
Method	BLASTX
NCBI GI	g2335100
BLAST score	695
E value	1.0e-73

Match length	148
% identity	86
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	193257
Contig ID	9124_1.R1039
5'-most EST	LIB3146-055-Q1-K1-G1
Method	BLASTX
NCBI GI	g3668097
BLAST score	629
E value	2.0e-65
Match length	155
% identity	77
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	193258
Contig ID	9126_1.R1039
5'-most EST	uC-gsflmaxxa028c06b1

Seq. No.	193259
Contig ID	9126_2.R1039
5'-most EST	uC-gsflmaxxa093g01b1

Seq. No.	193260
Contig ID	9131_1.R1039
5'-most EST	LIB3083-099-Q1-L1-G4

Seq. No.	193261
Contig ID	9143_1.R1039
5'-most EST	g5046366
Method	BLASTX
NCBI GI	g2689720
BLAST score	707
E value	1.0e-74
Match length	200
% identity	68
NCBI Description	(AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No.	193262
Contig ID	9149_1.R1039
5'-most EST	LIB3083-100-Q1-L1-A11
Method	BLASTX
NCBI GI	g3513727
BLAST score	487
E value	3.0e-49
Match length	119
% identity	35
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi|4539358|emb|CAB40052.1| (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	193263
Contig ID	9151_1.R1039
5'-most EST	g3326502

Method	BLASTX
NCBI GI	g2275215
BLAST score	737
E value	4.0e-78
Match length	264
% identity	56
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193264
Contig ID	9153_1.R1039
5'-most EST	g5047081
Method	BLASTX
NCBI GI	g2739376
BLAST score	400
E value	9.0e-39
Match length	108
% identity	69
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	193265
Contig ID	9154_1.R1039
5'-most EST	uC-gsflnu33B108e09b1
Method	BLASTX
NCBI GI	g112717
BLAST score	194
E value	9.0e-15
Match length	57
% identity	63
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi|82050|pir||S10911 hypothetical protein precursor - carrot >gi|18312|emb|CAA36642| (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

Seq. No.	193266
Contig ID	9163_3.R1039
5'-most EST	LIB3083-100-Q1-L1-B4
Method	BLASTX
NCBI GI	g4234768
BLAST score	664
E value	6.0e-70
Match length	126
% identity	89
NCBI Description	(AF069468) sterol-C5-desaturase [Arabidopsis thaliana]

Seq. No.	193267
Contig ID	9164_1.R1039
5'-most EST	LIB3166-009-P1-K1-F8
Method	BLASTX
NCBI GI	g4455192
BLAST score	347
E value	6.0e-42
Match length	188
% identity	50
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	193268
Contig ID	9165_1.R1039

5'-most EST	g5049299
Seq. No.	193269
Contig ID	9166_1.R1039
5'-most EST	LIB3148-029-Q1-K1-A3
Method	BLASTX
NCBI GI	g1928960
BLAST score	810
E value	1.0e-86
Match length	192
% identity	80
NCBI Description	(U92286) pyrroline-5-carboxylate synthetase [Actinidia deliciosa]
Seq. No.	193270
Contig ID	9168_2.R1039
5'-most EST	LIB3189-041-P1-K1-H12
Method	BLASTX
NCBI GI	g1762309
BLAST score	782
E value	2.0e-83
Match length	161
% identity	93
NCBI Description	(U53345) AP-1 Golgi-related complex component; clathrin coated vesicles; clathrin assembly protein [Camptotheca acuminata]
Seq. No.	193271
Contig ID	9177_1.R1039
5'-most EST	LIB3166-002-Q1-K1-G4
Method	BLASTX
NCBI GI	g123650
BLAST score	841
E value	7.0e-90
Match length	346
% identity	88
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi|82245|pir||S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi|20557|emb|CAA30018| (X06932) heat shock protein 70 [Petunia x hybrida]
Seq. No.	193272
Contig ID	9177_2.R1039
5'-most EST	g3326038
Method	BLASTX
NCBI GI	g3962377
BLAST score	614
E value	7.0e-64
Match length	131
% identity	92
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]
Seq. No.	193273
Contig ID	9177_3.R1039
5'-most EST	LIB3189-005-P1-K1-A6
Method	BLASTX
NCBI GI	g3986110

BLAST score 845
E value 8.0e-91
Match length 188
% identity 88
NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No. 193274
Contig ID 9178_1.R1039
5'-most EST LIB3166-028-P1-K1-B3
Method BLASTX
NCBI GI g2760317
BLAST score 547
E value 5.0e-56
Match length 175
% identity 61
NCBI Description (AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No. 193275
Contig ID 9186_1.R1039
5'-most EST LIB3166-049-P1-K1-C1

Seq. No. 193276
Contig ID 9191_1.R1039
5'-most EST LIB3083-109-Q1-L1-H4
Method BLASTX
NCBI GI g2160169
BLAST score 318
E value 3.0e-29
Match length 110
% identity 58
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 193277
Contig ID 9195_1.R1039
5'-most EST g5048069
Method BLASTX
NCBI GI g3983665
BLAST score 562
E value 8.0e-58
Match length 133
% identity 80
NCBI Description (AB011271) importin-beta2 [Oryza sativa]

Seq. No. 193278
Contig ID 9198_1.R1039
5'-most EST LIB3189-017-P1-K1-H1
Method BLASTX
NCBI GI g4510428
BLAST score 575
E value 3.0e-59
Match length 205
% identity 55
NCBI Description (AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 193279
Contig ID 9199_1.R1039

5'-most EST	uC-gsflnu33B145b09b1
Method	BLASTX
NCBI GI	g2244975
BLAST score	539
E value	3.0e-55
Match length	137
% identity	72
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193280
Contig ID	9201_1.R1039
5'-most EST	LIB3146-019-Q1-K1-A2
Method	BLASTX
NCBI GI	g2500589
BLAST score	446
E value	9.0e-44
Match length	242
% identity	23
NCBI Description	NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN) >gi|1592563 (U55861) RNA binding protein TIAR [Mus musculus]

Seq. No.	193281
Contig ID	9201_3.R1039
5'-most EST	LIB3196-022-P1-M1-A4
Method	BLASTX
NCBI GI	g267131
BLAST score	187
E value	8.0e-14
Match length	87
% identity	15
NCBI Description	NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN) >gi|423120|pir||A46174 RNA-binding protein TIAR - human >gi|189310 (M96954) nucleolysin TIAR [Homo sapiens] >gi|4507499|ref|NP_003243.1|pTIAL1| TIA1 cytotoxic granule-associated RNA-binding protein-like

Seq. No.	193282
Contig ID	9209_1.R1039
5'-most EST	LIB3083-100-Q1-L1-F2
Method	BLASTX
NCBI GI	g1717967
BLAST score	223
E value	5.0e-18
Match length	98
% identity	48
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) >gi|1345584|emb|CAA53582| (X75968) 3-O-glucsyltransferase [Vitis vinifera]

Seq. No.	193283
Contig ID	9216_1.R1039
5'-most EST	LIB3083-100-Q1-L1-G1

Seq. No.	193284
Contig ID	9230_1.R1039
5'-most EST	LIB3083-100-Q1-L1-H11

Seq. No.	193285
Contig ID	9250_1.R1039
5'-most EST	LIB3083-101-Q1-L1-B1

Seq. No.	193286
Contig ID	9253_1.R1039
5'-most EST	LIB3083-101-Q1-L1-B12
Method	BLASTX
NCBI GI	g3414809
BLAST score	387
E value	4.0e-37
Match length	254
% identity	4
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	193287
Contig ID	9260_1.R1039
5'-most EST	uC-gsronu33B004b03b1
Method	BLASTX
NCBI GI	g2181180
BLAST score	459
E value	2.0e-45
Match length	301
% identity	37
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	193288
Contig ID	9261_1.R1039
5'-most EST	g5049055
Method	BLASTX
NCBI GI	g2655037
BLAST score	139
E value	2.0e-15
Match length	146
% identity	35
NCBI Description	(AF019952) tumor suppressing STF cDNA 1 [Homo sapiens] >gi|4507703|ref|NP_003301.1|pTSSC1| tumor suppressing subtransferable candidate

Seq. No.	193289
Contig ID	9261_2.R1039
5'-most EST	uC-gsflmaxxa058d03b1
Method	BLASTX
NCBI GI	g2655037
BLAST score	322
E value	2.0e-29
Match length	188
% identity	39
NCBI Description	(AF019952) tumor suppressing STF cDNA 1 [Homo sapiens] >gi|4507703|ref|NP_003301.1|pTSSC1| tumor suppressing subtransferable candidate

Seq. No.	193290
Contig ID	9273_1.R1039
5'-most EST	g5046379
Method	BLASTX
NCBI GI	g2245109

BLAST score 635
E value 4.0e-66
Match length 173
% identity 71
NCBI Description (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]

Seq. No. 193291
Contig ID 9280_1.R1039
5'-most EST g5046128
Method BLASTX
NCBI GI g4454307
BLAST score 878
E value 9.0e-95
Match length 180
% identity 86
NCBI Description (AJ132763) cyclophilin [Pseudotsuga menziesii]

Seq. No. 193292
Contig ID 9286_1.R1039
5'-most EST LIB3083-101-Q1-L1-E8
Method BLASTX
NCBI GI g4325371
BLAST score 195
E value 1.0e-14
Match length 227
% identity 30
NCBI Description (AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No. 193293
Contig ID 9287_1.R1039
5'-most EST g3325983

Seq. No. 193294
Contig ID 9287_2.R1039
5'-most EST LIB3146-058-Q1-K1-A11

Seq. No. 193295
Contig ID 9289_1.R1039
5'-most EST LIB3083-104-Q1-L1-F4

Seq. No. 193296
Contig ID 9297_1.R1039
5'-most EST g5050849

Seq. No. 193297
Contig ID 9298_1.R1039
5'-most EST LIB3083-101-Q1-L1-G10
Method BLASTX
NCBI GI g3402701
BLAST score 197
E value 6.0e-15
Match length 56
% identity 71
NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	193298
Contig ID	9301_1.R1039
5'-most EST	LIB3083-101-Q1-L1-G2
Method	BLASTX
NCBI GI	g1743354
BLAST score	702
E value	5.0e-74
Match length	191
% identity	68
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	193299
Contig ID	9302_1.R1039
5'-most EST	LIB3166-059-P1-K1-C2
Method	BLASTX
NCBI GI	g4008441
BLAST score	435
E value	1.0e-42
Match length	143
% identity	61
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	193300
Contig ID	9306_1.R1039
5'-most EST	uC-gsflnu33B031c11b1
Method	BLASTX
NCBI GI	g2570338
BLAST score	1160
E value	1.0e-127
Match length	327
% identity	68
NCBI Description	(U90927) glyoxalase II isozyme [Arabidopsis thaliana]

Seq. No.	193301
Contig ID	9308_1.R1039
5'-most EST	LIB3146-008-Q1-K1-H11

Seq. No.	193302
Contig ID	9316_1.R1039
5'-most EST	g3326792
Method	BLASTX
NCBI GI	g3757522
BLAST score	526
E value	1.0e-56
Match length	193
% identity	66
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	193303
Contig ID	9318_1.R1039
5'-most EST	LIB3083-101-Q1-L1-H7
Method	BLASTX
NCBI GI	g1881585
BLAST score	347

E value	8.0e-33
Match length	143
% identity	57
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	193304
Contig ID	9323_1.R1039
5'-most EST	uC-gsflmaxxa001h08b1
Method	BLASTX
NCBI GI	g2213877
BLAST score	1698
E value	0.0e+00
Match length	356
% identity	90
NCBI Description	(AF003197) glutamine synthetase [Hevea brasiliensis]

Seq. No.	193305
Contig ID	9327_1.R1039
5'-most EST	g5047157
Method	BLASTX
NCBI GI	g3702368
BLAST score	1190
E value	1.0e-131
Match length	299
% identity	74
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	193306
Contig ID	9331_1.R1039
5'-most EST	LIB3148-036-Q1-K1-H12
Method	BLASTX
NCBI GI	g1561774
BLAST score	863
E value	6.0e-98
Match length	222
% identity	85
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	193307
Contig ID	9333_1.R1039
5'-most EST	g5049051
Method	BLASTX
NCBI GI	g1561774
BLAST score	1751
E value	0.0e+00
Match length	423
% identity	79
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	193308
Contig ID	9333_2.R1039
5'-most EST	LIB3149-031-Q1-K1-C2
Method	BLASTN
NCBI GI	g1561773
BLAST score	121
E value	3.0e-61

Match length	642
% identity	84
NCBI Description	Vitis vinifera malate dehydrogenase (VVME2) mRNA, complete cds

Seq. No.	193309
Contig ID	9334_1.R1039
5'-most EST	LIB3083-102-Q1-L1-B7

Seq. No.	193310
Contig ID	9337_1.R1039
5'-most EST	uC-gsflnu33B146g02b1

Seq. No.	193311
Contig ID	9341_1.R1039
5'-most EST	LIB3272-058-P1-K1-H12
Method	BLASTX
NCBI GI	g1173104
BLAST score	799
E value	3.0e-85
Match length	219
% identity	65
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi|289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi|2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	193312
Contig ID	9349_1.R1039
5'-most EST	uC-gsflnu33B113d12b1
Method	BLASTX
NCBI GI	g2982451
BLAST score	426
E value	2.0e-77
Match length	223
% identity	62
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	193313
Contig ID	9350_1.R1039
5'-most EST	LIB3083-102-Q1-L1-E1
Method	BLASTX
NCBI GI	g3935147
BLAST score	370
E value	2.0e-35
Match length	148
% identity	51
NCBI Description	(AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No.	193314
Contig ID	9353_1.R1039
5'-most EST	LIB3165-040-Q1-K1-G10
Method	BLASTX
NCBI GI	g2129752
BLAST score	362
E value	2.0e-34
Match length	93
% identity	67

NCBI Description	thioredoxin - Arabidopsis thaliana >gi|992964|emb|CAA84612| (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.	193315
Contig ID	9357_1.R1039
5'-most EST	LIB3145-037-Q1-K1-A11
Method	BLASTX
NCBI GI	g1169238
BLAST score	794
E value	6.0e-85
Match length	203
% identity	73
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) >gi|1076648|pir||A48767 glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia >gi|294112 (L16797) glutamate decarboxylase [Petunia hybrida] >gi|309680 (L16977) glutamate decarboxylase [Petunia hybrida]
Seq. No.	193316
Contig ID	9370_1.R1039
5'-most EST	LIB3083-104-Q1-L1-H2
Method	BLASTX
NCBI GI	g3913295
BLAST score	580
E value	7.0e-60
Match length	187
% identity	58
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi|602588|emb|CAA58218| (X83217) caffeic O-methyltransferase [Prunus dulcis]
Seq. No.	193317
Contig ID	9372_1.R1039
5'-most EST	LIB3120-013-Q1-K1-F9
Method	BLASTX
NCBI GI	g2982301
BLAST score	520
E value	1.0e-52
Match length	190
% identity	40
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]
Seq. No.	193318
Contig ID	9377_1.R1039
5'-most EST	uC-gsronu33B001a11b1
Method	BLASTX
NCBI GI	g3746064
BLAST score	177
E value	8.0e-13
Match length	87
% identity	37
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.	193319
Contig ID	9383_1.R1039
5'-most EST	uC-gsronu33B168d08b1

Seq. No. 193320
Contig ID 9383_2.R1039
5'-most EST LIB3148-053-Q1-K1-D10

Seq. No. 193321
Contig ID 9383_4.R1039
5'-most EST uC-gsflnu33B090d11b1

Seq. No. 193322
Contig ID 9383_5.R1039
5'-most EST LIB3083-105-Q1-L1-F8
Method BLASTX
NCBI GI g3184281
BLAST score 206
E value 3.0e-24
Match length 123
% identity 49
NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 193323
Contig ID 9383_6.R1039
5'-most EST LIB3083-103-Q1-L1-B9
Method BLASTX
NCBI GI g3184281
BLAST score 482
E value 2.0e-48
Match length 160
% identity 57
NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 193324
Contig ID 9385_1.R1039
5'-most EST uC-gsflmaxxa004g03b1
Method BLASTX
NCBI GI g2459446
BLAST score 454
E value 4.0e-45
Match length 139
% identity 63
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 193325
Contig ID 9393_1.R1039
5'-most EST LIB3272-016-P1-K1-F12

Seq. No. 193326
Contig ID 9395_1.R1039
5'-most EST LIB3145-023-Q1-K1-B7
Method BLASTX
NCBI GI g3915083
BLAST score 1172
E value 1.0e-129
Match length 225
% identity 98
NCBI Description TUBULIN BETA CHAIN >gi|1403143|emb|CAA67056| (X98406)

beta-tubulin [Cicer arietinum]

Seq. No.	193327
Contig ID	9398_1.R1039
5'-most EST	LIB3189-034-P1-K1-A1
Method	BLASTX
NCBI GI	g2271477
BLAST score	375
E value	5.0e-36
Match length	100
% identity	75
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	193328
Contig ID	9405_1.R1039
5'-most EST	LIB3145-023-Q1-K1-B10
Method	BLASTX
NCBI GI	g4033735
BLAST score	1500
E value	1.0e-175
Match length	362
% identity	86
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	193329
Contig ID	9413_1.R1039
5'-most EST	LIB3083-104-Q1-L1-A8

Seq. No.	193330
Contig ID	9414_1.R1039
5'-most EST	g5050062
Method	BLASTX
NCBI GI	g266567
BLAST score	337
E value	2.0e-31
Match length	143
% identity	52
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi|421956|pir||S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi|21493|emb|CAA46990| (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	193331
Contig ID	9417_1.R1039
5'-most EST	LIB3147-050-Q1-K1-B7

Seq. No.	193332
Contig ID	9420_1.R1039
5'-most EST	LIB3197-054-Q1-M1-C4
Method	BLASTX
NCBI GI	g2791806
BLAST score	414
E value	4.0e-40
Match length	125
% identity	62

NCBI Description (AF041433) bet3 [Mus musculus]

Seq. No. 193333
Contig ID 9420_2.R1039
5'-most EST LIB3147-049-Q1-K1-B1
Method BLASTX
NCBI GI g2791806
BLAST score 210
E value 1.0e-16
Match length 59
% identity 66
NCBI Description (AF041433) bet3 [Mus musculus]

Seq. No. 193334
Contig ID 9425_1.R1039
5'-most EST uC-gsronu33B136c08b1

Seq. No. 193335
Contig ID 9429_1.R1039
5'-most EST g5050576
Method BLASTX
NCBI GI g2506139
BLAST score 507
E value 7.0e-54
Match length 307
% identity 66
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi|1314049|emb|CAA91901| (Z67962) archain/delta-COP [Oryza sativa]

Seq. No. 193336
Contig ID 9429_2.R1039
5'-most EST LIB3083-104-Q1-L1-C8
Method BLASTX
NCBI GI g2506139
BLAST score 413
E value 2.0e-40
Match length 107
% identity 75
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi|1314049|emb|CAA91901| (Z67962) archain/delta-COP [Oryza sativa]

Seq. No. 193337
Contig ID 9430_1.R1039
5'-most EST LIB3147-019-Q1-K1-F1
Method BLASTX
NCBI GI g1174870
BLAST score 273
E value 5.0e-24
Match length 72
% identity 74
NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi|633685|emb|CAA55861| (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No. 193338

Contig ID	9430_3.R1039
5'-most EST	uC-gsronu33b023g07b1
Method	BLASTX
NCBI GI	g1174870
BLAST score	265
E value	4.0e-23
Match length	73
% identity	74
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi|633685|emb|CAA55861| (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	193339
Contig ID	9462_1.R1039
5'-most EST	LIB3272-026-P1-K1-D5
Method	BLASTX
NCBI GI	g119640
BLAST score	293
E value	3.0e-26
Match length	116
% identity	53
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi|82109|pir||S01642 ripening protein E8 - tomato >gi|19199|emb|CAA31789| (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	193340
Contig ID	9466_1.R1039
5'-most EST	LIB3083-104-Q1-L1-H5
Method	BLASTX
NCBI GI	g2088646
BLAST score	428
E value	4.0e-42
Match length	86
% identity	87
NCBI Description	(AF002109) Su1p isolog [Arabidopsis thaliana]

Seq. No.	193341
Contig ID	9471_1.R1039
5'-most EST	LIB3083-105-Q1-L1-A11
Method	BLASTX
NCBI GI	g4455198
BLAST score	364
E value	3.0e-42
Match length	171
% identity	39
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	193342
Contig ID	9475_1.R1039
5'-most EST	g5049480
Method	BLASTX
NCBI GI	g4417287
BLAST score	539
E value	6.0e-55
Match length	165
% identity	63

NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.	193343
Contig ID	9485_1.R1039
5'-most EST	LIB3083-105-Q1-L1-B4
Method	BLASTX
NCBI GI	g3213000
BLAST score	170
E value	2.0e-11
Match length	213
% identity	30
NCBI Description	(AC004997) similar to squid retinal-binding protein P49193 (PID:g1346953) [Homo sapiens]
Seq. No.	193344
Contig ID	9488_1.R1039
5'-most EST	g5047301
Method	BLASTX
NCBI GI	g1731181
BLAST score	260
E value	3.0e-22
Match length	195
% identity	35
NCBI Description	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi|3874230|emb|CAA90107| (Z49909) weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]
Seq. No.	193345
Contig ID	9490_1.R1039
5'-most EST	LIB3145-044-Q1-K1-D12
Method	BLASTX
NCBI GI	g464981
BLAST score	407
E value	2.0e-39
Match length	134
% identity	64
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	193346
Contig ID	9490_2.R1039
5'-most EST	uC-gsflnu33B126c03b1
Method	BLASTX
NCBI GI	g464981
BLAST score	480
E value	4.0e-48
Match length	101
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	193347
Contig ID	9494_1.R1039

5'-most EST	LIB3083-105-Q1-L1-C2
Method	BLASTX
NCBI GI	g461999
BLAST score	1870
E value	0.0e+00
Match length	391
% identity	94
NCBI Description	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No.	193348
Contig ID	9501_1.R1039
5'-most EST	uC-gsflmaxxa043f12b1
Method	BLASTX
NCBI GI	g3386597
BLAST score	234
E value	3.0e-19
Match length	70
% identity	69
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi|3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No.	193349
Contig ID	9508_1.R1039
5'-most EST	LIB3146-047-Q1-K1-H6
Method	BLASTX
NCBI GI	g4406819
BLAST score	216
E value	2.0e-17
Match length	87
% identity	52
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	193350
Contig ID	9512_1.R1039
5'-most EST	LIB3083-105-Q1-L1-D8
Method	BLASTX
NCBI GI	g1871192
BLAST score	506
E value	4.0e-51
Match length	207
% identity	59
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	193351
Contig ID	9513_1.R1039
5'-most EST	g5045418
Method	BLASTX
NCBI GI	g4531443
BLAST score	880
E value	9.0e-95
Match length	239
% identity	73
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	193352
Contig ID	9517_1.R1039
5'-most EST	LIB3165-048-Q1-K1-E2
Method	BLASTX
NCBI GI	g3341679
BLAST score	1235
E value	1.0e-136
Match length	311
% identity	77
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	193353
Contig ID	9518_1.R1039
5'-most EST	g3326505
Method	BLASTX
NCBI GI	g3738332
BLAST score	563
E value	9.0e-58
Match length	185
% identity	59
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	193354
Contig ID	9518_2.R1039
5'-most EST	g5044473
Method	BLASTX
NCBI GI	g3738332
BLAST score	606
E value	8.0e-63
Match length	223
% identity	58
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	193355
Contig ID	9528_1.R1039
5'-most EST	LIB3083-105-Q1-L1-F11
Method	BLASTX
NCBI GI	g2244971
BLAST score	359
E value	2.0e-34
Match length	92
% identity	76
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193356
Contig ID	9534_1.R1039
5'-most EST	LIB3083-105-Q1-L1-F6
Method	BLASTX
NCBI GI	g2191145
BLAST score	192
E value	2.0e-14
Match length	204
% identity	34
NCBI Description	(AF007269) A_IG002N01.4 gene product [Arabidopsis thaliana]

Seq. No.	193357
Contig ID	9538_1.R1039
5'-most EST	LIB3189-006-P1-K1-A5
Method	BLASTN
NCBI GI	g12218
BLAST score	100
E value	7.0e-49
Match length	180
% identity	89
NCBI Description	Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No.	193358
Contig ID	9549_1.R1039
5'-most EST	LIB3145-014-Q1-K1-E11
Method	BLASTX
NCBI GI	g3461821
BLAST score	410
E value	1.0e-39
Match length	153
% identity	56
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	193359
Contig ID	9551_1.R1039
5'-most EST	uC-gsronu33B078d09b1
Method	BLASTX
NCBI GI	g4056457
BLAST score	478
E value	1.0e-47
Match length	128
% identity	70
NCBI Description	(AC005990) ESTs gb|234051 and gb|F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	193360
Contig ID	9560_1.R1039
5'-most EST	uC-gsronu33B158c06b2
Method	BLASTX
NCBI GI	g2129471
BLAST score	914
E value	7.0e-99
Match length	228
% identity	78
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi|1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	193361
Contig ID	9563_1.R1039
5'-most EST	LIB3189-032-P1-K1-A6
Method	BLASTX
NCBI GI	g2465015
BLAST score	172
E value	3.0e-12
Match length	137

% identity	35
NCBI Description	(AJ001449) ripening-induced protein [Fragaria vesca]

Seq. No.	193362
Contig ID	9565_1.R1039
5'-most EST	LIB3083-106-Q1-L1-B11
Method	BLASTX
NCBI GI	g2462733
BLAST score	252
E value	1.0e-21
Match length	69
% identity	70
NCBI Description	(AC002292) Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]

Seq. No.	193363
Contig ID	9568_1.R1039
5'-most EST	LIB3197-056-Q1-M1-A11
Method	BLASTX
NCBI GI	g462187
BLAST score	343
E value	3.0e-32
Match length	108
% identity	69
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi|282928|pir||A42906 serine hydroxymethyltransferase - garden pea >gi|169158 (M87649) serine hydroxymethyltransferase [Pisum sativum]

Seq. No.	193364
Contig ID	9571_1.R1039
5'-most EST	uC-gsflmaxxa064b03b1
Method	BLASTX
NCBI GI	g421843
BLAST score	520
E value	8.0e-53
Match length	155
% identity	68
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi|217861|dbj|BAA01715| (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	193365
Contig ID	9571_2.R1039
5'-most EST	LIB3166-039-P1-K1-D4
Method	BLASTX
NCBI GI	g421843
BLAST score	649
E value	5.0e-68
Match length	159
% identity	77
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi|217861|dbj|BAA01715| (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	193366

Contig ID	9571_3.R1039
5'-most EST	LIB3148-002-P1-K1-A5
Method	BLASTX
NCBI GI	g421843
BLAST score	544
E value	2.0e-85
Match length	215
% identity	76
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi|217861|dbj|BAA01715| (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	193367
Contig ID	9577_1.R1039
5'-most EST	LIB3145-028-Q1-K1-H6
Method	BLASTX
NCBI GI	g3337361
BLAST score	1324
E value	1.0e-146
Match length	328
% identity	70
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	193368
Contig ID	9580_1.R1039
5'-most EST	LIB3146-003-P1-K1-A9
Method	BLASTX
NCBI GI	g2464855
BLAST score	177
E value	1.0e-12
Match length	163
% identity	40
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	193369
Contig ID	9593_1.R1039
5'-most EST	g5045055
Method	BLASTX
NCBI GI	g3080420
BLAST score	883
E value	3.0e-95
Match length	271
% identity	62
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	193370
Contig ID	9609_1.R1039
5'-most EST	LIB3083-107-Q1-L1-C12
Method	BLASTX
NCBI GI	g1519680
BLAST score	185
E value	2.0e-13
Match length	149
% identity	30
NCBI Description	(U67953) contains similarity to C3HC4-class zinc finger (PS:PS00518) [Caenorhabditis elegans]

Seq. No.	193371
Contig ID	9610_1.R1039
5'-most EST	LIB3272-015-P1-K1-D4
Method	BLASTX
NCBI GI	g2191150
BLAST score	948
E value	1.0e-103
Match length	220
% identity	38
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	193372
Contig ID	9610_2.R1039
5'-most EST	LIB3120-023-Q1-K1-E4
Method	BLASTX
NCBI GI	g2191150
BLAST score	501
E value	2.0e-50
Match length	136
% identity	42
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	193373
Contig ID	9611_1.R1039
5'-most EST	g5048917
Method	BLASTX
NCBI GI	g2760362
BLAST score	657
E value	6.0e-69
Match length	138
% identity	90
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]

Seq. No.	193374
Contig ID	9615_1.R1039
5'-most EST	LIB3083-107-Q1-L1-C7
Method	BLASTX
NCBI GI	g3834309
BLAST score	640
E value	1.0e-66
Match length	271
% identity	46
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb|L16983 Daucus carota and a member of S locus glycoprotein family PF|00954. ESTs gb|F13813, gb|T21052, gb|R30218 and gb|W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	193375
Contig ID	9621_1.R1039
5'-most EST	uC-gsronu33B134b03b1
Method	BLASTX
NCBI GI	g1943751
BLAST score	657

E value	4.0e-69
Match length	137
% identity	90
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi|2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	193376
Contig ID	9630_1.R1039
5'-most EST	LIB3145-049-Q1-K1-B6
Method	BLASTX
NCBI GI	g4558556
BLAST score	237
E value	7.0e-20
Match length	141
% identity	41
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	193377
Contig ID	9645_1.R1039
5'-most EST	g5045724
Method	BLASTX
NCBI GI	g4191778
BLAST score	550
E value	3.0e-56
Match length	148
% identity	71
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	193378
Contig ID	9646_1.R1039
5'-most EST	uC-gsronu33B147b07b1

Seq. No.	193379
Contig ID	9650_1.R1039
5'-most EST	LIB3145-044-Q1-K1-B4
Method	BLASTX
NCBI GI	g3096922
BLAST score	209
E value	2.0e-16
Match length	45
% identity	91
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	193380
Contig ID	9655_1.R1039
5'-most EST	LIB3147-044-Q1-K1-E1
Method	BLASTX
NCBI GI	g544861
BLAST score	356
E value	8.0e-34
Match length	69
% identity	100
NCBI Description	(S68003) actin [Striga asiatica=witchweed, Kuntze, Peptide Partial, 114 aa] [Striga asiatica]

Seq. No. 193381
Contig ID 9659_1.R1039
5'-most EST uC-gsronu33B127e02b1

Seq. No. 193382
Contig ID 9661_1.R1039
5'-most EST LIB3147-019-Q1-K1-B1
Method BLASTX
NCBI GI g4510354
BLAST score 209
E value 3.0e-16
Match length 157
% identity 40
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 193383
Contig ID 9666_1.R1039
5'-most EST LIB3120-010-Q1-K1-C8

Seq. No. 193384
Contig ID 9669_1.R1039
5'-most EST uC-gsronu33B060h12b1
Method BLASTX
NCBI GI g3135265
BLAST score 366
E value 5.0e-35
Match length 89
% identity 73
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 193385
Contig ID 9670_1.R1039
5'-most EST uC-gsflnu33B003g06b1
Method BLASTX
NCBI GI g4309738
BLAST score 283
E value 2.0e-25
Match length 73
% identity 70
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 193386
Contig ID 9671_1.R1039
5'-most EST LIB3189-013-P1-K1-C4
Method BLASTX
NCBI GI g2828293
BLAST score 685
E value 6.0e-72
Match length 278
% identity 48
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 193387
Contig ID 9673_1.R1039
5'-most EST g5047708
Method BLASTX

NCBI GI g421843
BLAST score 819
E value 2.0e-87
Match length 275
% identity 59
NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi|217861|dbj|BAA01715| (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 193388
Contig ID 9676_1.R1039
5'-most EST uC-gsflmaxxa010a04b1
Method BLASTX
NCBI GI g3548818
BLAST score 275
E value 3.0e-24
Match length 91
% identity 60
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 193389
Contig ID 9679_1.R1039
5'-most EST LIB3197-058-Q1-M1-G2
Method BLASTX
NCBI GI g1351014
BLAST score 842
E value 2.0e-90
Match length 218
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi|968902|dbj|BAA07207| (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 193390
Contig ID 9679_2.R1039
5'-most EST LIB3148-035-Q1-K1-H7
Method BLASTX
NCBI GI g1498053
BLAST score 527
E value 6.0e-89
Match length 209
% identity 82
NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 193391
Contig ID 9679_3.R1039
5'-most EST g5049899
Method BLASTX
NCBI GI g1351014
BLAST score 833
E value 3.0e-89
Match length 219
% identity 75
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi|968902|dbj|BAA07207| (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 193392
Contig ID 9679_4.R1039

5'-most EST	LIB3272-010-P1-K1-B12
Method	BLASTX
NCBI GI	g3264759
BLAST score	543
E value	1.0e-55
Match length	132
% identity	82
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	193393
Contig ID	9682_1.R1039
5'-most EST	LIB3083-108-Q1-L1-B1
Method	BLASTX
NCBI GI	g4204265
BLAST score	156
E value	4.0e-10
Match length	131
% identity	37
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	193394
Contig ID	9683_1.R1039
5'-most EST	LIB3083-108-Q1-L1-B10
Method	BLASTX
NCBI GI	g2281102
BLAST score	168
E value	1.0e-11
Match length	86
% identity	48
NCBI Description	(AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No.	193395
Contig ID	9687_1.R1039
5'-most EST	LIB3083-108-Q1-L1-B3
Method	BLASTX
NCBI GI	g1173327
BLAST score	399
E value	6.0e-39
Match length	86
% identity	90
NCBI Description	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') >gi|322619|pir||S30580 U2 snRNP protein A' - Arabidopsis thaliana >gi|17669|emb|CAA48890| (X69137) U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]

Seq. No.	193396
Contig ID	9693_1.R1039
5'-most EST	LIB3083-108-Q1-L1-B9

Seq. No.	193397
Contig ID	9695_1.R1039
5'-most EST	uC-gsronu33B015d09b1

Seq. No.	193398
Contig ID	9700_1.R1039
5'-most EST	uC-gsflnu33B144e07b1
Method	BLASTX

NCBI GI	g1421730
BLAST score	337
E value	1.0e-31
Match length	87
% identity	75
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	193399
Contig ID	9703_1.R1039
5'-most EST	LIB3197-055-Q1-M1-B6
Method	BLASTX
NCBI GI	g3212869
BLAST score	1475
E value	1.0e-164
Match length	595
% identity	71
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	193400
Contig ID	9703_3.R1039
5'-most EST	LIB3149-048-Q1-K1-E9
Method	BLASTX
NCBI GI	g3212869
BLAST score	722
E value	1.0e-76
Match length	148
% identity	90
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	193401
Contig ID	9705_1.R1039
5'-most EST	uC-gsronu33B078b10b1
Method	BLASTX
NCBI GI	g2642448
BLAST score	457
E value	2.0e-45
Match length	184
% identity	53
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi|3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193402
Contig ID	9707_1.R1039
5'-most EST	LIB3166-048-P1-K1-C4
Method	BLASTX
NCBI GI	g3201615
BLAST score	316
E value	4.0e-29
Match length	112
% identity	60
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	193403
Contig ID	9715_1.R1039
5'-most EST	LIB3083-108-Q1-L1-D7

Seq. No.	193404
Contig ID	9721_1.R1039
5'-most EST	g5046129
Method	BLASTX
NCBI GI	g2213643
BLAST score	538
E value	7.0e-55
Match length	141
% identity	72
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	193405
Contig ID	9723_1.R1039
5'-most EST	g5045072
Method	BLASTX
NCBI GI	g2498464
BLAST score	224
E value	5.0e-18
Match length	74
% identity	62
NCBI Description	28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN) >gi|1136584 (U41745) PDGF associated protein [Homo sapiens] >gi|1589642|prf||2211382B platelet-derived growth factor-associated protein [Homo sapiens]

Seq. No.	193406
Contig ID	9723_2.R1039
5'-most EST	LIB3146-028-Q1-K1-B6
Method	BLASTX
NCBI GI	g1136586
BLAST score	166
E value	3.0e-11
Match length	74
% identity	49
NCBI Description	(U41744) PDGF associated protein [Rattus norvegicus] >gi|1589641|prf||2211382A platelet-derived growth factor-associated protein [Rattus norvegicus]

Seq. No.	193407
Contig ID	9743_1.R1039
5'-most EST	uC-gsflmaxxa041e05b1
Method	BLASTX
NCBI GI	g4263712
BLAST score	482
E value	3.0e-48
Match length	120
% identity	72
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	193408
Contig ID	9751_1.R1039
5'-most EST	uC-gsflnu33B023c05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34

E value 3.0e-09
Match length 35
% identity 59
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 193409
Contig ID 9752_1.R1039
5'-most EST LIB3083-108-Q1-L1-H2

Seq. No. 193410
Contig ID 9754_1.R1039
5'-most EST LIB3196-047-P1-M1-C5
Method BLASTX
NCBI GI g3123100
BLAST score 236
E value 9.0e-20
Match length 93
% identity 49
NCBI Description HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I >gi|4490640|emb|CAB11472.1| (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ _ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E(): 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe]

Seq. No. 193411
Contig ID 9758_1.R1039
5'-most EST LIB3145-001-P1-K1-C8
Method BLASTX
NCBI GI g729882
BLAST score 754
E value 2.0e-80
Match length 151
% identity 88
NCBI Description CASEIN KINASE II BETA' CHAIN (CK II) >gi|1076300|pir||S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi|467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi|2245122|emb|CAB10544| (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 193412
Contig ID 9761_1.R1039
5'-most EST LIB3166-010-P1-K1-H9
Method BLASTX
NCBI GI g1524370
BLAST score 268
E value 5.0e-43
Match length 134
% identity 65
NCBI Description (X92491) TOM20 [Solanum tuberosum]

Seq. No. 193413
Contig ID 9762_1.R1039
5'-most EST LIB3083-112-Q1-L1-G7
Method BLASTX
NCBI GI g3080420

BLAST score 835
E value 8.0e-98
Match length 292
% identity 65
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 193414
Contig ID 9763_1.R1039
5'-most EST g5049574
Method BLASTX
NCBI GI g3309168
BLAST score 192
E value 2.0e-14
Match length 149
% identity 32
NCBI Description (AF071313) COP9 complex subunit 3 [Mus musculus]

Seq. No. 193415
Contig ID 9765_1.R1039
5'-most EST LIB3166-011-P1-K1-A1
Method BLASTX
NCBI GI g4469023
BLAST score 562
E value 1.0e-57
Match length 184
% identity 64
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 193416
Contig ID 9778_1.R1039
5'-most EST LIB3148-041-Q1-K1-D2
Method BLASTX
NCBI GI g2252841
BLAST score 339
E value 1.0e-31
Match length 152
% identity 49
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 193417
Contig ID 9785_1.R1039
5'-most EST LIB3083-109-Q1-L1-C11
Method BLASTX
NCBI GI g2829870
BLAST score 351
E value 4.0e-33
Match length 185
% identity 49
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 193418
Contig ID 9795_1.R1039
5'-most EST g5048206
Method BLASTX
NCBI GI g3309170
BLAST score 886

E value 2.0e-95
Match length 375
% identity 50
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No. 193419
Contig ID 9807_1.R1039
5'-most EST LIB3083-109-Q1-L1-E1
Method BLASTX
NCBI GI g2558654
BLAST score 554
E value 8.0e-57
Match length 193
% identity 50
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 193420
Contig ID 9824_1.R1039
5'-most EST LIB3083-109-Q1-L1-F4
Method BLASTX
NCBI GI g3413716
BLAST score 303
E value 4.0e-27
Match length 287
% identity 22
NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >gi|3643589 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 193421
Contig ID 9832_1.R1039
5'-most EST LIB3083-109-Q1-L1-G11
Method BLASTX
NCBI GI g3877951
BLAST score 193
E value 2.0e-14
Match length 132
% identity 34
NCBI Description (Z81555) predicted using Genefinder [Caenorhabditis elegans]

Seq. No. 193422
Contig ID 9840_1.R1039
5'-most EST LIB3197-046-Q1-M1-B2

Seq. No. 193423
Contig ID 9842_1.R1039
5'-most EST LIB3083-109-Q1-L1-H1
Method BLASTX
NCBI GI g4539460
BLAST score 436
E value 7.0e-43
Match length 243
% identity 4
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 193424

Contig ID 9851_1.R1039
5'-most EST LIB3083-109-Q1-L1-H8

Seq. No. 193425
Contig ID 9855_2.R1039
5'-most EST LIB3149-048-Q1-K1-B7

Seq. No. 193426
Contig ID 9856_1.R1039
5'-most EST LIB3135-035-Q1-K1-C8
Method BLASTX
NCBI GI g2500354
BLAST score 1087
E value 1.0e-119
Match length 219
% identity 93
NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi|1902894|dbj|BAA19462| (AB001891) QM family protein [Solanum melongena]

Seq. No. 193427
Contig ID 9860_1.R1039
5'-most EST uC-gsronu33B055d02b1
Method BLASTX
NCBI GI g464621
BLAST score 521
E value 6.0e-53
Match length 159
% identity 68
NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi|280374|pir||S28586 ribosomal protein ML16 - common ice plant >gi|19539|emb|CAA49175| (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No. 193428
Contig ID 9862_1.R1039
5'-most EST LIB3083-110-Q1-L1-C11

Seq. No. 193429
Contig ID 9867_1.R1039
5'-most EST LIB3083-110-Q1-L1-D12

Seq. No. 193430
Contig ID 9869_1.R1039
5'-most EST LIB3083-110-Q1-L1-E10
Method BLASTX
NCBI GI g2739389
BLAST score 455
E value 3.0e-45
Match length 141
% identity 36
NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No. 193431
Contig ID 9872_2.R1039
5'-most EST LIB3083-110-Q1-L1-E9
Method BLASTX
NCBI GI g1009234

BLAST score	583
E value	2.0e-72
Match length	190
% identity	74
NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	193432
Contig ID	9875_1.R1039
5'-most EST	LIB3083-111-Q1-L1-E3
Method	BLASTX
NCBI GI	g3152559
BLAST score	655
E value	2.0e-68
Match length	162
% identity	73
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	193433
Contig ID	9881_1.R1039
5'-most EST	uC-gsronu33B144f09b1
Method	BLASTX
NCBI GI	g2980777
BLAST score	691
E value	1.0e-72
Match length	273
% identity	56
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	193434
Contig ID	9883_1.R1039
5'-most EST	LIB3083-110-Q1-L1-H12
Method	BLASTX
NCBI GI	g129594
BLAST score	922
E value	1.0e-105
Match length	231
% identity	79
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi|2146799|pir||S66343 phenylalanine ammonialyase (EC 4.3.1.5) 1 - common tobacco >gi|170350 (M84466) phenylalanine ammonia lyase [Nicotiana tabacum] >gi|2564057|dbj|BAA22948| (AB008200) phenylalanine ammonia-lyase [Nicotiana tabacum]

Seq. No.	193435
Contig ID	9885_1.R1039
5'-most EST	LIB3083-111-Q1-L1-A1
Method	BLASTX
NCBI GI	g1732587
BLAST score	216
E value	2.0e-17
Match length	69
% identity	59
NCBI Description	(U73203) farnesyltransferase beta subunit [Nicotiana glutinosa]

Seq. No.	193436
Contig ID	9887_1.R1039
5'-most EST	LIB3083-111-Q1-L1-A3

Seq. No.	193437
Contig ID	9889_1.R1039
5'-most EST	uC-gsflmaxxa054b04b1
Method	BLASTX
NCBI GI	g3269293
BLAST score	155
E value	6.0e-11
Match length	153
% identity	32
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	193438
Contig ID	9891_1.R1039
5'-most EST	LIB3135-026-Q1-K1-G7
Method	BLASTX
NCBI GI	g4544399
BLAST score	774
E value	1.0e-82
Match length	174
% identity	85
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	193439
Contig ID	9894_1.R1039
5'-most EST	LIB3083-111-Q1-L1-B2
Method	BLASTN
NCBI GI	g4544381
BLAST score	42
E value	3.0e-14
Match length	221
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	193440
Contig ID	9896_1.R1039
5'-most EST	LIB3189-039-P1-K1-F6
Method	BLASTX
NCBI GI	g1808656
BLAST score	615
E value	4.0e-64
Match length	149
% identity	78
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	193441
Contig ID	9898_1.R1039
5'-most EST	LIB3135-046-Q1-K1-A8
Method	BLASTX
NCBI GI	g2244835
BLAST score	253
E value	1.0e-21

Match length	69
% identity	75
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	193442
Contig ID	9898_2.R1039
5'-most EST	LIB3147-056-Q1-K1-H8
Method	BLASTX
NCBI GI	g2494144
BLAST score	161
E value	6.0e-20
Match length	104
% identity	50
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	193443
Contig ID	9898_3.R1039
5'-most EST	LIB3272-048-P1-K1-H2
Method	BLASTX
NCBI GI	g2244835
BLAST score	246
E value	1.0e-20
Match length	69
% identity	71
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	193444
Contig ID	9903_1.R1039
5'-most EST	g5044849
Method	BLASTX
NCBI GI	g3341694
BLAST score	348
E value	1.0e-32
Match length	146
% identity	48
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	193445
Contig ID	9919_1.R1039
5'-most EST	uC-gsflmaxxa015a02b1
Method	BLASTX
NCBI GI	g2959358
BLAST score	588
E value	3.0e-63
Match length	127
% identity	97
NCBI Description	(X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No.	193446
Contig ID	9921_1.R1039
5'-most EST	LIB3083-111-Q1-L1-E6
Method	BLASTX
NCBI GI	g3080420
BLAST score	503
E value	6.0e-51
Match length	121

% identity	78
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	193447
Contig ID	9930_1.R1039
5'-most EST	LIB3083-111-Q1-L1-F7
Method	BLASTX
NCBI GI	g2827661
BLAST score	538
E value	6.0e-55
Match length	193
% identity	60
NCBI Description	(AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No.	193448
Contig ID	9932_1.R1039
5'-most EST	uC-gsflnu33B083d05b1
Method	BLASTX
NCBI GI	g4335751
BLAST score	703
E value	3.0e-74
Match length	183
% identity	38
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	193449
Contig ID	9933_1.R1039
5'-most EST	LIB3147-042-Q1-K1-F6
Method	BLASTX
NCBI GI	g2677830
BLAST score	565
E value	4.0e-73
Match length	162
% identity	85
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	193450
Contig ID	9938_1.R1039
5'-most EST	uC-gsflnu33B023f06b1

Seq. No.	193451
Contig ID	9941_1.R1039
5'-most EST	LIB3146-007-Q1-K1-E11
Method	BLASTX
NCBI GI	g1351408
BLAST score	268
E value	1.0e-28
Match length	83
% identity	77
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease [Citrus sinensis]

Seq. No.	193452
Contig ID	9948_1.R1039
5'-most EST	LIB3083-112-Q1-L1-A2
Method	BLASTX
NCBI GI	g3063448
BLAST score	734
E value	9.0e-78
Match length	248
% identity	58
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	193453
Contig ID	9949_1.R1039
5'-most EST	LIB3166-023-P1-K1-H5
Method	BLASTX
NCBI GI	g2982458
BLAST score	648
E value	8.0e-68
Match length	171
% identity	75
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	193454
Contig ID	9952_1.R1039
5'-most EST	LIB3189-053-P1-K1-B12
Method	BLASTX
NCBI GI	g456568
BLAST score	786
E value	7.0e-84
Match length	148
% identity	98
NCBI Description	(L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No.	193455
Contig ID	9952_2.R1039
5'-most EST	LIB3165-027-P1-K1-E6
Method	BLASTX
NCBI GI	g464987
BLAST score	785
E value	9.0e-84
Match length	148
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi|421858|pir||S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi|297878|emb|CAA78715| (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi|349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	193456
Contig ID	9952_5.R1039
5'-most EST	LIB3165-026-P1-K1-D3
Method	BLASTX
NCBI GI	g464981
BLAST score	470
E value	3.0e-47

Match length	95
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	193457
Contig ID	9957_1.R1039
5'-most EST	LIB3165-027-P1-K1-E12
Method	BLASTX
NCBI GI	g3142301
BLAST score	207
E value	3.0e-16
Match length	114
% identity	48
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb|M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb|Q05946. ESTs gb|N65081 gb|Z30910, gb|Z34190, gb|Z34611, gb|R30101, gb|H3630

Seq. No.	193458
Contig ID	9960_1.R1039
5'-most EST	LIB3083-112-Q1-L1-B8

Seq. No.	193459
Contig ID	9962_1.R1039
5'-most EST	g5045643
Method	BLASTX
NCBI GI	g3402282
BLAST score	412
E value	5.0e-40
Match length	154
% identity	50
NCBI Description	(AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No.	193460
Contig ID	9964_1.R1039
5'-most EST	LIB3146-033-Q1-K1-G1

Seq. No.	193461
Contig ID	9967_1.R1039
5'-most EST	LIB3083-112-Q1-L1-D1
Method	BLASTX
NCBI GI	g4567235
BLAST score	365
E value	1.0e-34
Match length	114
% identity	61
NCBI Description	(AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	193462
Contig ID	9969_1.R1039
5'-most EST	LIB3083-112-Q1-L1-D3
Method	BLASTX
NCBI GI	g4455367

BLAST score 262
E value 8.0e-23
Match length 128
% identity 31
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 193463
Contig ID 9971_1.R1039
5'-most EST LIB3197-028-Q1-M1-A7
Method BLASTX
NCBI GI g4539390
BLAST score 1097
E value 1.0e-120
Match length 227
% identity 92
NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]

Seq. No. 193464
Contig ID 9971_2.R1039
5'-most EST LIB3166-023-P1-K1-A10
Method BLASTX
NCBI GI g4539390
BLAST score 511
E value 7.0e-52
Match length 112
% identity 88
NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]

Seq. No. 193465
Contig ID 9979_1.R1039
5'-most EST LIB3083-112-Q1-L1-F8
Method BLASTX
NCBI GI g4426565
BLAST score 166
E value 3.0e-11
Match length 84
% identity 39
NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 193466
Contig ID 9985_1.R1039
5'-most EST g3326500

Seq. No. 193467
Contig ID 9990_1.R1039
5'-most EST LIB3083-113-Q1-L1-A11
Method BLASTX
NCBI GI g3643603
BLAST score 477
E value 4.0e-88
Match length 253
% identity 65
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 193468

Contig ID 10003_1.R1039
5'-most EST LIB3189-035-P1-K1-A7

Seq. No. 193469
Contig ID 10008_1.R1039
5'-most EST LIB3083-113-Q1-L1-B7
Method BLASTN
NCBI GI g2342495
BLAST score 49
E value 2.0e-18
Match length 172
% identity 85
NCBI Description Ananas comosus mRNA for bromelain, complete cds

Seq. No. 193470
Contig ID 10014_1.R1039
5'-most EST uC-gsronu33B057g06b1
Method BLASTX
NCBI GI g1762130
BLAST score 739
E value 1.0e-78
Match length 164
% identity 91
NCBI Description (U46136) chaperonin-60 beta subunit [Solanum tuberosum]

Seq. No. 193471
Contig ID 10024_1.R1039
5'-most EST LIB3189-008-P1-K1-C11
Method BLASTX
NCBI GI g2088649
BLAST score 341
E value 4.0e-35
Match length 126
% identity 63
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 193472
Contig ID 10030_1.R1039
5'-most EST LIB3165-001-Q1-K1-E1
Method BLASTX
NCBI GI g3747111
BLAST score 355
E value 9.0e-41
Match length 151
% identity 58
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 193473
Contig ID 10032_1.R1039
5'-most EST g3326039
Method BLASTX
NCBI GI g2967452
BLAST score 252
E value 2.0e-21
Match length 131
% identity 44
NCBI Description (AB010882) hSNF2H [Homo sapiens]

>gi|4507075|ref|NP_003592.1|pSMARCA5| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member

Seq. No.	193474
Contig ID	10034_1.R1039
5'-most EST	LIB3083-113-Q1-L1-D9
Method	BLASTX
NCBI GI	g4406775
BLAST score	285
E value	3.0e-25
Match length	154
% identity	42
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	193475
Contig ID	10036_1.R1039
5'-most EST	uC-gsronu33B114c03b1
Method	BLASTX
NCBI GI	g4567226
BLAST score	166
E value	2.0e-11
Match length	46
% identity	65
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	193476
Contig ID	10040_1.R1039
5'-most EST	g5046060

Seq. No.	193477
Contig ID	10043_1.R1039
5'-most EST	LIB3083-113-Q1-L1-E7
Method	BLASTX
NCBI GI	g4314378
BLAST score	231
E value	7.0e-19
Match length	103
% identity	44
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	193478
Contig ID	10048_1.R1039
5'-most EST	LIB3135-022-Q1-K1-E7
Method	BLASTX
NCBI GI	g3367591
BLAST score	161
E value	1.0e-10
Match length	109
% identity	36
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	193479
Contig ID	10049_1.R1039
5'-most EST	uC-gsronu33B111a11b1

Seq. No.	193480

Contig ID	10051_1.R1039
5'-most EST	LIB3189-033-P1-K1-D1
Method	BLASTX
NCBI GI	g3776005
BLAST score	220
E value	9.0e-35
Match length	147
% identity	61
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	193481
Contig ID	10058_1.R1039
5'-most EST	uC-gsronu33B021g10b1
Method	BLASTX
NCBI GI	g1718097
BLAST score	1091
E value	1.0e-119
Match length	340
% identity	58
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi|626048|pir||A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi|532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	193482
Contig ID	10058_2.R1039
5'-most EST	LIB3083-113-Q1-L1-G11
Method	BLASTX
NCBI GI	g1718097
BLAST score	487
E value	9.0e-49
Match length	166
% identity	56
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi|626048|pir||A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi|532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	193483
Contig ID	10061_1.R1039
5'-most EST	LIB3083-113-Q1-L1-G3
Method	BLASTX
NCBI GI	g2281102
BLAST score	271
E value	1.0e-23
Match length	188
% identity	44
NCBI Description	(AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No.	193484
Contig ID	10064_1.R1039
5'-most EST	g5045301
Method	BLASTX
NCBI GI	g2245127
BLAST score	258

E value	4.0e-22
Match length	93
% identity	57
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193485
Contig ID	10065_1.R1039
5'-most EST	uC-gsronu33B038c07b1
Method	BLASTN
NCBI GI	g3819163
BLAST score	65
E value	4.0e-28
Match length	165
% identity	85
NCBI Description	Glycine max cctd gene

Seq. No.	193486
Contig ID	10068_1.R1039
5'-most EST	LIB3083-113-Q1-L1-H2
Method	BLASTX
NCBI GI	g3819164
BLAST score	1222
E value	1.0e-135
Match length	261
% identity	93
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	193487
Contig ID	10068_2.R1039
5'-most EST	LIB3145-045-Q1-K1-C4
Method	BLASTX
NCBI GI	g3819164
BLAST score	273
E value	4.0e-24
Match length	59
% identity	95
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	193488
Contig ID	10069_1.R1039
5'-most EST	LIB3135-034-Q1-K1-C6
Method	BLASTX
NCBI GI	g1173218
BLAST score	664
E value	1.0e-69
Match length	130
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193489
Contig ID	10069_2.R1039
5'-most EST	LIB3166-004-P1-K1-D5
Method	BLASTX

NCBI GI	g1173218
BLAST score	664
E value	1.0e-69
Match length	130
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193490
Contig ID	10069_3.R1039
5'-most EST	g5050845
Method	BLASTX
NCBI GI	g1173218
BLAST score	415
E value	1.0e-40
Match length	87
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193491
Contig ID	10069_4.R1039
5'-most EST	uC-gsflnu33B026g09b1
Method	BLASTX
NCBI GI	g1173218
BLAST score	664
E value	1.0e-69
Match length	130
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193492
Contig ID	10069_5.R1039
5'-most EST	g5045408
Method	BLASTX
NCBI GI	g1173218
BLAST score	643
E value	4.0e-67
Match length	130
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193493
Contig ID	10069_6.R1039
5'-most EST	LIB3189-010-P1-K1-G9
Method	BLASTX
NCBI GI	g1173218
BLAST score	487
E value	3.0e-49
Match length	107
% identity	97

NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi|440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi|2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	193494
Contig ID	10073_1.R1039
5'-most EST	g5046312
Method	BLASTX
NCBI GI	g2497538
BLAST score	649
E value	2.0e-87
Match length	458
% identity	43
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	193495
Contig ID	10073_2.R1039
5'-most EST	LIB3147-037-Q1-K2-G4
Method	BLASTX
NCBI GI	g2497543
BLAST score	735
E value	1.0e-77
Match length	328
% identity	47
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|542061|pir||S41379 pyruvate kinase - common tobacco >gi|444023|emb|CAA82628| (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	193496
Contig ID	10073_3.R1039
5'-most EST	LIB3166-043-P1-K1-A8

Seq. No.	193497
Contig ID	10078_1.R1039
5'-most EST	LIB3083-114-Q1-L1-A12
Method	BLASTX
NCBI GI	g4558553
BLAST score	512
E value	1.0e-51
Match length	172
% identity	59
NCBI Description	(AC007138) putative potassium channel [Arabidopsis thaliana]

Seq. No.	193498
Contig ID	10079_1.R1039
5'-most EST	LIB3083-114-Q1-L1-A3
Method	BLASTX
NCBI GI	g1817584
BLAST score	218
E value	2.0e-17
Match length	94
% identity	44
NCBI Description	(Y08991) adaptor protein [Homo sapiens]

Seq. No.	193499

Contig ID 10081_1.R1039
5'-most EST g5047911
Method BLASTX
NCBI GI g1945611
BLAST score 912
E value 3.0e-98
Match length 434
% identity 43
NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens] >gi|4506221|ref|NP_002807.1|pPSMD12| proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No. 193500
Contig ID 10081_2.R1039
5'-most EST LIB3145-014-Q1-K1-D11
Method BLASTX
NCBI GI g2827544
BLAST score 157
E value 2.0e-10
Match length 44
% identity 68
NCBI Description (AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No. 193501
Contig ID 10081_3.R1039
5'-most EST LIB3147-013-Q1-K1-E9

Seq. No. 193502
Contig ID 10087_1.R1039
5'-most EST uC-gsflmaxxa096f02b1

Seq. No. 193503
Contig ID 10102_1.R1039
5'-most EST LIB3189-001-P1-K1-F12
Method BLASTX
NCBI GI g285741
BLAST score 263
E value 7.0e-23
Match length 148
% identity 42
NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 193504
Contig ID 10105_1.R1039
5'-most EST LIB3083-114-Q1-L1-C7
Method BLASTX
NCBI GI g3075391
BLAST score 583
E value 1.0e-64
Match length 230
% identity 56
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 193505
Contig ID 10131_1.R1039
5'-most EST g5045390

Method	BLASTX
NCBI GI	g2914706
BLAST score	608
E value	5.0e-63
Match length	217
% identity	78
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	193506
Contig ID	10131_2.R1039
5'-most EST	g5047800
Method	BLASTX
NCBI GI	g2914706
BLAST score	625
E value	1.0e-70
Match length	198
% identity	76
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	193507
Contig ID	10137_1.R1039
5'-most EST	g5045723
Method	BLASTX
NCBI GI	g3402279
BLAST score	1582
E value	1.0e-177
Match length	329
% identity	89
NCBI Description	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq. No.	193508
Contig ID	10144_1.R1039
5'-most EST	LIB3083-114-Q1-L1-G11

Seq. No.	193509
Contig ID	10145_1.R1039
5'-most EST	g5046304
Method	BLASTX
NCBI GI	g3096944
BLAST score	360
E value	4.0e-34
Match length	156
% identity	49
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	193510
Contig ID	10158_1.R1039
5'-most EST	LIB3166-036-P1-K1-A5
Method	BLASTX
NCBI GI	g3193287
BLAST score	575
E value	4.0e-59
Match length	201
% identity	57
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	193511
Contig ID	10159_1.R1039
5'-most EST	LIB3148-015-Q1-K1-C7
Method	BLASTX
NCBI GI	g4490705
BLAST score	582
E value	4.0e-60
Match length	131
% identity	88
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	193512
Contig ID	10159_2.R1039
5'-most EST	uC-gsronu33B160a08b1
Method	BLASTX
NCBI GI	g4490705
BLAST score	147
E value	2.0e-09
Match length	37
% identity	86
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	193513
Contig ID	10161_1.R1039
5'-most EST	LIB3197-054-Q1-M1-D4
Method	BLASTX
NCBI GI	g4006941
BLAST score	410
E value	7.0e-40
Match length	155
% identity	52
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	193514
Contig ID	10169_1.R1039
5'-most EST	LIB3083-116-Q1-L1-A4
Method	BLASTX
NCBI GI	g4006873
BLAST score	476
E value	1.0e-47
Match length	236
% identity	44
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193515
Contig ID	10171_1.R1039
5'-most EST	LIB3145-010-Q1-K1-C7
Method	BLASTX
NCBI GI	g4210948
BLAST score	473
E value	2.0e-47
Match length	94
% identity	94

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 193516
Contig ID 10178_1.R1039
5'-most EST uC-gsflmaxxa041d07b1
Method BLASTX
NCBI GI g2493052
BLAST score 333
E value 5.0e-31
Match length 69
% identity 86
NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi|1655486|dbj|BAA13602| (D88377) epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No. 193517
Contig ID 10183_1.R1039
5'-most EST LIB3135-024-Q1-K1-C1

Seq. No. 193518
Contig ID 10187_1.R1039
5'-most EST LIB3146-033-Q1-K1-F12
Method BLASTX
NCBI GI g1172873
BLAST score 891
E value 4.0e-96
Match length 223
% identity 69
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi|541857|pir||JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi|435619|dbj|BAA02374| (D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 193519
Contig ID 10191_1.R1039
5'-most EST g5050553
Method BLASTX
NCBI GI g2731377
BLAST score 431
E value 3.0e-42
Match length 227
% identity 41
NCBI Description (U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]

Seq. No. 193520
Contig ID 10194_1.R1039
5'-most EST LIB3165-013-P1-K1-D4
Method BLASTX
NCBI GI g1304227
BLAST score 327
E value 6.0e-30
Match length 81
% identity 68
NCBI Description (D63781) Epoxide hydrolase [Glycine max] >gi|2764804|emb|CAA55293| (X78547) epoxide hydrolase [Glycine max]

Seq. No.	193521
Contig ID	10198_1.R1039
5'-most EST	LIB3120-018-Q1-K1-D4
Method	BLASTN
NCBI GI	g1350521
BLAST score	34
E value	2.0e-09
Match length	62
% identity	89
NCBI Description	Picea glauca late embryogenesis abundant protein (EMB2) mRNA, complete cds

Seq. No.	193522
Contig ID	10201_1.R1039
5'-most EST	LIB3135-031-Q1-K1-B9
Method	BLASTX
NCBI GI	g1730108
BLAST score	737
E value	1.0e-144
Match length	346
% identity	74
NCBI Description	LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN HYDROXYLASE) >gi|486848|pir||S36233 flavanone 3-hydroxylase homolog - garden petunia

Seq. No.	193523
Contig ID	10206_1.R1039
5'-most EST	LIB3083-116-Q1-L1-F4

Seq. No.	193524
Contig ID	10207_1.R1039
5'-most EST	LIB3189-013-P1-K1-F10
Method	BLASTX
NCBI GI	g3785983
BLAST score	457
E value	2.0e-45
Match length	148
% identity	57
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193525
Contig ID	10208_1.R1039
5'-most EST	LIB3146-043-Q1-K1-C11

Seq. No.	193526
Contig ID	10208_2.R1039
5'-most EST	LIB3146-052-Q1-K1-A2
Method	BLASTN
NCBI GI	g3449327
BLAST score	51
E value	1.0e-19
Match length	127
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 193527
Contig ID 10209_1.R1039
5'-most EST LIB3083-116-Q1-L1-F7

Seq. No. 193528
Contig ID 10232_1.R1039
5'-most EST LIB3148-024-Q1-K1-D9

Seq. No. 193529
Contig ID 10246_1.R1039
5'-most EST LIB3083-119-Q1-L1-B6
Method BLASTX
NCBI GI g2213590
BLAST score 371
E value 1.0e-35
Match length 139
% identity 54
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 193530
Contig ID 10254_1.R1039
5'-most EST LIB3083-119-Q1-L1-C2
Method BLASTX
NCBI GI g1351408
BLAST score 207
E value 3.0e-16
Match length 61
% identity 66
NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease [Citrus sinensis]

Seq. No. 193531
Contig ID 10257_1.R1039
5'-most EST LIB3083-119-Q1-L1-C5

Seq. No. 193532
Contig ID 10258_1.R1039
5'-most EST LIB3197-026-Q1-M1-B2
Method BLASTX
NCBI GI g2661840
BLAST score 392
E value 4.0e-38
Match length 109
% identity 67
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 193533
Contig ID 10262_1.R1039
5'-most EST g3325787
Method BLASTN
NCBI GI g2264309
BLAST score 69
E value 3.0e-30
Match length 213

% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.	193534
Contig ID	10262_2.R1039
5'-most EST	LIB3197-030-Q1-M1-C10
Method	BLASTX
NCBI GI	g4049341
BLAST score	274
E value	1.0e-23
Match length	261
% identity	32
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	193535
Contig ID	10266_1.R1039
5'-most EST	LIB3149-003-P1-K1-H8
Seq. No.	193536
Contig ID	10266_2.R1039
5'-most EST	LIB3197-027-Q1-M1-E3
Method	BLASTX
NCBI GI	g1518388
BLAST score	409
E value	2.0e-44
Match length	166
% identity	55
NCBI Description	(X91172) korean-radish isoperoxidase [Raphanus sativus]
Seq. No.	193537
Contig ID	10272_1.R1039
5'-most EST	LIB3083-119-Q1-L1-E2
Seq. No.	193538
Contig ID	10278_1.R1039
5'-most EST	LIB3197-031-Q1-M1-C12
Method	BLASTX
NCBI GI	g1495251
BLAST score	466
E value	9.0e-47
Match length	97
% identity	91
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.	193539
Contig ID	10280_1.R1039
5'-most EST	LIB3146-003-P1-K1-D1
Method	BLASTX
NCBI GI	g2739000
BLAST score	678
E value	1.0e-75
Match length	256
% identity	54
NCBI Description	(AF022459) CYP71D10p [Glycine max]
Seq. No.	193540

Contig ID	10287_1.R1039
5'-most EST	LIB3146-025-Q1-K1-F8
Method	BLASTX
NCBI GI	g2914706
BLAST score	445
E value	7.0e-44
Match length	108
% identity	76
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	193541
Contig ID	10287_2.R1039
5'-most EST	uC-gsronu33B005b12b1
Method	BLASTX
NCBI GI	g2924792
BLAST score	920
E value	2.0e-99
Match length	219
% identity	78
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	193542
Contig ID	10288_1.R1039
5'-most EST	LIB3083-119-Q1-L1-F8
Method	BLASTX
NCBI GI	g3273243
BLAST score	648
E value	5.0e-68
Match length	150
% identity	28
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi|3273245|dbj|BAA31166| (AB004814) NLS receptor [Oryza sativa]

Seq. No.	193543
Contig ID	10290_1.R1039
5'-most EST	LIB3197-052-Q1-M1-B6
Method	BLASTX
NCBI GI	g3046731
BLAST score	228
E value	7.0e-19
Match length	53
% identity	89
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	193544
Contig ID	10293_1.R1039
5'-most EST	uC-gsflnu33B061b02b1
Method	BLASTX
NCBI GI	g2497542
BLAST score	1120
E value	1.0e-123
Match length	263
% identity	83
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi|629696|pir||S44287 pyruvate kinase, plastid - common tobacco >gi|482938|emb|CAA82223| (Z28374) Pyruvate kinase;

plastid isozyme [Nicotiana tabacum]

Seq. No.	193545
Contig ID	10306_1.R1039
5'-most EST	LIB3189-005-P1-K1-E12

Seq. No.	193546
Contig ID	10308_1.R1039
5'-most EST	LIB3135-035-Q1-K1-H7
Method	BLASTX
NCBI GI	g3790569
BLAST score	183
E value	2.0e-13
Match length	49
% identity	59
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	193547
Contig ID	10311_1.R1039
5'-most EST	LIB3166-005-P1-K1-C8

Seq. No.	193548
Contig ID	10313_1.R1039
5'-most EST	LIB3272-058-P1-K1-C11
Method	BLASTX
NCBI GI	g3023195
BLAST score	1111
E value	1.0e-122
Match length	245
% identity	89
NCBI Description	14-3-3-LIKE PROTEIN B (SGF14B) >gi|1575727 (U70534) SGF14B [Glycine max]

Seq. No.	193549
Contig ID	10313_2.R1039
5'-most EST	uC-gsflnu33B026h11b1
Method	BLASTX
NCBI GI	g3023195
BLAST score	768
E value	7.0e-82
Match length	179
% identity	84
NCBI Description	14-3-3-LIKE PROTEIN B (SGF14B) >gi|1575727 (U70534) SGF14B [Glycine max]

Seq. No.	193550
Contig ID	10330_1.R1039
5'-most EST	uC-gsflmaxxa119h01b1

Seq. No.	193551
Contig ID	10334_1.R1039
5'-most EST	g5049757
Method	BLASTX
NCBI GI	g1256259
BLAST score	950
E value	1.0e-103

Match length	225
% identity	80
NCBI Description	(U50900) voltage-dependent anion channel protein [Spinacia oleracea]

Seq. No.	193552
Contig ID	10346_1.R1039
5'-most EST	LIB3145-056-Q1-K1-B7
Method	BLASTX
NCBI GI	g2827655
BLAST score	166
E value	1.0e-11
Match length	67
% identity	24
NCBI Description	(AL021637) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193553
Contig ID	10348_1.R1039
5'-most EST	LIB3083-120-Q1-L1-D8
Method	BLASTX
NCBI GI	g2281093
BLAST score	584
E value	1.0e-135
Match length	277
% identity	55
NCBI Description	(AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No.	193554
Contig ID	10352_1.R1039
5'-most EST	LIB3197-037-Q1-M1-C9
Method	BLASTX
NCBI GI	g4115377
BLAST score	515
E value	3.0e-52
Match length	150
% identity	69
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	193555
Contig ID	10360_1.R1039
5'-most EST	g5049615
Method	BLASTX
NCBI GI	g4539335
BLAST score	981
E value	1.0e-106
Match length	266
% identity	68
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	193556
Contig ID	10362_1.R1039
5'-most EST	LIB3083-120-Q1-L1-F12
Method	BLASTX
NCBI GI	g3184283
BLAST score	235
E value	1.0e-19
Match length	68

% identity	69
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
Seq. No.	193557
Contig ID	10363_1.R1039
5'-most EST	LIB3120-012-P1-K1-F6
Method	BLASTX
NCBI GI	g131972
BLAST score	378
E value	2.0e-36
Match length	88
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi|68151|pir||RKCNLU ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain precursor - upland cotton chloroplast >gi|11563|emb|CAA33896| (X15886) precursor [Gossypium hirsutum]
Seq. No.	193558
Contig ID	10370_1.R1039
5'-most EST	LIB3120-030-Q1-K1-G2
Method	BLASTX
NCBI GI	g4455351
BLAST score	300
E value	4.0e-27
Match length	78
% identity	71
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	193559
Contig ID	10375_1.R1039
5'-most EST	LIB3083-120-Q1-L1-G4
Method	BLASTN
NCBI GI	g3985934
BLAST score	90
E value	8.0e-43
Match length	194
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.	193560
Contig ID	10390_1.R1039
5'-most EST	LIB3120-007-Q1-K1-F8
Method	BLASTX
NCBI GI	g100362
BLAST score	1017
E value	1.0e-111
Match length	268
% identity	74
NCBI Description	photosystem II oxygen-evolving complex protein 2 precursor (clone T23-5B) - common tobacco (fragment) >gi|1345550|emb|CAA44292| (X62426) 23-kDa ploypeptide of photosystem II oxygen-evolving complex [Nicotiana tabacum]

Seq. No.	193561
Contig ID	10390_2.R1039
5'-most EST	LIB3166-025-P1-K1-C7
Method	BLASTX
NCBI GI	g1769905
BLAST score	570
E value	1.0e-103
Match length	257
% identity	74
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	193562
Contig ID	10391_1.R1039
5'-most EST	LIB3120-001-Q1-K1-A11

Seq. No.	193563
Contig ID	10392_1.R1039
5'-most EST	LIB3166-002-Q1-K1-D11
Method	BLASTX
NCBI GI	g1469930
BLAST score	472
E value	4.0e-47
Match length	135
% identity	74
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No.	193564
Contig ID	10396_1.R1039
5'-most EST	LIB3120-005-Q1-K1-C10
Method	BLASTX
NCBI GI	g289920
BLAST score	1400
E value	1.0e-155
Match length	264
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	193565
Contig ID	10396_2.R1039
5'-most EST	LIB3120-015-Q1-K1-H12
Method	BLASTX
NCBI GI	g289920
BLAST score	870
E value	1.0e-93
Match length	198
% identity	85
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	193566
Contig ID	10396_4.R1039
5'-most EST	LIB3165-046-Q1-K1-A12
Method	BLASTX
NCBI GI	g289920

BLAST score	447
E value	2.0e-44
Match length	121
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	193567
Contig ID	10398_1.R1039
5'-most EST	LIB3166-040-P1-K1-D6
Method	BLASTX
NCBI GI	g2864617
BLAST score	596
E value	2.0e-61
Match length	220
% identity	59
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	193568
Contig ID	10401_1.R1039
5'-most EST	LIB3120-001-Q1-K1-B1

Seq. No.	193569
Contig ID	10402_1.R1039
5'-most EST	LIB3165-018-P1-K1-B9
Method	BLASTX
NCBI GI	g1352821
BLAST score	850
E value	2.0e-91
Match length	162
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193570
Contig ID	10402_2.R1039
5'-most EST	LIB3165-034-P1-K6-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	870
E value	1.0e-93
Match length	162
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193571
Contig ID	10402_3.R1039
5'-most EST	LIB3120-008-Q1-K1-A7
Method	BLASTX

NCBI GI	g1352821
BLAST score	354
E value	8.0e-67
Match length	153
% identity	77
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193572
Contig ID	10402_4.R1039
5'-most EST	LIB3165-053-Q1-K1-G3
Method	BLASTX
NCBI GI	g1352821
BLAST score	452
E value	8.0e-45
Match length	97
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193573
Contig ID	10402_6.R1039
5'-most EST	LIB3165-040-Q1-K1-A1
Method	BLASTX
NCBI GI	g1352821
BLAST score	549
E value	3.0e-56
Match length	133
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193574
Contig ID	10402_7.R1039
5'-most EST	LIB3120-053-P1-K1-C5
Method	BLASTX
NCBI GI	g1352821
BLAST score	354
E value	2.0e-33
Match length	120
% identity	67
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi|279581|pir||RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi|450505|emb|CAA38026| (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	193575

Contig ID	10402_8.R1039
5'-most EST	LIB3165-053-Q1-K1-H4
Method	BLASTX
NCBI GI	g132091
BLAST score	336
E value	2.0e-51
Match length	208
% identity	75
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR (RUBISCO SMALL SUBUNIT F1) >gi|68065|pir||RKRPF1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (gene rbcSF1) - rape >gi|17852|emb|CAA39402| (X55937) ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

Seq. No.	193576
Contig ID	10402_11.R1039
5'-most EST	LIB3165-045-Q1-K1-E2
Method	BLASTN
NCBI GI	g450504
BLAST score	89
E value	2.0e-42
Match length	238
% identity	96
NCBI Description	G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No.	193577
Contig ID	10405_1.R1039
5'-most EST	LIB3165-016-P1-K1-G4

Seq. No.	193578
Contig ID	10406_1.R1039
5'-most EST	LIB3146-020-Q1-K1-A11
Method	BLASTX
NCBI GI	g2499535
BLAST score	564
E value	4.0e-66
Match length	227
% identity	63
NCBI Description	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi|595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]

Seq. No.	193579
Contig ID	10407_1.R1039
5'-most EST	LIB3120-001-Q1-K1-B4
Method	BLASTX
NCBI GI	g3913651
BLAST score	963
E value	1.0e-104
Match length	212
% identity	86
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi|2225993|emb|CAA74359| (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	193580
Contig ID	10410_1.R1039
5'-most EST	LIB3197-008-P1-M1-F6
Method	BLASTX
NCBI GI	g547683
BLAST score	1198
E value	1.0e-132
Match length	298
% identity	80
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi|170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi|445601|prf||1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	193581
Contig ID	10410_2.R1039
5'-most EST	LIB3135-025-Q1-K1-A9
Method	BLASTX
NCBI GI	g1708313
BLAST score	557
E value	2.0e-57
Match length	117
% identity	96
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi|999396|bbs|163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	193582
Contig ID	10410_3.R1039
5'-most EST	uC-gsflnu33B050a11b1
Method	BLASTX
NCBI GI	g1708313
BLAST score	475
E value	9.0e-48
Match length	100
% identity	95
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi|999396|bbs|163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	193583
Contig ID	10412_1.R1039
5'-most EST	LIB3165-028-P1-K1-H9
Method	BLASTX
NCBI GI	g3914605
BLAST score	723
E value	1.0e-76
Match length	197
% identity	72
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi|541930|pir||S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi|415852|emb|CAA79857| (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	193584
Contig ID	10412_2.R1039
5'-most EST	LIB3165-008-P1-K1-A3
Method	BLASTX
NCBI GI	g100616
BLAST score	1610
E value	0.0e+00
Match length	410
% identity	81
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi|167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi|167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	193585
Contig ID	10412_3.R1039
5'-most EST	LIB3165-021-P1-K1-H5
Method	BLASTX
NCBI GI	g132168
BLAST score	638
E value	5.0e-74
Match length	180
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi|81488|pir||A31082 ribulose-bisphosphate carboxylase activase precursor - spinach >gi|170129 (J03610) rubisco activase precursor [Spinacia oleracea]

Seq. No.	193586
Contig ID	10412_4.R1039
5'-most EST	LIB3165-014-P1-K1-F1

Seq. No.	193587
Contig ID	10412_5.R1039
5'-most EST	LIB3165-006-P1-K3-G7
Method	BLASTX
NCBI GI	g4406530
BLAST score	705
E value	1.0e-74
Match length	171
% identity	83
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	193588
Contig ID	10412_6.R1039
5'-most EST	LIB3166-044-P1-K1-B11
Method	BLASTX
NCBI GI	g100616
BLAST score	164
E value	8.0e-11
Match length	69
% identity	55
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi|167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi|167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	193589
Contig ID	10412_7.R1039
5'-most EST	LIB3165-021-P1-K1-H7
Method	BLASTX
NCBI GI	g3914603
BLAST score	540
E value	5.0e-63
Match length	199
% identity	66
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi|1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	193590
Contig ID	10412_8.R1039
5'-most EST	LIB3165-026-P1-K1-G10
Method	BLASTX
NCBI GI	g100616
BLAST score	249
E value	3.0e-21
Match length	60
% identity	80
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi|167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi|167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	193591
Contig ID	10412_13.R1039
5'-most EST	LIB3165-036-P1-K1-G6
Method	BLASTX
NCBI GI	g3687652
BLAST score	632
E value	4.0e-66
Match length	131
% identity	95
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	193592
Contig ID	10412_14.R1039
5'-most EST	LIB3165-019-P1-K1-E10
Method	BLASTX
NCBI GI	g166834
BLAST score	128
E value	1.0e-16
Match length	142
% identity	48
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi|2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	193593
Contig ID	10416_1.R1039
5'-most EST	LIB3165-046-Q1-K1-G5
Method	BLASTX
NCBI GI	g421826
BLAST score	1179
E value	1.0e-130
Match length	272
% identity	82
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi|298036|emb|CAA50712| (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	193594
Contig ID	10421_1.R1039
5'-most EST	LIB3120-044-P1-K1-E2
Method	BLASTX
NCBI GI	g2754849
BLAST score	1624
E value	0.0e+00
Match length	354
% identity	87
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	193595
Contig ID	10428_1.R1039
5'-most EST	g5045987
Method	BLASTX
NCBI GI	g2129944
BLAST score	376
E value	6.0e-36
Match length	136
% identity	56
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi|1395193|dbj|BAA12064| (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi|1435062|dbj|BAA06012| (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No.	193596
Contig ID	10431_1.R1039
5'-most EST	LIB3166-009-P1-K1-F9
Method	BLASTX
NCBI GI	g1345698
BLAST score	910
E value	2.0e-98
Match length	202
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi|99601|pir||S20917 chlorophyll a/b-binding protein - upland cotton >gi|452314|emb|CAA38025| (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	193597
Contig ID	10431_2.R1039
5'-most EST	LIB3120-032-Q1-K1-F1

Method	BLASTX
NCBI GI	g99600
BLAST score	499
E value	1.0e-50
Match length	98
% identity	96
NCBI Description	chlorophyll a/b-binding protein - upland cotton

Seq. No.	193598
Contig ID	10431_4.R1039
5'-most EST	LIB3165-004-P1-K1-B1
Method	BLASTX
NCBI GI	g1345698
BLAST score	247
E value	1.0e-50
Match length	113
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi|99601|pir||S20917 chlorophyll a/b-binding protein - upland cotton >gi|452314|emb|CAA38025| (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	193599
Contig ID	10432_1.R1039
5'-most EST	LIB3120-001-Q1-K1-E11
Method	BLASTX
NCBI GI	g2961378
BLAST score	569
E value	1.0e-58
Match length	190
% identity	36
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	193600
Contig ID	10433_1.R1039
5'-most EST	LIB3166-048-P1-K1-A1
Method	BLASTX
NCBI GI	g1730502
BLAST score	179
E value	1.0e-12
Match length	80
% identity	51
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi|110903|pir||A31351 probable transmembrane protein FT27 - mouse >gi|535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	193601
Contig ID	10435_1.R1039
5'-most EST	LIB3165-023-P1-K1-H11

Seq. No.	193602
Contig ID	10441_1.R1039
5'-most EST	LIB3165-007-P1-K1-E3
Method	BLASTX
NCBI GI	g2739375
BLAST score	243

E value	1.0e-20
Match length	107
% identity	50
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	193603
Contig ID	10444_1.R1039
5'-most EST	LIB3145-005-Q1-K1-D4
Method	BLASTX
NCBI GI	g464981
BLAST score	788
E value	5.0e-84
Match length	148
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	193604
Contig ID	10444_3.R1039
5'-most EST	LIB3146-049-Q1-K1-C3
Method	BLASTX
NCBI GI	g3721926
BLAST score	342
E value	5.0e-32
Match length	81
% identity	85
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	193605
Contig ID	10444_4.R1039
5'-most EST	LIB3165-049-Q1-K1-D1
Method	BLASTN
NCBI GI	g304040
BLAST score	62
E value	3.0e-26
Match length	62
% identity	100
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	193606
Contig ID	10444_5.R1039
5'-most EST	LIB3189-003-P1-K1-D11

Seq. No.	193607
Contig ID	10444_7.R1039
5'-most EST	LIB3165-033-P1-K1-D11
Method	BLASTX
NCBI GI	g2492514
BLAST score	845
E value	7.0e-91
Match length	177
% identity	93
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi|1483215|emb|CAA68141| (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	193608
Contig ID	10444_9.R1039
5'-most EST	uC-gsronu33B154d04b2
Method	BLASTN
NCBI GI	g304040
BLAST score	564
E value	0.0e+00
Match length	640
% identity	97
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	193609
Contig ID	10446_1.R1039
5'-most EST	LIB3120-054-P1-K1-E4
Method	BLASTX
NCBI GI	g100200
BLAST score	1173
E value	1.0e-129
Match length	279
% identity	80
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	193610
Contig ID	10448_1.R1039
5'-most EST	LIB3120-029-Q1-K1-E11
Method	BLASTX
NCBI GI	g100196
BLAST score	645
E value	1.0e-67
Match length	142
% identity	84
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	193611
Contig ID	10451_1.R1039
5'-most EST	LIB3189-053-P1-K1-A6
Method	BLASTX
NCBI GI	g1935914
BLAST score	240
E value	5.0e-20
Match length	78
% identity	56
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	193612
Contig ID	10452_1.R1039
5'-most EST	LIB3120-001-Q1-K1-F9

Seq. No.	193613
Contig ID	10453_1.R1039
5'-most EST	LIB3120-001-Q1-K1-G1

Seq. No.	193614
Contig ID	10454_1.R1039
5'-most EST	LIB3165-018-P1-K1-D12
Method	BLASTX
NCBI GI	g115765

BLAST score	1027
E value	1.0e-112
Match length	216
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi|100201|pir||S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi|19180|emb|CAA32197| (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi|170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi|226546|prf||1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	193615
Contig ID	10455_1.R1039
5'-most EST	LIB3165-017-P1-K1-F12
Method	BLASTX
NCBI GI	g2618731
BLAST score	1108
E value	1.0e-121
Match length	343
% identity	67
NCBI Description	(U49077) IAA21 [Arabidopsis thaliana]

Seq. No.	193616
Contig ID	10456_1.R1039
5'-most EST	uC-gsflmaxxa028f08b1
Method	BLASTX
NCBI GI	g1168655
BLAST score	335
E value	2.0e-31
Match length	102
% identity	55
NCBI Description	PROBABLE BETA-GLUCOSIDASE (GENTIOBIASE) (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGDALASE) >gi|710632|dbj|BAA06429| (D30762) beta-glucosidase [Bacillus subtilis] >gi|1805413|dbj|BAA08975| (D50453) homologue of beta-glucosidase of B. circulans [Bacillus subtilis] >gi|2632627|emb|CAB12135| (Z99105) similar to beta-glucosidase [Bacillus subtilis]

Seq. No.	193617
Contig ID	10459_1.R1039
5'-most EST	uC-gsronu33B004f03b1
Method	BLASTX
NCBI GI	g3641838
BLAST score	452
E value	4.0e-64
Match length	170
% identity	76
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	193618
Contig ID	10460_1.R1039
5'-most EST	LIB3120-031-Q1-K1-G6
Method	BLASTN

NCBI GI	g2529375
BLAST score	85
E value	9.0e-40
Match length	405
% identity	80
NCBI Description	Spinacia oleracea chloroplast sedoheptulose-1,7-bisphosphatase mRNA, complete cds

Seq. No.	193619
Contig ID	10461_1.R1039
5'-most EST	LIB3149-002-P1-K1-F9
Method	BLASTX
NCBI GI	g2583108
BLAST score	1215
E value	1.0e-134
Match length	315
% identity	75
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	193620
Contig ID	10466_1.R1039
5'-most EST	LIB3165-034-P1-K3-C12
Method	BLASTX
NCBI GI	g1181599
BLAST score	772
E value	3.0e-82
Match length	219
% identity	70
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	193621
Contig ID	10468_1.R1039
5'-most EST	LIB3165-040-Q1-K1-G5
Method	BLASTX
NCBI GI	g417256
BLAST score	182
E value	1.0e-12
Match length	222
% identity	30
NCBI Description	LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)

Seq. No.	193622
Contig ID	10468_2.R1039
5'-most EST	LIB3120-008-Q1-K1-F12
Method	BLASTX
NCBI GI	g1431629
BLAST score	1088
E value	1.0e-119
Match length	296
% identity	68
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	193623
Contig ID	10468_3.R1039
5'-most EST	LIB3147-060-Q1-K1-E7
Method	BLASTX
NCBI GI	g3080371

BLAST score	731
E value	2.0e-77
Match length	212
% identity	60
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	193624
Contig ID	10468_7.R1039
5'-most EST	LIB3145-045-Q1-K1-B5
Method	BLASTX
NCBI GI	g1431629
BLAST score	381
E value	2.0e-36
Match length	116
% identity	61
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	193625
Contig ID	10468_9.R1039
5'-most EST	LIB3147-047-Q1-K1-D1

Seq. No.	193626
Contig ID	10469_1.R1039
5'-most EST	LIB3166-022-P1-K1-A1
Method	BLASTX
NCBI GI	g2191138
BLAST score	290
E value	1.0e-25
Match length	138
% identity	54
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	193627
Contig ID	10469_2.R1039
5'-most EST	uC-gsflmaxxa097a07b1
Method	BLASTX
NCBI GI	g3218550
BLAST score	460
E value	5.0e-46
Match length	116
% identity	77
NCBI Description	(AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]

Seq. No.	193628
Contig ID	10471_1.R1039
5'-most EST	uC-gsronu33B150f09b1
Method	BLASTX
NCBI GI	g1169494
BLAST score	256
E value	5.0e-22
Match length	85
% identity	61
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi|2119915|pir||S60659 EF-Tu protein precursor - soybean >gi|949873|emb|CAA61444| (X89058) EF-Tu protein [Glycine

max]

Seq. No.	193629
Contig ID	10471_2.R1039
5'-most EST	LIB3165-051-Q1-K1-H4
Method	BLASTX
NCBI GI	g120663
BLAST score	785
E value	8.0e-84
Match length	191
% identity	80
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi|66027|pir||DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi|309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	193630
Contig ID	10472_1.R1039
5'-most EST	LIB3120-011-Q1-K1-A7
Method	BLASTX
NCBI GI	g1653230
BLAST score	158
E value	2.0e-10
Match length	62
% identity	52
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	193631
Contig ID	10474_1.R1039
5'-most EST	LIB3120-002-Q1-K1-A3
Method	BLASTX
NCBI GI	g729478
BLAST score	179
E value	6.0e-13
Match length	111
% identity	45
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi|442481|dbj|BAA04616| (D17790) ferredoxin-NADP+ reductase [Oryza sativa]

Seq. No.	193632
Contig ID	10476_1.R1039
5'-most EST	LIB3120-020-Q1-K1-A1
Method	BLASTX
NCBI GI	g1709825
BLAST score	565
E value	5.0e-58
Match length	170
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi|1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	193633
Contig ID	10476_2.R1039
5'-most EST	LIB3165-004-P1-K1-A11

Method	BLASTX
NCBI GI	g1709825
BLAST score	279
E value	8.0e-25
Match length	131
% identity	49
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi|1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	193634
Contig ID	10477_1.R1039
5'-most EST	LIB3120-002-Q1-K1-A7
Method	BLASTX
NCBI GI	g3334200
BLAST score	2003
E value	0.0e+00
Match length	419
% identity	89
NCBI Description	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi|2894362|emb|CAB16918| (Z99770) P-Protein precursor [Solanum tuberosum]

Seq. No.	193635
Contig ID	10479_1.R1039
5'-most EST	LIB3120-008-Q1-K1-G12
Method	BLASTN
NCBI GI	g2894361
BLAST score	440
E value	0.0e+00
Match length	1228
% identity	84
NCBI Description	Solanum tuberosum cv. Desire mRNA for P-protein

Seq. No.	193636
Contig ID	10484_1.R1039
5'-most EST	LIB3165-049-Q1-K1-G8
Method	BLASTX
NCBI GI	g3983125
BLAST score	506
E value	3.0e-51
Match length	168
% identity	64
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	193637
Contig ID	10485_1.R1039
5'-most EST	LIB3272-006-P1-K1-D4
Method	BLASTX
NCBI GI	g3142292
BLAST score	316
E value	2.0e-33
Match length	106
% identity	67
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb|U46571 from home sapiens. EST gb|Z47802 and

gb|Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	193638
Contig ID	10487_1.R1039
5'-most EST	LIB3145-017-Q1-K1-G11

Seq. No.	193639
Contig ID	10488_1.R1039
5'-most EST	LIB3120-036-Q1-K1-E5
Method	BLASTX
NCBI GI	g3914442
BLAST score	438
E value	3.0e-43
Match length	99
% identity	84
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi|1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	193640
Contig ID	10500_1.R1039
5'-most EST	LIB3165-055-P1-K1-H8
Method	BLASTX
NCBI GI	g2435517
BLAST score	409
E value	5.0e-40
Match length	132
% identity	58
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	193641
Contig ID	10501_1.R1039
5'-most EST	LIB3120-002-Q1-K1-D10
Method	BLASTX
NCBI GI	g133028
BLAST score	582
E value	4.0e-60
Match length	181
% identity	64
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi|71257|pir||R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi|16499|emb|CAA77480| (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi|16501|emb|CAA77594| (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	193642
Contig ID	10503_1.R1039
5'-most EST	LIB3166-027-P1-K1-C1
Method	BLASTN
NCBI GI	g3108248
BLAST score	328
E value	0.0e+00
Match length	391
% identity	96
NCBI Description	Gossypium barbadense clone pXP027 repetitive DNA sequence

Seq. No.	193643
Contig ID	10509_1.R1039
5'-most EST	g5047569
Method	BLASTX
NCBI GI	g4567202
BLAST score	2469
E value	0.0e+00
Match length	510
% identity	92
NCBI Description	(AC007168) putative myo-inositol 1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	193644
Contig ID	10511_1.R1039
5'-most EST	LIB3120-002-Q1-K1-E1

Seq. No.	193645
Contig ID	10514_1.R1039
5'-most EST	LIB3166-009-P1-K1-F4
Method	BLASTX
NCBI GI	g4335750
BLAST score	283
E value	6.0e-25
Match length	82
% identity	57
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	193646
Contig ID	10514_2.R1039
5'-most EST	uC-gsronu33B002d11b1
Method	BLASTX
NCBI GI	g4335750
BLAST score	274
E value	6.0e-24
Match length	84
% identity	55
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	193647
Contig ID	10516_1.R1039
5'-most EST	uC-gsflmaxxa098h02b1
Method	BLASTX
NCBI GI	g4512651
BLAST score	728
E value	4.0e-77
Match length	226
% identity	60
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	193648
Contig ID	10524_1.R1039
5'-most EST	uC-gsflnu33B084h07b1
Method	BLASTX

NCBI GI g3980415
BLAST score 473
E value 2.0e-47
Match length 161
% identity 58
NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 193649
Contig ID 10527_1.R1039
5'-most EST LIB3120-002-Q1-K1-F5

Seq. No. 193650
Contig ID 10528_1.R1039
5'-most EST uC-gsflmaxxa009e07b1
Method BLASTX
NCBI GI g1351408
BLAST score 806
E value 2.0e-86
Match length 175
% identity 82
NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease [Citrus sinensis]

Seq. No. 193651
Contig ID 10530_1.R1039
5'-most EST g5045572
Method BLASTX
NCBI GI g1175381
BLAST score 284
E value 3.0e-25
Match length 134
% identity 40
NCBI Description HYPOTHETICAL 44.9 KD PROTEIN C18B11.02C IN CHROMOSOME I >gi|2130286|pir||S58301 hypothetical protein SPAC18B11.02c - fission yeast (Schizosaccharomyces pombe) >gi|929888|emb|CAA90587| (Z50728) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 193652
Contig ID 10535_1.R1039
5'-most EST LIB3165-034-P1-K6-G1
Method BLASTX
NCBI GI g82080
BLAST score 1073
E value 1.0e-117
Match length 272
% identity 77
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi|226872|prf||1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 193653
Contig ID 10536_1.R1039

5'-most EST	LIB3165-032-P1-K1-H1
Method	BLASTX
NCBI GI	g1773330
BLAST score	970
E value	1.0e-179
Match length	369
% identity	88
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	193654
Contig ID	10537_1.R1039
5'-most EST	uC-gsronu33B111c08b1
Method	BLASTX
NCBI GI	g1076414
BLAST score	1723
E value	0.0e+00
Match length	462
% identity	71
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi|757534|emb|CAA59963| (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	193655
Contig ID	10537_2.R1039
5'-most EST	LIB3146-025-Q1-K1-E5
Method	BLASTX
NCBI GI	g1771160
BLAST score	224
E value	3.0e-18
Match length	64
% identity	67
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi|3687305|emb|CAA06999| (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	193656
Contig ID	10539_1.R1039
5'-most EST	LIB3120-005-Q1-K1-F10
Method	BLASTX
NCBI GI	g479406
BLAST score	980
E value	1.0e-106
Match length	205
% identity	64
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi|20671|emb|CAA49149| (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	193657
Contig ID	10539_2.R1039
5'-most EST	LIB3120-002-Q1-K1-G6
Method	BLASTX
NCBI GI	g479406
BLAST score	569
E value	1.0e-58
Match length	123
% identity	62

NCBI Description	chlorophyll a/b-binding protein - garden pea >gi|20671|emb|CAA49149| (X69215) chlorophyll a/b-binding protein [Pisum sativum]
Seq. No.	193658
Contig ID	10542_1.R1039
5'-most EST	LIB3165-027-P1-K1-F9
Seq. No.	193659
Contig ID	10543_1.R1039
5'-most EST	uC-gsflnu33B061e09b1
Method	BLASTX
NCBI GI	g4469014
BLAST score	325
E value	5.0e-30
Match length	180
% identity	40
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	193660
Contig ID	10551_1.R1039
5'-most EST	LIB3165-017-P1-K1-H3
Method	BLASTX
NCBI GI	g542100
BLAST score	723
E value	1.0e-76
Match length	165
% identity	84
NCBI Description	H-protein - Flaveria pringlei >gi|2147453|pir||S60195 H-protein precursor (clone HFC1) - Flaveria cronquistii >gi|437993|emb|CAA81073| (Z25854) H-protein [Flaveria cronquistii] >gi|437999|emb|CAA81074| (Z25855) H-protein [Flaveria pringlei] >gi|3688299|emb|CAB16912| (Z99763) H-protein [Flaveria pringlei]
Seq. No.	193661
Contig ID	10554_1.R1039
5'-most EST	LIB3120-007-Q1-K1-G7
Method	BLASTX
NCBI GI	g417544
BLAST score	754
E value	3.0e-80
Match length	195
% identity	75
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi|320209|pir||A60695 photosystem I chain II precursor - cucumber >gi|625966|pir||JQ2132 photosystem I complex 20K protein precursor - cucumber >gi|227772|prf||1710320A photosystem I 20kD protein [Cucumis sativus]
Seq. No.	193662
Contig ID	10556_1.R1039
5'-most EST	LIB3166-051-P1-K1-D6
Method	BLASTX
NCBI GI	g115833
BLAST score	741

E value	1.0e-78
Match length	174
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi|100195|pir||S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi|170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	193663
Contig ID	10566_1.R1039
5'-most EST	LIB3165-048-Q1-K1-E9
Method	BLASTX
NCBI GI	g3582021
BLAST score	375
E value	6.0e-36
Match length	134
% identity	55
NCBI Description	(Y09423) cytochrome P450 [Nepeta racemosa]

Seq. No.	193664
Contig ID	10569_1.R1039
5'-most EST	LIB3189-018-P1-K1-E9
Method	BLASTX
NCBI GI	g2894378
BLAST score	311
E value	2.0e-28
Match length	132
% identity	51
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	193665
Contig ID	10570_1.R1039
5'-most EST	uC-gsflnu33B085b09b1
Method	BLASTX
NCBI GI	g81601
BLAST score	319
E value	3.0e-29
Match length	118
% identity	59
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	193666
Contig ID	10572_1.R1039
5'-most EST	LIB3120-003-Q1-K1-C1
Method	BLASTX
NCBI GI	g4249385
BLAST score	634
E value	7.0e-66
Match length	298
% identity	49
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	193667
Contig ID	10573_1.R1039
5'-most EST	LIB3120-003-Q1-K1-C10
Method	BLASTX
NCBI GI	g4027895

BLAST score	163
E value	3.0e-11
Match length	42
% identity	74
NCBI Description	(AF049352) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	193668
Contig ID	10577_1.R1039
5'-most EST	LIB3120-003-Q1-K1-C3
Method	BLASTX
NCBI GI	g535780
BLAST score	818
E value	1.0e-87
Match length	173
% identity	90
NCBI Description	(D26609) transmembrane protein [Arabidopsis thaliana]

Seq. No.	193669
Contig ID	10578_1.R1039
5'-most EST	LIB3120-003-Q1-K1-C4
Method	BLASTX
NCBI GI	g1651865
BLAST score	158
E value	3.0e-10
Match length	72
% identity	54
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	193670
Contig ID	10583_1.R1039
5'-most EST	LIB3120-003-Q1-K1-D2
Method	BLASTX
NCBI GI	g1709651
BLAST score	586
E value	2.0e-60
Match length	167
% identity	68
NCBI Description	PLASTOCYANIN A PRECURSOR >gi|2117431|pir||S58209 plastocyanin a precursor - black poplar >gi|929813|emb|CAA90564| (Z50185) plastocyanin a [Populus nigra]

Seq. No.	193671
Contig ID	10589_1.R1039
5'-most EST	LIB3120-023-Q1-K1-F4
Method	BLASTN
NCBI GI	g166695
BLAST score	55
E value	9.0e-22
Match length	110
% identity	94
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	193672
Contig ID	10591_1.R1039
5'-most EST	LIB3120-003-Q1-K1-F1

Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	193673
Contig ID	10600_1.R1039
5'-most EST	uC-gsflmaxxa058f05b1
Method	BLASTX
NCBI GI	g2464872
BLAST score	365
E value	1.0e-34
Match length	165
% identity	47
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193674
Contig ID	10602_1.R1039
5'-most EST	LIB3120-003-Q1-K1-G2
Method	BLASTX
NCBI GI	g131399
BLAST score	523
E value	4.0e-53
Match length	129
% identity	78
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi|82277|pir||S00411 photosystem II 10K protein precursor - potato >gi|21489|emb|CAA28450| (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	193675
Contig ID	10605_1.R1039
5'-most EST	LIB3120-018-Q1-K1-B12
Method	BLASTX
NCBI GI	g3023752
BLAST score	403
E value	6.0e-39
Match length	130
% identity	64
NCBI Description	FERREDOXIN I PRECURSOR >gi|1418982|emb|CAA99756| (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	193676
Contig ID	10605_4.R1039
5'-most EST	LIB3165-043-Q1-K1-H6
Method	BLASTX
NCBI GI	g3023752
BLAST score	183
E value	3.0e-18
Match length	100
% identity	56
NCBI Description	FERREDOXIN I PRECURSOR >gi|1418982|emb|CAA99756| (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	193677
Contig ID	10606_1.R1039
5'-most EST	LIB3120-003-Q1-K1-H10
Method	BLASTX
NCBI GI	g2507458
BLAST score	315
E value	6.0e-29
Match length	142
% identity	43
NCBI Description	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi|81491|pir||S20496 thioredoxin m precursor - spinach >gi|21348|emb|CAA35826| (X51462) thioredoxin M precursor (AA -67 to 114) [Spinacia oleracea]

Seq. No.	193678
Contig ID	10607_1.R1039
5'-most EST	LIB3120-008-Q1-K1-D8

Seq. No.	193679
Contig ID	10610_1.R1039
5'-most EST	LIB3120-016-Q1-K1-A10

Seq. No.	193680
Contig ID	10613_1.R1039
5'-most EST	LIB3120-004-Q1-K1-A6
Method	BLASTX
NCBI GI	g2895866
BLAST score	737
E value	2.0e-85
Match length	255
% identity	67
NCBI Description	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]

Seq. No.	193681
Contig ID	10616_1.R1039
5'-most EST	LIB3166-004-P1-K1-H12
Method	BLASTX
NCBI GI	g505482
BLAST score	1455
E value	1.0e-162
Match length	331
% identity	86
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	193682
Contig ID	10621_1.R1039
5'-most EST	LIB3120-014-Q1-K1-E12
Method	BLASTX
NCBI GI	g2695931
BLAST score	376
E value	7.0e-36
Match length	82
% identity	82
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	193683
Contig ID	10629_1.R1039
5'-most EST	LIB3272-010-P1-K1-D1
Method	BLASTX
NCBI GI	g2760834
BLAST score	879
E value	1.0e-105
Match length	295
% identity	69
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	193684
Contig ID	10631_1.R1039
5'-most EST	LIB3272-029-P1-K1-E2
Method	BLASTX
NCBI GI	g1666173
BLAST score	509
E value	2.0e-51
Match length	156
% identity	67
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	193685
Contig ID	10631_3.R1039
5'-most EST	LIB3135-021-Q1-K1-A9

Seq. No.	193686
Contig ID	10638_1.R1039
5'-most EST	uC-gsflmaxxa028g04b1
Method	BLASTX
NCBI GI	g3183185
BLAST score	179
E value	5.0e-13
Match length	52
% identity	67
NCBI Description	GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG >gi|2224766|emb|CAB09712| (Z97025) product highly similar to elongation factor EF-G [Bacillus subtilis] >gi|2633848|emb|CAB13350| (Z99111) similar to GTP-binding elongation factor [Bacillus subtilis]

Seq. No.	193687
Contig ID	10641_1.R1039
5'-most EST	LIB3120-004-Q1-K1-E8
Method	BLASTX
NCBI GI	g2760834
BLAST score	487
E value	5.0e-49
Match length	161
% identity	63
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	193688
Contig ID	10641_2.R1039

5'-most EST	LIB3272-020-P1-K1-D1
Method	BLASTX
NCBI GI	g4490321
BLAST score	455
E value	3.0e-45
Match length	116
% identity	78
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	193689
Contig ID	10642_1.R1039
5'-most EST	LIB3165-014-P1-K1-B5
Method	BLASTX
NCBI GI	g1346809
BLAST score	581
E value	6.0e-60
Match length	189
% identity	58
NCBI Description	PATHOGEN-RELATED PROTEIN >gi|499074|emb|CAA34641| (X16648) pathogenesis related protein [Hordeum vulgare]

Seq. No.	193690
Contig ID	10642_2.R1039
5'-most EST	LIB3120-019-Q1-K1-G4
Method	BLASTX
NCBI GI	g3834316
BLAST score	313
E value	2.0e-28
Match length	127
% identity	49
NCBI Description	(AC005679) Similar to gb|X16648 pathogenesis related protein from Hordeum vulgare. EST gb|Z18206 comes from this gene. [Arabidopsis thaliana]

Seq. No.	193691
Contig ID	10645_1.R1039
5'-most EST	LIB3120-004-Q1-K1-F4
Method	BLASTX
NCBI GI	g3885334
BLAST score	938
E value	1.0e-102
Match length	210
% identity	82
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	193692
Contig ID	10651_1.R1039
5'-most EST	LIB3165-016-P1-K1-H5
Method	BLASTX
NCBI GI	g3913018
BLAST score	1677
E value	0.0e+00
Match length	396
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi|218155|dbj|BAA02730| (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No.	193693
Contig ID	10659_1.R1039
5'-most EST	g5047277
Method	BLASTX
NCBI GI	g132659
BLAST score	577
E value	6.0e-76
Match length	218
% identity	63
NCBI Description	50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13) >gi|81483|pir||A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi|170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No.	193694
Contig ID	10664_1.R1039
5'-most EST	uC-gsflnu33B011g10b1
Method	BLASTX
NCBI GI	g1008904
BLAST score	1470
E value	1.0e-164
Match length	289
% identity	89
NCBI Description	(L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No.	193695
Contig ID	10667_1.R1039
5'-most EST	LIB3166-014-P1-K1-B7
Method	BLASTX
NCBI GI	g2970654
BLAST score	864
E value	7.0e-93
Match length	247
% identity	72
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	193696
Contig ID	10668_1.R1039
5'-most EST	LIB3120-005-Q1-K1-B10

Seq. No.	193697
Contig ID	10671_1.R1039
5'-most EST	LIB3148-017-Q1-K1-C2
Method	BLASTX
NCBI GI	g4006924
BLAST score	1174
E value	1.0e-129
Match length	312
% identity	66
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	193698
Contig ID	10675_1.R1039

5'-most EST	LIB3145-058-Q1-K1-E1
Method	BLASTX
NCBI GI	g3914136
BLAST score	268
E value	3.0e-23
Match length	116
% identity	46
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi|2632171|emb|CAA05771| (AJ002958) lipid transfer protein [Cicer arietinum]

Seq. No.	193699
Contig ID	10680_1.R1039
5'-most EST	LIB3120-005-Q1-K1-D2

Seq. No.	193700
Contig ID	10682_1.R1039
5'-most EST	LIB3120-005-Q1-K1-D7
Method	BLASTX
NCBI GI	g2982453
BLAST score	1184
E value	1.0e-130
Match length	258
% identity	90
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	193701
Contig ID	10682_2.R1039
5'-most EST	LIB3165-034-P1-K3-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	251
E value	2.0e-21
Match length	56
% identity	91
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi|2118268|pir||S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi|927507|emb|CAA61946| (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	193702
Contig ID	10686_1.R1039
5'-most EST	uC-gsflmaxxa060h08b1
Method	BLASTX
NCBI GI	g4455223
BLAST score	1021
E value	1.0e-111
Match length	296
% identity	67
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	193703
Contig ID	10686_2.R1039
5'-most EST	uC-gsflmaxxa009g06b1

Seq. No.	193704
Contig ID	10689_2.R1039
5'-most EST	LIB3165-002-Q1-K1-F7
Method	BLASTX
NCBI GI	g4096662
BLAST score	839
E value	3.0e-90
Match length	168
% identity	96
NCBI Description	(U35026) Rab1-like small GTP-binding protein [Petunia x hybrida]

Seq. No.	193705
Contig ID	10691_1.R1039
5'-most EST	LIB3165-008-P1-K1-E5
Method	BLASTX
NCBI GI	g2499497
BLAST score	1893
E value	0.0e+00
Match length	444
% identity	87
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi|1161600|emb|CAA88841| (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No.	193706
Contig ID	10700_1.R1039
5'-most EST	g5046187
Method	BLASTN
NCBI GI	g4220640
BLAST score	34
E value	2.0e-09
Match length	130
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	193707
Contig ID	10705_1.R1039
5'-most EST	LIB3165-057-P1-K1-A5
Method	BLASTX
NCBI GI	g1791309
BLAST score	203
E value	7.0e-16
Match length	106
% identity	50
NCBI Description	(U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi|2852454|dbj|BAA24699| (AB010888) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	193708
Contig ID	10707_1.R1039
5'-most EST	LIB3146-055-Q1-K1-B9
Method	BLASTX
NCBI GI	g3281846
BLAST score	261
E value	4.0e-22

Match length	289
% identity	30
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	193709
Contig ID	10707_2.R1039
5'-most EST	LIB3120-006-Q1-K1-A5
Method	BLASTX
NCBI GI	g3281846
BLAST score	275
E value	4.0e-24
Match length	186
% identity	39
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	193710
Contig ID	10709_1.R1039
5'-most EST	uC-gsflmaxxa043f06b1
Method	BLASTX
NCBI GI	g2980793
BLAST score	911
E value	1.0e-98
Match length	241
% identity	70
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	193711
Contig ID	10729_1.R1039
5'-most EST	LIB3120-006-Q1-K1-D1
Method	BLASTX
NCBI GI	g4160300
BLAST score	152
E value	8.0e-10
Match length	59
% identity	47
NCBI Description	(AJ011893) cyclin D3.1 protein [Nicotiana tabacum]

Seq. No.	193712
Contig ID	10731_1.R1039
5'-most EST	LIB3120-034-Q1-K1-E2
Method	BLASTX
NCBI GI	g2244749
BLAST score	2206
E value	0.0e+00
Match length	471
% identity	88
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	193713
Contig ID	10731_2.R1039
5'-most EST	uC-gsflnu33B011e12b1
Method	BLASTX
NCBI GI	g2244749
BLAST score	753
E value	3.0e-80
Match length	151
% identity	93

NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	193714
Contig ID	10731_3.R1039
5'-most EST	LIB3135-053-Q1-K1-C7
Method	BLASTX
NCBI GI	g2244749
BLAST score	496
E value	5.0e-50
Match length	113
% identity	84
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	193715
Contig ID	10739_1.R1039
5'-most EST	LIB3165-003-P1-K1-D10
Method	BLASTX
NCBI GI	g4056456
BLAST score	170
E value	5.0e-12
Match length	52
% identity	65
NCBI Description	(AC005990) Strong similarity to gb|U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF|00107. ESTs gb|T43674, gb|H77006 and gb|AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	193716
Contig ID	10741_1.R1039
5'-most EST	LIB3120-006-Q1-K1-E2

Seq. No.	193717
Contig ID	10757_1.R1039
5'-most EST	LIB3120-037-P1-K1-F2

Seq. No.	193718
Contig ID	10759_1.R1039
5'-most EST	g5048438
Method	BLASTX
NCBI GI	g1001449
BLAST score	168
E value	2.0e-11
Match length	132
% identity	35
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	193719
Contig ID	10759_2.R1039
5'-most EST	LIB3120-020-Q1-K1-F11

Seq. No.	193720
Contig ID	10760_1.R1039
5'-most EST	LIB3120-006-Q1-K1-G5
Method	BLASTX
NCBI GI	g115794
BLAST score	445
E value	5.0e-60

Match length	122
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB-13) >gi|72748|pir||CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi|19277|emb|CAA42818| (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	193721
Contig ID	10761_1.R1039
5'-most EST	LIB3165-058-P1-K1-G1
Method	BLASTX
NCBI GI	g2501578
BLAST score	1343
E value	1.0e-149
Match length	309
% identity	87
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi|2129913|pir||S60047 ethylene-responsive protein 1 - Para rubber tree >gi|1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	193722
Contig ID	10762_1.R1039
5'-most EST	LIB3165-017-P1-K1-E3
Method	BLASTX
NCBI GI	g3510256
BLAST score	236
E value	1.0e-19
Match length	127
% identity	41
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	193723
Contig ID	10763_1.R1039
5'-most EST	LIB3165-045-Q1-K1-D10
Method	BLASTX
NCBI GI	g120663
BLAST score	685
E value	3.0e-72
Match length	178
% identity	75
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi|66027|pir||DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi|309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	193724
Contig ID	10767_1.R1039
5'-most EST	LIB3189-045-P1-K1-B8
Method	BLASTX
NCBI GI	g1362065
BLAST score	828
E value	1.0e-88
Match length	201

% identity	82
NCBI Description	small GTP-binding protein - garden pea >gi|871506|emb|CAA90081| (Z49901) small GTP-binding protein [Pisum sativum]
Seq. No.	193725
Contig ID	10767_2.R1039
5'-most EST	LIB3197-027-Q1-M1-A8
Method	BLASTX
NCBI GI	g114088
BLAST score	402
E value	1.0e-38
Match length	99
% identity	82
NCBI Description	RAS-RELATED PROTEIN ARA-3 >gi|320560|pir||JS0640 GTP-binding protein ara-3 - Arabidopsis thaliana >gi|217837|dbj|BAA00830| (D01025) small GTP-binding protein [Arabidopsis thaliana]
Seq. No.	193726
Contig ID	10767_3.R1039
5'-most EST	g5050098
Method	BLASTX
NCBI GI	g1362065
BLAST score	803
E value	1.0e-85
Match length	201
% identity	80
NCBI Description	small GTP-binding protein - garden pea >gi|871506|emb|CAA90081| (Z49901) small GTP-binding protein [Pisum sativum]
Seq. No.	193727
Contig ID	10769_1.R1039
5'-most EST	LIB3165-049-Q1-K1-H11
Method	BLASTX
NCBI GI	g4455226
BLAST score	157
E value	1.0e-13
Match length	115
% identity	41
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	193728
Contig ID	10772_1.R1039
5'-most EST	LIB3120-025-Q1-K1-E8
Method	BLASTX
NCBI GI	g2129538
BLAST score	1022
E value	1.0e-111
Match length	199
% identity	95
NCBI Description	AT103 protein - Arabidopsis thaliana >gi|1033195 (U38232) AT103 [Arabidopsis thaliana]
Seq. No.	193729
Contig ID	10773_1.R1039

5'-most EST	LIB3120-007-Q1-K1-A5
Method	BLASTX
NCBI GI	g3929651
BLAST score	430
E value	2.0e-42
Match length	95
% identity	88
NCBI Description	(AJ131206) microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	193730
Contig ID	10781_1.R1039
5'-most EST	LIB3120-007-Q1-K1-B4

Seq. No.	193731
Contig ID	10783_1.R1039
5'-most EST	LIB3120-032-Q1-K1-H6
Method	BLASTX
NCBI GI	g3047405
BLAST score	253
E value	5.0e-30
Match length	172
% identity	40
NCBI Description	(AF058333) tyrosine phosphorylated protein A [Escherichia coli]

Seq. No.	193732
Contig ID	10785_1.R1039
5'-most EST	LIB3146-006-Q1-K1-E3
Method	BLASTX
NCBI GI	g2558962
BLAST score	449
E value	2.0e-44
Match length	92
% identity	99
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	193733
Contig ID	10785_2.R1039
5'-most EST	LIB3149-063-Q1-K1-E11
Method	BLASTX
NCBI GI	g3021485
BLAST score	449
E value	2.0e-44
Match length	102
% identity	89
NCBI Description	(AJ224932) histone H2B-3 [Lycopersicon esculentum]

Seq. No.	193734
Contig ID	10793_1.R1039
5'-most EST	LIB3120-007-Q1-K1-C5
Method	BLASTX
NCBI GI	g1621268
BLAST score	760
E value	8.0e-81
Match length	170
% identity	84

NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	193735
Contig ID	10794_1.R1039
5'-most EST	LIB3120-007-Q1-K1-C6
Method	BLASTX
NCBI GI	g2832625
BLAST score	283
E value	4.0e-25
Match length	124
% identity	44
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	193736
Contig ID	10800_1.R1039
5'-most EST	LIB3120-046-P1-K1-G11
Method	BLASTX
NCBI GI	g625547
BLAST score	822
E value	3.0e-88
Match length	191
% identity	83
NCBI Description	chlorophyll a/b-binding protein type I - common tobacco >gi|493723|emb|CAA45523| (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]

Seq. No.	193737
Contig ID	10800_2.R1039
5'-most EST	LIB3120-026-Q1-K1-B12
Method	BLASTX
NCBI GI	g282865
BLAST score	608
E value	3.0e-63
Match length	137
% identity	84
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi|16207|emb|CAA39534| (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi|166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	193738
Contig ID	10801_1.R1039
5'-most EST	LIB3145-056-Q1-K1-G7
Method	BLASTN
NCBI GI	g18511
BLAST score	494
E value	0.0e+00
Match length	522
% identity	99
NCBI Description	G.hirsutum light regulated unknown reading frame DNA

Seq. No.	193739
Contig ID	10803_1.R1039
5'-most EST	LIB3120-007-Q1-K1-D3
Method	BLASTX
NCBI GI	g2970051

BLAST score 461
E value 4.0e-46
Match length 118
% identity 74
NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 193740
Contig ID 10807_1.R1039
5'-most EST LIB3145-010-Q1-K1-A11
Method BLASTX
NCBI GI g3738320
BLAST score 456
E value 3.0e-45
Match length 184
% identity 49
NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No. 193741
Contig ID 10808_1.R1039
5'-most EST LIB3165-040-Q1-K1-H8
Method BLASTX
NCBI GI g119748
BLAST score 635
E value 2.0e-66
Match length 135
% identity 90
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi|67241|pir||PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi|21245|emb|CAA43860| (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No. 193742
Contig ID 10809_1.R1039
5'-most EST uC-gsronu33B099g11b1
Method BLASTX
NCBI GI g478318
BLAST score 204
E value 5.0e-16
Match length 85
% identity 53
NCBI Description immunophilin p59 - mouse >gi|410499|emb|CAA50231| (X70887) p59 immunophilin [Mus musculus]

Seq. No. 193743
Contig ID 10810_1.R1039
5'-most EST LIB3120-007-Q1-K1-E4
Method BLASTX
NCBI GI g2341024
BLAST score 150
E value 2.0e-09
Match length 58
% identity 52
NCBI Description (AC000104) F19P19.1 [Arabidopsis thaliana]

Seq. No. 193744

Contig ID 10814_1.R1039
5'-most EST g5045563

Seq. No. 193745
Contig ID 10815_1.R1039
5'-most EST LIB3120-007-Q1-K1-F1
Method BLASTX
NCBI GI g2191138
BLAST score 207
E value 3.0e-16
Match length 106
% identity 46
NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 193746
Contig ID 10818_1.R1039
5'-most EST LIB3166-034-P1-K1-F7
Method BLASTX
NCBI GI g3915089
BLAST score 1994
E value 0.0e+00
Match length 472
% identity 82
NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi|2144269|pir||JC5129 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) A - Populus kitakamiensis >gi|1139561|dbj|BAA11579| (D82815) cinnamic acid 4-hydroxylase [Populus kitakamiensis] >gi|1777370|dbj|BAA11576| (D82812) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No. 193747
Contig ID 10818_2.R1039
5'-most EST LIB3145-020-Q1-K1-F5
Method BLASTX
NCBI GI g2144271
BLAST score 244
E value 1.0e-20
Match length 54
% identity 89
NCBI Description trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus kitakamiensis (fragment) >gi|1777372|dbj|BAA11578| (D82814) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No. 193748
Contig ID 10829_1.R1039
5'-most EST uC-gsronu33B145b01b1
Method BLASTX
NCBI GI g1199772
BLAST score 301
E value 5.0e-27
Match length 85
% identity 68
NCBI Description (D83226) extensin like protein [Populus nigra] >gi|1199774|dbj|BAA11855| (D83227) extensin like protein

[Populus nigra]

Seq. No.	193749
Contig ID	10829_2.R1039
5'-most EST	uC-gsronu33B136e11b1
Method	BLASTX
NCBI GI	g2583134
BLAST score	348
E value	9.0e-33
Match length	79
% identity	81
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	193750
Contig ID	10829_3.R1039
5'-most EST	LIB3120-015-Q1-K1-C12
Method	BLASTX
NCBI GI	g1199772
BLAST score	342
E value	4.0e-32
Match length	131
% identity	58
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi|1199774|dbj|BAA11855| (D83227) extensin like protein [Populus nigra]

Seq. No.	193751
Contig ID	10829_4.R1039
5'-most EST	g5048713
Method	BLASTX
NCBI GI	g4206199
BLAST score	272
E value	1.0e-23
Match length	253
% identity	15
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193752
Contig ID	10832_1.R1039
5'-most EST	LIB3120-008-Q1-K1-A11
Method	BLASTX
NCBI GI	g2335099
BLAST score	909
E value	4.0e-98
Match length	299
% identity	39
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	193753
Contig ID	10833_1.R1039
5'-most EST	LIB3120-031-Q1-K1-D1

Seq. No.	193754
Contig ID	10834_1.R1039
5'-most EST	LIB3146-007-Q1-K1-E9
Method	BLASTX

NCBI GI g115764
BLAST score 488
E value 1.0e-67
Match length 147
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN) >gi|170494 (J03558) chlorophyll a/b binding protein precursor [Lycopersicon esculentum]

Seq. No. 193755
Contig ID 10836_1.R1039
5'-most EST LIB3120-009-Q1-K1-H12
Method BLASTX
NCBI GI g2565275
BLAST score 566
E value 2.0e-58
Match length 121
% identity 84
NCBI Description (AF023611) Dim1p homolog [Homo sapiens]

Seq. No. 193756
Contig ID 10837_1.R1039
5'-most EST LIB3120-008-Q1-K1-A6
Method BLASTX
NCBI GI g3953473
BLAST score 355
E value 1.0e-43
Match length 153
% identity 67
NCBI Description (AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No. 193757
Contig ID 10837_2.R1039
5'-most EST LIB3165-058-P1-K1-B8
Method BLASTX
NCBI GI g3953473
BLAST score 502
E value 9.0e-51
Match length 146
% identity 74
NCBI Description (AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No. 193758
Contig ID 10843_1.R1039
5'-most EST LIB3120-008-Q1-K1-B12

Seq. No. 193759
Contig ID 10845_1.R1039
5'-most EST LIB3166-032-P1-K1-A5

Seq. No. 193760
Contig ID 10848_1.R1039
5'-most EST LIB3165-039-Q1-K1-B7
Method BLASTX
NCBI GI g4115357
BLAST score 488

E value	4.0e-49
Match length	187
% identity	52
NCBI Description	(AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193761
Contig ID	10849_1.R1039
5'-most EST	LIB3120-060-Q1-K1-F12

Seq. No.	193762
Contig ID	10849_2.R1039
5'-most EST	LIB3165-034-P1-K3-D8

Seq. No.	193763
Contig ID	10851_1.R1039
5'-most EST	LIB3165-053-Q1-K1-F12
Method	BLASTX
NCBI GI	g1346155
BLAST score	1553
E value	1.0e-173
Match length	321
% identity	93
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi|481942|pir||S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi|437995|emb|CAA81078| (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	193764
Contig ID	10853_1.R1039
5'-most EST	LIB3120-008-Q1-K1-C12
Method	BLASTX
NCBI GI	g2827888
BLAST score	571
E value	1.0e-58
Match length	172
% identity	67
NCBI Description	(AF016621) ATP-dependent Clp protease proteolytic subunit [Arabidopsis thaliana]

Seq. No.	193765
Contig ID	10858_1.R1039
5'-most EST	LIB3120-008-Q1-K1-C6

Seq. No.	193766
Contig ID	10862_1.R1039
5'-most EST	LIB3120-008-Q1-K1-D1
Method	BLASTX
NCBI GI	g2832669
BLAST score	155
E value	4.0e-10
Match length	102
% identity	42
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 193767

Contig ID	10865_1.R1039
5'-most EST	LIB3146-050-Q1-K1-B6
Method	BLASTX
NCBI GI	g1345969
BLAST score	741
E value	1.0e-78
Match length	219
% identity	66
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi|414732 (L25897) linoleoyl desaturase [Ricinus communis]

Seq. No.	193768
Contig ID	10868_1.R1039
5'-most EST	uC-gsflmaxxa041c01b1
Method	BLASTX
NCBI GI	g2864602
BLAST score	253
E value	1.0e-21
Match length	125
% identity	53
NCBI Description	(Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No.	193769
Contig ID	10872_1.R1039
5'-most EST	uC-gsflnu33B140e09b1
Method	BLASTX
NCBI GI	g2339978
BLAST score	811
E value	7.0e-87
Match length	228
% identity	70
NCBI Description	(Y11336) RGA1 protein [Arabidopsis thaliana]

Seq. No.	193770
Contig ID	10873_1.R1039
5'-most EST	LIB3165-006-P1-K3-C6

Seq. No.	193771
Contig ID	10874_1.R1039
5'-most EST	uC-gsflnu33B064b03b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	41
E value	2.0e-13
Match length	143
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	193772
Contig ID	10874_2.R1039
5'-most EST	uC-gsronu33B015g03b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	43
E value	1.0e-14
Match length	189

% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	193773
Contig ID	10877_1.R1039
5'-most EST	LIB3120-008-Q1-K1-E5
Method	BLASTX
NCBI GI	g2129636
BLAST score	237
E value	1.0e-19
Match length	184
% identity	35
NCBI Description	lipase - Arabidopsis thaliana >gi|1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	193774
Contig ID	10882_1.R1039
5'-most EST	LIB3120-037-P1-K1-H3
Method	BLASTX
NCBI GI	g2493694
BLAST score	227
E value	1.0e-18
Match length	92
% identity	52
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi|1076268|pir||S53025 photosystem II protein - spinach >gi|728716|emb|CAA59409| (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	193775
Contig ID	10890_1.R1039
5'-most EST	LIB3197-052-Q1-M1-D5
Method	BLASTX
NCBI GI	g3075399
BLAST score	110
E value	4.0e-09
Match length	67
% identity	57
NCBI Description	(AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No.	193776
Contig ID	10891_1.R1039
5'-most EST	g5048088
Method	BLASTX
NCBI GI	g4249388
BLAST score	782
E value	3.0e-93
Match length	231
% identity	73
NCBI Description	(AC005966) Similar to gb|AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	193777
Contig ID	10891_3.R1039
5'-most EST	LIB3197-031-Q1-M1-E8

Seq. No.	193778
Contig ID	10891_4.R1039
5'-most EST	uC-gsronu33B141a07b1

Seq. No.	193779
Contig ID	10891_5.R1039
5'-most EST	LIB3197-001-P1-M1-F9

Seq. No.	193780
Contig ID	10894_1.R1039
5'-most EST	uC-gsflnu33B100e03b1
Method	BLASTX
NCBI GI	g2894603
BLAST score	201
E value	1.0e-15
Match length	105
% identity	39
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	193781
Contig ID	10904_1.R1039
5'-most EST	LIB3272-042-P1-K1-F4
Method	BLASTX
NCBI GI	g487046
BLAST score	809
E value	1.0e-86
Match length	214
% identity	74
NCBI Description	photosystem I chain II precursor - wood tobacco >gi|407769|dbj|BAA02871| (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	193782
Contig ID	10909_1.R1039
5'-most EST	LIB3120-025-Q1-K1-E12
Method	BLASTX
NCBI GI	g3202030
BLAST score	458
E value	9.0e-46
Match length	137
% identity	69
NCBI Description	(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum crystallinum]

Seq. No.	193783
Contig ID	10914_1.R1039
5'-most EST	LIB3165-006-P1-K2-A11
Method	BLASTX
NCBI GI	g2239089
BLAST score	290
E value	6.0e-26
Match length	137
% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi|3288180|emb|CAB11466| (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	193784
Contig ID	10914_2.R1039
5'-most EST	LIB3120-009-Q1-K1-A12
Method	BLASTX
NCBI GI	g2239083
BLAST score	380
E value	4.0e-66
Match length	313
% identity	50
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi|2239087|emb|CAB06429| (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	193785
Contig ID	10914_3.R1039
5'-most EST	LIB3120-022-Q1-K1-C3

Seq. No.	193786
Contig ID	10916_1.R1039
5'-most EST	LIB3120-009-Q1-K1-A3
Method	BLASTX
NCBI GI	g1084321
BLAST score	688
E value	1.0e-72
Match length	175
% identity	74
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - cucumber >gi|2244614|dbj|BAA21089| (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No.	193787
Contig ID	10922_1.R1039
5'-most EST	LIB3165-019-P1-K1-D5

Seq. No.	193788
Contig ID	10937_1.R1039
5'-most EST	uC-gsronu33B156d06b1
Method	BLASTX
NCBI GI	g3759184
BLAST score	1038
E value	1.0e-113
Match length	293
% identity	67
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	193789
Contig ID	10944_1.R1039
5'-most EST	g5047424
Method	BLASTX
NCBI GI	g2979553
BLAST score	655
E value	2.0e-68
Match length	271
% identity	47
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193790
Contig ID	10945_1.R1039
5'-most EST	LIB3120-009-Q1-K1-D1

Seq. No.	193791
Contig ID	10946_1.R1039
5'-most EST	uC-gsflnu33B058g01b1
Method	BLASTX
NCBI GI	g2982243
BLAST score	260
E value	2.0e-22
Match length	70
% identity	66
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	193792
Contig ID	10950_1.R1039
5'-most EST	LIB3146-011-Q1-K1-F2
Method	BLASTX
NCBI GI	g2493694
BLAST score	273
E value	7.0e-24
Match length	117
% identity	53
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi|1076268|pir||S53025 photosystem II protein - spinach >gi|728716|emb|CAA59409| (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	193793
Contig ID	10951_1.R1039
5'-most EST	LIB3189-049-P1-K1-C7
Method	BLASTX
NCBI GI	g1931639
BLAST score	347
E value	2.0e-32
Match length	194
% identity	37
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	193794
Contig ID	10952_1.R1039
5'-most EST	LIB3146-003-P1-K1-F11
Method	BLASTX
NCBI GI	g3218467
BLAST score	192
E value	2.0e-14
Match length	129
% identity	35
NCBI Description	(AJ006529) putative phosphatase [Gallus gallus]

Seq. No.	193795
Contig ID	10954_1.R1039
5'-most EST	LIB3272-035-P1-K1-E11
Method	BLASTX
NCBI GI	g2511691

BLAST score 1477
E value 1.0e-164
Match length 343
% identity 78
NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 193796
Contig ID 10955_1.R1039
5'-most EST LIB3148-010-Q1-K1-E8

Seq. No. 193797
Contig ID 10956_1.R1039
5'-most EST LIB3165-023-P1-K1-E6
Method BLASTX
NCBI GI g4454459
BLAST score 177
E value 8.0e-13
Match length 90
% identity 51
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 193798
Contig ID 10958_1.R1039
5'-most EST LIB3272-009-P1-K1-A10
Method BLASTX
NCBI GI g3319354
BLAST score 417
E value 5.0e-41
Match length 106
% identity 81
NCBI Description (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No. 193799
Contig ID 10961_1.R1039
5'-most EST LIB3165-031-P1-K1-A11
Method BLASTX
NCBI GI g3808101
BLAST score 448
E value 1.0e-44
Match length 131
% identity 69
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 193800
Contig ID 10971_1.R1039
5'-most EST g5049973
Method BLASTX
NCBI GI g2245118
BLAST score 384
E value 7.0e-37
Match length 159
% identity 49
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 193801
Contig ID 10976_1.R1039

5'-most EST	LIB3189-018-P1-K1-G4
Method	BLASTX
NCBI GI	g2827634
BLAST score	153
E value	9.0e-10
Match length	145
% identity	36
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	193802
Contig ID	10977_1.R1039
5'-most EST	LIB3165-018-P1-K1-H12
Method	BLASTX
NCBI GI	g1354515
BLAST score	379
E value	2.0e-36
Match length	158
% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	193803
Contig ID	10977_2.R1039
5'-most EST	LIB3165-040-Q1-K1-C1
Method	BLASTX
NCBI GI	g1354515
BLAST score	255
E value	5.0e-22
Match length	103
% identity	55
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	193804
Contig ID	10979_1.R1039
5'-most EST	LIB3197-035-Q1-M1-E3
Method	BLASTX
NCBI GI	g1076627
BLAST score	690
E value	1.0e-72
Match length	190
% identity	74
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi|790479|emb|CAA58701| (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	193805
Contig ID	10984_1.R1039
5'-most EST	uC-gsflnu33B009e07b1
Method	BLASTX
NCBI GI	g1076283
BLAST score	570
E value	1.0e-58
Match length	151
% identity	73
NCBI Description	adenylylsulfate kinase (EC 2.7.1.25) precursor - Arabidopsis thaliana >gi|414737|emb|CAA53426| (X75782) APS

kinase [Arabidopsis thaliana] >gi|450235 (U05238) APS
kinase [Arabidopsis thaliana] >gi|1575322 (U59759) APS
kinase [Arabidopsis thaliana] >gi|3252812 (AC004705) APS
kinase [Arabidopsis thaliana]

Seq. No.	193806
Contig ID	10985_1.R1039
5'-most EST	LIB3147-045-Q1-K1-D4
Method	BLASTX
NCBI GI	g3236235
BLAST score	373
E value	2.0e-35
Match length	189
% identity	41
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi|4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	193807
Contig ID	10990_1.R1039
5'-most EST	uC-gsflnu33B101e03b1
Method	BLASTX
NCBI GI	g2529663
BLAST score	426
E value	6.0e-42
Match length	154
% identity	58
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi|3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	193808
Contig ID	10991_1.R1039
5'-most EST	g5047098
Method	BLASTX
NCBI GI	g2809246
BLAST score	650
E value	6.0e-68
Match length	237
% identity	66
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	193809
Contig ID	10998_1.R1039
5'-most EST	LIB3120-025-Q1-K1-C3
Method	BLASTX
NCBI GI	g1871577
BLAST score	425
E value	2.0e-41
Match length	169
% identity	46
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	193810
Contig ID	11002_1.R1039
5'-most EST	g5050506
Method	BLASTX

NCBI GI	g1213629
BLAST score	1288
E value	1.0e-142
Match length	284
% identity	83
NCBI Description	(X95991) pectinesterase [Prunus persica]

Seq. No.	193811
Contig ID	11004_1.R1039
5'-most EST	uC-gsronu33B021e06b1
Method	BLASTX
NCBI GI	g3256770
BLAST score	305
E value	3.0e-27
Match length	314
% identity	32
NCBI Description	(AP000002) 318aa long hypothetical UDP-glucose 4-epimerase [Pyrococcus horikoshii]

Seq. No.	193812
Contig ID	11004_3.R1039
5'-most EST	uC-gsflnu33B144e04b1

Seq. No.	193813
Contig ID	11004_4.R1039
5'-most EST	uC-gsronu33B168b01b1
Method	BLASTX
NCBI GI	g2129578
BLAST score	163
E value	7.0e-11
Match length	113
% identity	34
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi|928932|emb|CAA89205| (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi|1585435|prf||2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	193814
Contig ID	11006_1.R1039
5'-most EST	LIB3120-054-P1-K1-E3
Method	BLASTX
NCBI GI	g3850111
BLAST score	262
E value	1.0e-22
Match length	149
% identity	41
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	193815
Contig ID	11008_1.R1039
5'-most EST	LIB3120-010-Q1-K1-A6
Method	BLASTX
NCBI GI	g3063695
BLAST score	286
E value	1.0e-25

Match length	78
% identity	68
NCBI Description	(AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193816
Contig ID	11016_1.R1039
5'-most EST	LIB3120-010-Q1-K1-F7

Seq. No.	193817
Contig ID	11028_1.R1039
5'-most EST	LIB3166-046-P1-K1-F5
Method	BLASTX
NCBI GI	g4103324
BLAST score	1558
E value	1.0e-174
Match length	323
% identity	92
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	193818
Contig ID	11029_1.R1039
5'-most EST	LIB3120-018-Q1-K2-D2
Method	BLASTX
NCBI GI	g1170897
BLAST score	599
E value	4.0e-62
Match length	131
% identity	89
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi|1076276|pir||S52039 NAD-malate dehydrogenase - cucumber >gi|695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	193819
Contig ID	11030_1.R1039
5'-most EST	g5049544
Method	BLASTX
NCBI GI	g2088654
BLAST score	742
E value	8.0e-79
Match length	162
% identity	90
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	193820
Contig ID	11030_3.R1039
5'-most EST	LIB3272-044-P1-K1-G9
Method	BLASTX
NCBI GI	g2088654
BLAST score	552
E value	1.0e-56
Match length	123
% identity	88
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	193821
Contig ID	11030_4.R1039
5'-most EST	LIB3197-030-Q1-M1-H5
Method	BLASTX
NCBI GI	g1710587
BLAST score	388
E value	2.0e-37
Match length	117
% identity	72
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi|1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	193822
Contig ID	11031_1.R1039
5'-most EST	LIB3120-018-Q1-K2-C8
Method	BLASTX
NCBI GI	g1350625
BLAST score	264
E value	9.0e-23
Match length	66
% identity	82
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 PRECURSOR >gi|577089|emb|CAA58020| (X82776) chloroplast ribosomal protein L1 [Pisum sativum]

Seq. No.	193823
Contig ID	11035_1.R1039
5'-most EST	LIB3120-010-Q1-K1-E3

Seq. No.	193824
Contig ID	11038_1.R1039
5'-most EST	LIB3165-055-P1-K1-G9

Seq. No.	193825
Contig ID	11050_1.R1039
5'-most EST	LIB3120-010-Q1-K1-G3
Method	BLASTX
NCBI GI	g1076315
BLAST score	143
E value	7.0e-09
Match length	98
% identity	39
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi|853719|emb|CAA60793| (X87367) CYP90 protein [Arabidopsis thaliana] >gi|871988|emb|CAA60794| (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	193826
Contig ID	11051_1.R1039
5'-most EST	LIB3148-006-Q1-K1-D12
Method	BLASTX
NCBI GI	g542127
BLAST score	281
E value	2.0e-46
Match length	129
% identity	74

NCBI Description	chlorophyll a/b-binding protein type Ib, 20K chain precursor - barley (fragment) >gi|544702|bbs|143260 (S68729) light-harvesting complex I, LHC I [Hordeum vulgare=barley, Prato, Peptide Chloroplast, 231 aa] [Hordeum vulgare]
Seq. No.	193827
Contig ID	11052_1.R1039
5'-most EST	LIB3120-010-Q1-K1-G5
Method	BLASTX
NCBI GI	g132794
BLAST score	439
E value	2.0e-43
Match length	112
% identity	75
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi|71288|pir||R5NT22 ribosomal protein L22 - common tobacco chloroplast >gi|11866|emb|CAA77382| (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi|225236|prf||1211235BU ribosomal protein L22 [Nicotiana tabacum]
Seq. No.	193828
Contig ID	11057_1.R1039
5'-most EST	LIB3120-010-Q1-K1-H4
Method	BLASTX
NCBI GI	g2702270
BLAST score	356
E value	8.0e-34
Match length	115
% identity	61
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]
Seq. No.	193829
Contig ID	11068_1.R1039
5'-most EST	LIB3120-025-Q1-K1-A8
Method	BLASTX
NCBI GI	g3298439
BLAST score	464
E value	4.0e-46
Match length	149
% identity	62
NCBI Description	(AB010878) chloroplast ribosomal protein L4 [Nicotiana tabacum]
Seq. No.	193830
Contig ID	11068_2.R1039
5'-most EST	LIB3165-048-Q1-K1-E3
Method	BLASTX
NCBI GI	g3298439
BLAST score	451
E value	9.0e-45
Match length	149
% identity	35
NCBI Description	(AB010878) chloroplast ribosomal protein L4 [Nicotiana tabacum]
Seq. No.	193831

Contig ID	11074_1.R1039
5'-most EST	LIB3165-028-P1-K1-C10
Method	BLASTX
NCBI GI	g400890
BLAST score	386
E value	3.0e-37
Match length	156
% identity	47
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi|282837|pir||S26953 photosystem II 22K protein precursor - spinach >gi|21307|emb|CAA48557| (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi|260917|bbs|119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	193832
Contig ID	11074_2.R1039
5'-most EST	LIB3120-027-Q1-K1-D7
Method	BLASTX
NCBI GI	g400890
BLAST score	154
E value	4.0e-10
Match length	111
% identity	32
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi|282837|pir||S26953 photosystem II 22K protein precursor - spinach >gi|21307|emb|CAA48557| (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi|260917|bbs|119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	193833
Contig ID	11086_1.R1039
5'-most EST	LIB3135-039-Q1-K1-D4

Seq. No.	193834
Contig ID	11089_1.R1039
5'-most EST	LIB3120-011-Q1-K1-C7
Method	BLASTX
NCBI GI	g1122288
BLAST score	157
E value	2.0e-29
Match length	148
% identity	49
NCBI Description	(X94184) aspartate aminotransferase [Lotus japonicus]

Seq. No.	193835
Contig ID	11099_1.R1039
5'-most EST	LIB3120-011-Q1-K1-D7
Method	BLASTX
NCBI GI	g2342723
BLAST score	165
E value	6.0e-11
Match length	215
% identity	26
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	193836
Contig ID	11100_1.R1039
5'-most EST	LIB3166-038-P1-K1-B7

Seq. No.	193837
Contig ID	11101_1.R1039
5'-most EST	LIB3165-033-P1-K1-A5
Method	BLASTX
NCBI GI	g118564
BLAST score	1745
E value	0.0e+00
Match length	380
% identity	86
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi|65955|pir||DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi|18264|emb|CAA41434| (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi|18275|emb|CAA32764| (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	193838
Contig ID	11103_1.R1039
5'-most EST	LIB3120-011-Q1-K1-E10
Method	BLASTX
NCBI GI	g399940
BLAST score	1147
E value	1.0e-126
Match length	258
% identity	89
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi|100004|pir||S25005 heat shock protein, 70K - kidney bean >gi|22636|emb|CAA47345| (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	193839
Contig ID	11111_1.R1039
5'-most EST	LIB3165-006-P1-K2-G3
Method	BLASTX
NCBI GI	g100069
BLAST score	739
E value	2.0e-78
Match length	198
% identity	70
NCBI Description	cysteine proteinase tpp (EC 3.4.22.-) - garden pea >gi|3980198|emb|CAA46863| (X66061) thiolprotease [Pisum sativum]

Seq. No.	193840
Contig ID	11112_1.R1039
5'-most EST	LIB3120-011-Q1-K1-E8
Method	BLASTX
NCBI GI	g2811031
BLAST score	877
E value	1.0e-94
Match length	225
% identity	73

NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi|2109299|gb|AAB58165.1| (AF000132) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]
Seq. No.	193841
Contig ID	11115_1.R1039
5'-most EST	LIB3145-006-Q1-K1-D9
Seq. No.	193842
Contig ID	11116_1.R1039
5'-most EST	LIB3120-011-Q1-K1-F11
Seq. No.	193843
Contig ID	11120_1.R1039
5'-most EST	g5049084
Method	BLASTX
NCBI GI	g4490318
BLAST score	550
E value	3.0e-56
Match length	138
% identity	75
NCBI Description	(AL035678) 2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana]
Seq. No.	193844
Contig ID	11125_1.R1039
5'-most EST	LIB3135-010-Q1-K1-A9
Method	BLASTX
NCBI GI	g1345979
BLAST score	617
E value	2.0e-64
Match length	125
% identity	86
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi|459962 (L29215) plastid omega-6 desaturase [Glycine max]
Seq. No.	193845
Contig ID	11128_1.R1039
5'-most EST	LIB3120-022-Q1-K1-G11
Method	BLASTX
NCBI GI	g2315140
BLAST score	347
E value	5.0e-42
Match length	101
% identity	89
NCBI Description	(AB006187) S-adenosylmethionine synthase [Nicotiana tabacum]
Seq. No.	193846
Contig ID	11129_1.R1039
5'-most EST	LIB3120-011-Q1-K1-G12
Method	BLASTX
NCBI GI	g11837
BLAST score	486
E value	1.0e-64
Match length	141

% identity	91
NCBI Description	(Z00044) NADH dehydrogenase 27kD subunit [Nicotiana tabacum] >gi|225205|prf||1211235AK bhpB gene [Nicotiana tabacum]

Seq. No.	193847
Contig ID	11131_1.R1039
5'-most EST	LIB3149-043-Q1-K1-F6
Method	BLASTX
NCBI GI	g4335719
BLAST score	215
E value	4.0e-17
Match length	108
% identity	44
NCBI Description	(AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No.	193848
Contig ID	11132_1.R1039
5'-most EST	LIB3146-012-Q1-K1-F2
Method	BLASTX
NCBI GI	g4469003
BLAST score	164
E value	7.0e-11
Match length	75
% identity	44
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	193849
Contig ID	11138_1.R1039
5'-most EST	LIB3120-011-Q1-K1-H10
Method	BLASTX
NCBI GI	g2494261
BLAST score	701
E value	5.0e-74
Match length	147
% identity	92
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi|99903|pir||S21567 translation elongation factor Tu precursor - soybean chloroplast >gi|18776|emb|CAA46864| (X66062) EF-Tu [Glycine max] >gi|448921|prf||1918220A elongation factor Tu [Glycine max]

Seq. No.	193850
Contig ID	11148_1.R1039
5'-most EST	uC-gsronu33B078g04b1
Method	BLASTX
NCBI GI	g548852
BLAST score	361
E value	3.0e-34
Match length	82
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi|481227|pir||S38357 ribosomal protein S21 - rice >gi|303839|dbj|BAA02158| (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	193851

Contig ID	11148_2.R1039
5'-most EST	LIB3135-024-Q1-K1-B9
Method	BLASTX
NCBI GI	g548852
BLAST score	361
E value	3.0e-34
Match length	82
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi|481227|pir||S38357 ribosomal protein S21 - rice >gi|303839|dbj|BAA02158| (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	193852
Contig ID	11151_2.R1039
5'-most EST	LIB3120-012-P1-K1-A3

Seq. No.	193853
Contig ID	11157_1.R1039
5'-most EST	LIB3197-022-Q1-M1-H11
Method	BLASTX
NCBI GI	g1397319
BLAST score	268
E value	4.0e-23
Match length	184
% identity	35
NCBI Description	(U61953) No definition line found [Caenorhabditis elegans]

Seq. No.	193854
Contig ID	11163_1.R1039
5'-most EST	LIB3165-044-Q1-K1-B12
Method	BLASTX
NCBI GI	g2494076
BLAST score	1133
E value	1.0e-124
Match length	234
% identity	92
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi|1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	193855
Contig ID	11175_1.R1039
5'-most EST	LIB3120-012-P1-K1-C9
Method	BLASTX
NCBI GI	g585564
BLAST score	450
E value	2.0e-51
Match length	114
% identity	88
NCBI Description	FERREDOXIN--NITRITE REDUCTASE PRECURSOR >gi|81443|pir||S20495 ferredoxin--nitrite reductase (EC 1.7.7.1) precursor - European white birch >gi|17927|emb|CAA42690| (X60093) ferredoxin--nitrite reductase [Betula pendula]

Seq. No.	193856
Contig ID	11180_1.R1039
5'-most EST	LIB3120-018-Q1-K1-B3
Method	BLASTX
NCBI GI	g3885511
BLAST score	445
E value	4.0e-44
Match length	107
% identity	81
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	193857
Contig ID	11181_1.R1039
5'-most EST	LIB3120-012-P1-K1-D6
Method	BLASTX
NCBI GI	g2244910
BLAST score	302
E value	3.0e-27
Match length	202
% identity	39
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	193858
Contig ID	11185_1.R1039
5'-most EST	LIB3120-012-P1-K1-E12

Seq. No.	193859
Contig ID	11186_1.R1039
5'-most EST	LIB3149-002-P1-K1-C12

Seq. No.	193860
Contig ID	11195_1.R1039
5'-most EST	LIB3120-012-P1-K1-F3
Method	BLASTX
NCBI GI	g125578
BLAST score	498
E value	2.0e-50
Match length	128
% identity	75
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi|167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	193861
Contig ID	11196_1.R1039
5'-most EST	LIB3197-017-P1-M1-H11

Seq. No.	193862
Contig ID	11205_1.R1039
5'-most EST	LIB3165-022-P1-K1-A7
Method	BLASTX
NCBI GI	g125578
BLAST score	1740
E value	0.0e+00
Match length	390

% identity	85
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi|167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	193863
Contig ID	11205_2.R1039
5'-most EST	LIB3120-036-Q1-K1-F4
Method	BLASTN
NCBI GI	g167265
BLAST score	86
E value	2.0e-40
Match length	294
% identity	82
NCBI Description	Mesembryanthemum crystallinum phosphoribulokinase mRNA, complete CDS

Seq. No.	193864
Contig ID	11206_1.R1039
5'-most EST	LIB3120-012-P1-K1-G5

Seq. No.	193865
Contig ID	11207_1.R1039
5'-most EST	LIB3165-011-P1-K1-D5
Method	BLASTX
NCBI GI	g2244806
BLAST score	151
E value	1.0e-09
Match length	80
% identity	35
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193866
Contig ID	11208_1.R1039
5'-most EST	LIB3120-012-P1-K1-G9
Method	BLASTX
NCBI GI	g2950472
BLAST score	355
E value	3.0e-33
Match length	266
% identity	34
NCBI Description	(AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe]

Seq. No.	193867
Contig ID	11210_1.R1039
5'-most EST	LIB3120-012-P1-K1-H10

Seq. No.	193868
Contig ID	11212_1.R1039
5'-most EST	LIB3120-012-P1-K1-H2
Method	BLASTX
NCBI GI	g2921158
BLAST score	191
E value	3.0e-14
Match length	136
% identity	25

NCBI Description (AF022909) ClpC [Arabidopsis thaliana]

Seq. No. 193869
Contig ID 11217_1.R1039
5'-most EST LIB3145-040-Q1-K1-H1

Seq. No. 193870
Contig ID 11217_2.R1039
5'-most EST LIB3189-016-P1-K1-D11
Method BLASTN
NCBI GI g1465367
BLAST score 38
E value 1.0e-11
Match length 153
% identity 82
NCBI Description A.thaliana mRNA for RAP-1 protein

Seq. No. 193871
Contig ID 11220_1.R1039
5'-most EST g5050031
Method BLASTX
NCBI GI g586004
BLAST score 758
E value 1.0e-80
Match length 152
% identity 91
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi|421962|pir||S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi|542090|pir||S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi|311971|emb|CAA51654| (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No. 193872
Contig ID 11220_2.R1039
5'-most EST uC-gsronu33B078c07b1
Method BLASTX
NCBI GI g3176715
BLAST score 710
E value 4.0e-75
Match length 155
% identity 86
NCBI Description (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 193873
Contig ID 11220_3.R1039
5'-most EST LIB3147-056-Q1-K1-F6
Method BLASTX
NCBI GI g3915000
BLAST score 434
E value 6.0e-43
Match length 90
% identity 88
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi|2305109 (AF009734) Cu/Zn superoxide dismutase [Capsicum annuum]

Seq. No. 193874

Contig ID 11222_1.R1039
5'-most EST LIB3165-044-Q1-K1-E9
Method BLASTX
NCBI GI g3650033
BLAST score 345
E value 5.0e-32
Match length 212
% identity 39
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 193875
Contig ID 11230_1.R1039
5'-most EST LIB3272-032-P1-K1-A1
Method BLASTX
NCBI GI g2879867
BLAST score 412
E value 4.0e-40
Match length 115
% identity 68
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 193876
Contig ID 11230_2.R1039
5'-most EST LIB3196-050-P1-M1-G9
Method BLASTX
NCBI GI g2879867
BLAST score 418
E value 4.0e-41
Match length 115
% identity 70
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 193877
Contig ID 11232_1.R1039
5'-most EST LIB3120-013-Q1-K1-C10
Method BLASTX
NCBI GI g4325341
BLAST score 848
E value 4.0e-91
Match length 189
% identity 80
NCBI Description (AF128393) similar to the Drosophila DES-1 protein (GB:X94180) [Arabidopsis thaliana]

Seq. No. 193878
Contig ID 11240_1.R1039
5'-most EST LIB3120-013-Q1-K1-D12
Method BLASTX
NCBI GI g4218120
BLAST score 703
E value 3.0e-74
Match length 214
% identity 62
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	193879
Contig ID	11246_1.R1039
5'-most EST	LIB3120-013-Q1-K1-E10

Seq. No.	193880
Contig ID	11251_1.R1039
5'-most EST	LIB3149-022-Q1-K1-F6
Method	BLASTX
NCBI GI	g294062
BLAST score	217
E value	4.0e-17
Match length	145
% identity	34
NCBI Description	(L06469) major latex protein [Papaver somniferum]

Seq. No.	193881
Contig ID	11251_2.R1039
5'-most EST	LIB3166-028-P1-K1-B4
Method	BLASTN
NCBI GI	g2246457
BLAST score	265
E value	1.0e-147
Match length	825
% identity	84
NCBI Description	Ricinus communis sterol-C-methyltransferase mRNA, complete cds

Seq. No.	193882
Contig ID	11251_3.R1039
5'-most EST	uC-gsronu33B018b10b1
Method	BLASTX
NCBI GI	g1399380
BLAST score	1561
E value	1.0e-174
Match length	321
% identity	88
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	193883
Contig ID	11253_1.R1039
5'-most EST	LIB3120-013-Q1-K1-E7

Seq. No.	193884
Contig ID	11256_1.R1039
5'-most EST	LIB3149-034-Q1-K1-C1

Seq. No.	193885
Contig ID	11256_2.R1039
5'-most EST	LIB3120-013-Q1-K1-F11

Seq. No.	193886
Contig ID	11257_1.R1039
5'-most EST	LIB3120-013-Q1-K1-F12
Method	BLASTX
NCBI GI	g2500115

BLAST score	673
E value	6.0e-71
Match length	151
% identity	85
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi|529375|dbj|BAA07108| (D37870) Glutathione Reductase precursor [Spinacia oleracea]

Seq. No.	193887
Contig ID	11258_1.R1039
5'-most EST	LIB3149-040-Q1-K1-G7
Method	BLASTX
NCBI GI	g4539422
BLAST score	520
E value	5.0e-53
Match length	124
% identity	76
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	193888
Contig ID	11258_2.R1039
5'-most EST	LIB3165-027-P1-K1-D4
Method	BLASTX
NCBI GI	g4539422
BLAST score	374
E value	6.0e-36
Match length	115
% identity	68
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	193889
Contig ID	11259_1.R1039
5'-most EST	uC-gsflnu33B084d11b1
Method	BLASTX
NCBI GI	g1587206
BLAST score	2582
E value	0.0e+00
Match length	535
% identity	94
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	193890
Contig ID	11290_1.R1039
5'-most EST	uC-gsflnu33B004e07b1
Method	BLASTX
NCBI GI	g1073820
BLAST score	270
E value	5.0e-44
Match length	129
% identity	71
NCBI Description	adenylosuccinate lyase (purB) homolog - Haemophilus influenzae (strain Rd KW20)

Seq. No.	193891
Contig ID	11291_1.R1039
5'-most EST	LIB3120-014-Q1-K1-B12

Seq. No.	193892
Contig ID	11294_1.R1039
5'-most EST	g5045999
Method	BLASTX
NCBI GI	g2507455
BLAST score	1255
E value	1.0e-139
Match length	306
% identity	78
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi|322401|pir||A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi|170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	193893
Contig ID	11311_1.R1039
5'-most EST	LIB3272-005-P1-K1-F6

Seq. No.	193894
Contig ID	11322_1.R1039
5'-most EST	LIB3165-045-Q1-K1-G6
Method	BLASTX
NCBI GI	g4337177
BLAST score	1174
E value	1.0e-129
Match length	250
% identity	87
NCBI Description	(AC006416) Identical to gb|Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb|R30578, gb|R90475, gb|T22384, gb|T22425, gb|N64934 and gb|T46767 come from this gene. [Arabidopsis thaliana]

Seq. No.	193895
Contig ID	11329_1.R1039
5'-most EST	g5044894
Method	BLASTX
NCBI GI	g1172664
BLAST score	720
E value	5.0e-76
Match length	150
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi|419791|pir||S31165 photosystem I chain III precursor - Flaveria trinervia >gi|298482|bbs|127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi|168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	193896
Contig ID	11329_2.R1039
5'-most EST	LIB3165-013-P1-K1-A7
Method	BLASTX
NCBI GI	g1172664
BLAST score	379
E value	2.0e-36

Match length	80
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi|419791|pir||S31165 photosystem I chain III precursor - Flaveria trinervia >gi|298482|bbs|127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi|168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	193897
Contig ID	11336_1.R1039
5'-most EST	LIB3120-015-Q1-K1-B9
Method	BLASTX
NCBI GI	g117291
BLAST score	781
E value	3.0e-83
Match length	181
% identity	83
NCBI Description	CHLOROPLAST PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E29) >gi|81464|pir||S03638 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - spinach >gi|21274|emb|CAA32016| (X13754) phosphate translocator protein (AA 1 - 404) [Spinacia oleracea]

Seq. No.	193898
Contig ID	11337_1.R1039
5'-most EST	LIB3145-045-Q1-K1-D8
Method	BLASTX
NCBI GI	g585241
BLAST score	237
E value	9.0e-20
Match length	61
% identity	77
NCBI Description	HISTONE H1 >gi|629668|pir||S45662 histone H1 - tomato >gi|424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No.	193899
Contig ID	11337_2.R1039
5'-most EST	LIB3146-020-Q1-K1-D6
Method	BLASTX
NCBI GI	g4106696
BLAST score	264
E value	8.0e-23
Match length	67
% identity	78
NCBI Description	(AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No.	193900
Contig ID	11342_1.R1039
5'-most EST	uC-gsflnu33B126f04b1
Method	BLASTN
NCBI GI	g1773329
BLAST score	97
E value	4.0e-47
Match length	245

% identity	85
NCBI Description	Mesembryanthemum crystallinum glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	193901
Contig ID	11343_1.R1039
5'-most EST	uC-gsflnu33B093a10b1
Method	BLASTX
NCBI GI	g1928981
BLAST score	1055
E value	1.0e-115
Match length	251
% identity	81
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	193902
Contig ID	11345_1.R1039
5'-most EST	LIB3146-006-Q1-K1-F3
Method	BLASTX
NCBI GI	g1084321
BLAST score	278
E value	3.0e-29
Match length	117
% identity	66
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - cucumber >gi|2244614|dbj|BAA21089| (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No.	193903
Contig ID	11346_1.R1039
5'-most EST	LIB3120-015-Q1-K1-C8
Method	BLASTX
NCBI GI	g4559372
BLAST score	286
E value	2.0e-25
Match length	81
% identity	78
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	193904
Contig ID	11347_1.R1039
5'-most EST	LIB3120-015-Q1-K1-C9
Method	BLASTX
NCBI GI	g2651308
BLAST score	329
E value	1.0e-30
Match length	117
% identity	66
NCBI Description	(AC002336) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	193905
Contig ID	11351_1.R1039
5'-most EST	LIB3165-017-P1-K1-F5
Method	BLASTX
NCBI GI	g2494415

BLAST score	1156
E value	1.0e-127
Match length	275
% identity	85
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi|515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]

Seq. No.	193906
Contig ID	11352_1.R1039
5'-most EST	LIB3120-015-Q1-K1-D2

Seq. No.	193907
Contig ID	11364_1.R1039
5'-most EST	LIB3145-033-Q1-K1-E3

Seq. No.	193908
Contig ID	11365_1.R1039
5'-most EST	LIB3120-015-Q1-K1-E6

Seq. No.	193909
Contig ID	11366_1.R1039
5'-most EST	g5044754

Seq. No.	193910
Contig ID	11377_1.R1039
5'-most EST	LIB3272-052-P1-K1-A7
Method	BLASTX
NCBI GI	g2493144
BLAST score	568
E value	2.0e-58
Match length	165
% identity	73
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi|2118221|pir||S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi|926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	193911
Contig ID	11377_2.R1039
5'-most EST	uC-gsronu33B171f02b1
Method	BLASTX
NCBI GI	g2493144
BLAST score	580
E value	1.0e-59
Match length	165
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi|2118221|pir||S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi|926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	193912
Contig ID	11377_3.R1039
5'-most EST	LIB3166-005-P1-K1-H8
Method	BLASTX
NCBI GI	g2493146
BLAST score	404
E value	2.0e-39
Match length	115
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi|755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi|4519415|dbj|BAA75542.1| (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	193913
Contig ID	11377_5.R1039
5'-most EST	LIB3196-050-P1-M1-C4
Method	BLASTX
NCBI GI	g2493144
BLAST score	405
E value	1.0e-39
Match length	99
% identity	84
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi|2118221|pir||S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi|926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	193914
Contig ID	11380_1.R1039
5'-most EST	LIB3120-015-Q1-K1-G1
Method	BLASTX
NCBI GI	g2501647
BLAST score	480
E value	3.0e-48
Match length	134
% identity	74
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi|1362120|pir||S55732 uroporphyrinogen decarboxylase - common tobacco >gi|1009429|emb|CAA58040| (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No.	193915
Contig ID	11382_1.R1039
5'-most EST	LIB3120-015-Q1-K1-G11
Method	BLASTX
NCBI GI	g1172974
BLAST score	556
E value	4.0e-57
Match length	137
% identity	79
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 >gi|454860 (M80799) ribosomal protein L16 [Vigna unguiculata]

Seq. No. 193916

Contig ID	11383_1.R1039
5'-most EST	LIB3120-015-Q1-K1-G12
Method	BLASTX
NCBI GI	g122781
BLAST score	599
E value	7.0e-62
Match length	143
% identity	77
NCBI Description	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi|82210|pir||A05198 hypothetical protein 229 - common tobacco chloroplast >gi|11844|emb|CAA77364| (Z00044) hypothetical protein [Nicotiana tabacum] >gi|225212|prf||1211235AT ORF 229 [Nicotiana tabacum]

Seq. No.	193917
Contig ID	11389_1.R1039
5'-most EST	LIB3120-015-Q1-K1-G8

Seq. No.	193918
Contig ID	11397_1.R1039
5'-most EST	uC-gsronu33B154b12b2
Method	BLASTX
NCBI GI	g3335359
BLAST score	172
E value	6.0e-17
Match length	84
% identity	56
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	193919
Contig ID	11400_1.R1039
5'-most EST	LIB3120-027-Q1-K1-A2
Method	BLASTX
NCBI GI	g2791423
BLAST score	225
E value	3.0e-18
Match length	76
% identity	55
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	193920
Contig ID	11402_1.R1039
5'-most EST	LIB3120-016-Q1-K1-A11

Seq. No.	193921
Contig ID	11404_1.R1039
5'-most EST	LIB3272-003-P1-K1-D3
Method	BLASTX
NCBI GI	g1351408
BLAST score	907
E value	4.0e-98
Match length	246
% identity	69
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A

vascular processing protease [Citrus sinensis]

Seq. No.	193922
Contig ID	11405_1.R1039
5'-most EST	LIB3165-006-P1-K4-A10
Method	BLASTX
NCBI GI	g3913711
BLAST score	1583
E value	1.0e-177
Match length	333
% identity	89
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi|4379384|emb|CAA53076| (X75327) glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating,NADP+) [Pisum sativum]

Seq. No.	193923
Contig ID	11405_2.R1039
5'-most EST	LIB3165-008-P1-K1-F2
Method	BLASTX
NCBI GI	g2494076
BLAST score	486
E value	6.0e-49
Match length	104
% identity	88
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi|1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	193924
Contig ID	11414_2.R1039
5'-most EST	LIB3120-016-Q1-K1-B7
Method	BLASTX
NCBI GI	g4220481
BLAST score	559
E value	3.0e-57
Match length	167
% identity	61
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	193925
Contig ID	11418_1.R1039
5'-most EST	LIB3120-016-Q1-K1-C11

Seq. No.	193926
Contig ID	11429_1.R1039
5'-most EST	LIB3120-016-Q1-K1-E11
Method	BLASTX
NCBI GI	g4539315
BLAST score	305
E value	1.0e-27

Match length	63
% identity	55
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	193927
Contig ID	11430_1.R1039
5'-most EST	g5047420

Seq. No.	193928
Contig ID	11430_2.R1039
5'-most EST	uC-gsflnu33B114f10b1

Seq. No.	193929
Contig ID	11434_1.R1039
5'-most EST	LIB3165-060-Q1-K1-A12
Method	BLASTX
NCBI GI	g2194137
BLAST score	379
E value	6.0e-36
Match length	170
% identity	54
NCBI Description	(AC002062) ESTs gb|R29947,gb|H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	193930
Contig ID	11435_1.R1039
5'-most EST	LIB3165-037-P1-K1-H2
Method	BLASTX
NCBI GI	g4455251
BLAST score	367
E value	4.0e-35
Match length	115
% identity	63
NCBI Description	(AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	193931
Contig ID	11440_1.R1039
5'-most EST	LIB3120-016-Q1-K1-G9
Method	BLASTX
NCBI GI	g4454014
BLAST score	135
E value	3.0e-13
Match length	110
% identity	38
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	193932
Contig ID	11441_1.R1039
5'-most EST	LIB3145-043-Q1-K1-E4
Method	BLASTX
NCBI GI	g3510256
BLAST score	149
E value	2.0e-09
Match length	64
% identity	45

NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	193933
Contig ID	11446_1.R1039
5'-most EST	LIB3149-031-Q1-K1-C12
Method	BLASTX
NCBI GI	g1707878
BLAST score	1639
E value	0.0e+00
Match length	343
% identity	90
NCBI Description	AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi|2129976|pir||S59948 aminomethyltransferase (EC 2.1.2.10) precursor - potato >gi|438254|emb|CAA81081| (Z25862) T-protein [Solanum tuberosum]

Seq. No.	193934
Contig ID	11457_1.R1039
5'-most EST	LIB3165-027-P1-K1-A11
Method	BLASTX
NCBI GI	g1256259
BLAST score	274
E value	3.0e-24
Match length	112
% identity	51
NCBI Description	(U50900) voltage-dependent anion channel protein [Spinacia oleracea]

Seq. No.	193935
Contig ID	11458_1.R1039
5'-most EST	LIB3120-017-Q1-K1-B2
Method	BLASTX
NCBI GI	g4510387
BLAST score	599
E value	5.0e-62
Match length	172
% identity	65
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	193936
Contig ID	11461_1.R1039
5'-most EST	LIB3120-017-Q1-K1-B5
Method	BLASTX
NCBI GI	g1071913
BLAST score	290
E value	4.0e-26
Match length	72
% identity	79
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi|1066153|dbj|BAA07177| (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	193937
Contig ID	11469_1.R1039
5'-most EST	g5045824
Method	BLASTX
NCBI GI	g121349

BLAST score	1746
E value	0.0e+00
Match length	342
% identity	92
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS28) >gi|20368|emb|CAA32461| (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza sativa]

Seq. No.	193938
Contig ID	11470_1.R1039
5'-most EST	LIB3189-048-P1-K1-A2
Method	BLASTX
NCBI GI	g2244847
BLAST score	604
E value	1.0e-62
Match length	210
% identity	57
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	193939
Contig ID	11470_2.R1039
5'-most EST	LIB3165-045-Q1-K1-B9
Method	BLASTX
NCBI GI	g2244847
BLAST score	668
E value	5.0e-70
Match length	215
% identity	61
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	193940
Contig ID	11470_3.R1039
5'-most EST	LIB3165-041-Q1-K1-F1
Method	BLASTX
NCBI GI	g1708313
BLAST score	515
E value	3.0e-52
Match length	114
% identity	91
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi|999396|bbs|163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	193941
Contig ID	11472_1.R1039
5'-most EST	LIB3166-058-P1-K1-A12

Seq. No.	193942
Contig ID	11483_1.R1039
5'-most EST	LIB3120-017-Q1-K1-D7

Seq. No.	193943
Contig ID	11485_1.R1039

5'-most EST	LIB3272-046-P1-K1-B11
Method	BLASTX
NCBI GI	g303730
BLAST score	545
E value	7.0e-56
Match length	121
% identity	88
NCBI Description	(D12540) GTP-binding protein [Pisum sativum] >gi|738933|prf||2001457A GTP-binding protein [Pisum sativum]

Seq. No.	193944
Contig ID	11494_1.R1039
5'-most EST	g5050733
Method	BLASTX
NCBI GI	g4160280
BLAST score	1012
E value	1.0e-110
Match length	290
% identity	63
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	193945
Contig ID	11496_1.R1039
5'-most EST	LIB3149-064-Q1-K1-A2
Method	BLASTX
NCBI GI	g4538945
BLAST score	533
E value	3.0e-54
Match length	147
% identity	68
NCBI Description	(AL049483) putative thioredoxin [Arabidopsis thaliana]

Seq. No.	193946
Contig ID	11498_1.R1039
5'-most EST	uC-gsflmaxxa008e05b1
Method	BLASTX
NCBI GI	g121689
BLAST score	412
E value	4.0e-40
Match length	111
% identity	65
NCBI Description	GAST1 PROTEIN PRECURSOR >gi|100217|pir||S22151 GAST1 protein - tomato >gi|19247|emb|CAA44807| (X63093) gast1 [Lycopersicon esculentum]

Seq. No.	193947
Contig ID	11501_1.R1039
5'-most EST	LIB3120-017-Q1-K1-F2
Method	BLASTX
NCBI GI	g4512655
BLAST score	168
E value	1.0e-11
Match length	128
% identity	50
NCBI Description	(AC007048) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	193948
Contig ID	11503_1.R1039
5'-most EST	LIB3120-017-Q1-K1-F4
Method	BLASTX
NCBI GI	g132677
BLAST score	471
E value	4.0e-47
Match length	170
% identity	61
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi|71241|pir||R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi|16497|emb|CAA77593| (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	193949
Contig ID	11504_1.R1039
5'-most EST	LIB3197-030-Q1-M1-D6
Method	BLASTX
NCBI GI	g4454012
BLAST score	457
E value	2.0e-45
Match length	123
% identity	67
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	193950
Contig ID	11505_3.R1039
5'-most EST	LIB3145-014-Q1-K1-E2
Method	BLASTX
NCBI GI	g3668080
BLAST score	721
E value	2.0e-76
Match length	202
% identity	72
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	193951
Contig ID	11507_1.R1039
5'-most EST	LIB3165-006-P1-K1-A8
Method	BLASTX
NCBI GI	g1353352
BLAST score	1174
E value	1.0e-130
Match length	375
% identity	63
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	193952
Contig ID	11507_2.R1039
5'-most EST	LIB3165-036-P1-K1-B2
Method	BLASTX
NCBI GI	g1353352
BLAST score	183

E value	1.0e-13
Match length	48
% identity	75
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	193953
Contig ID	11508_1.R1039
5'-most EST	LIB3120-027-Q1-K1-C2
Method	BLASTX
NCBI GI	g1755156
BLAST score	393
E value	4.0e-38
Match length	130
% identity	59
NCBI Description	(U75189) germin-like protein [Arabidopsis thaliana] >gi|1755158 (U75190) germin-like protein [Arabidopsis thaliana] >gi|1755170 (U75196) germin-like protein [Arabidopsis thaliana] >gi|1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi|1755180 (U75201) germin-like protein [Arabidopsis thaliana] >gi|1755190 (U75206) germin-like protein [Arabidopsis thaliana] >gi|1934728 (U95035) germin-like protein [Arabidopsis thaliana] >gi|4154285 (AF090733) germin-like protein 1 [Arabidopsis thaliana]

Seq. No.	193954
Contig ID	11510_1.R1039
5'-most EST	LIB3165-034-P1-K2-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	652
E value	3.0e-68
Match length	151
% identity	84
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	193955
Contig ID	11513_1.R1039
5'-most EST	LIB3120-017-Q1-K1-G2
Method	BLASTX
NCBI GI	g3096945
BLAST score	440
E value	1.0e-43
Match length	102
% identity	82
NCBI Description	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	193956
Contig ID	11520_1.R1039
5'-most EST	LIB3120-017-Q1-K1-H1
Method	BLASTX
NCBI GI	g1170028
BLAST score	184
E value	4.0e-30
Match length	76

% identity	85
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi|454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]
Seq. No.	193957
Contig ID	11523_1.R1039
5'-most EST	LIB3120-017-Q1-K1-H3
Seq. No.	193958
Contig ID	11530_1.R1039
5'-most EST	LIB3120-018-Q1-K2-A1
Method	BLASTX
NCBI GI	g3395588
BLAST score	170
E value	5.0e-12
Match length	84
% identity	44
NCBI Description	(AL031179) serine-threonine protein phosphatase [Schizosaccharomyces pombe]
Seq. No.	193959
Contig ID	11533_1.R1039
5'-most EST	g5050321
Method	BLASTX
NCBI GI	g2245125
BLAST score	174
E value	3.0e-12
Match length	47
% identity	64
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	193960
Contig ID	11537_1.R1039
5'-most EST	LIB3120-018-Q1-K2-A5
Seq. No.	193961
Contig ID	11539_1.R1039
5'-most EST	LIB3120-018-Q1-K1-A8
Method	BLASTX
NCBI GI	g1894771
BLAST score	150
E value	1.0e-09
Match length	134
% identity	34
NCBI Description	(Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] >gi|2636109|emb|CAB15600.1| (Z99122) similar to metabolite transport protein [Bacillus subtilis]
Seq. No.	193962
Contig ID	11542_1.R1039
5'-most EST	uC-gsflnu33B012h08b1
Method	BLASTX
NCBI GI	g4176531

BLAST score 424
E value 1.0e-41
Match length 191
% identity 45
NCBI Description (AL035263) weak similarity to chick phosphatidylcholine-ste
rol acetyltransferase [Schizosaccharomyces pombe]

Seq. No. 193963
Contig ID 11545_1.R1039
5'-most EST LIB3120-018-Q1-K1-B2
Method BLASTX
NCBI GI g2506788
BLAST score 475
E value 2.0e-47
Match length 158
% identity 26
NCBI Description GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB
GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB
GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG
TRANSFERASE) (RAB GGTASE) >gi|1332508|emb|CAA66638|
(X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No. 193964
Contig ID 11548_1.R1039
5'-most EST LIB3272-018-P1-K1-H10

Seq. No. 193965
Contig ID 11554_1.R1039
5'-most EST LIB3120-018-Q1-K1-C11
Method BLASTX
NCBI GI g4415916
BLAST score 356
E value 2.0e-39
Match length 144
% identity 56
NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis
thaliana]

Seq. No. 193966
Contig ID 11556_1.R1039
5'-most EST uC-gsflmaxxa010a02b1

Seq. No. 193967
Contig ID 11558_1.R1039
5'-most EST LIB3120-018-Q1-K2-C6
Method BLASTX
NCBI GI g3249081
BLAST score 389
E value 2.0e-37
Match length 152
% identity 11
NCBI Description (AC004473) Strong similarity to AROGP2 gene gb|1762634 from
Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No. 193968
Contig ID 11562_1.R1039
5'-most EST LIB3165-024-P1-K1-E7

Method	BLASTX
NCBI GI	g2499967
BLAST score	268
E value	3.0e-23
Match length	129
% identity	49
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E B) >gi|632724|bbs|151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 143 aa] [Nicotiana sylvestris]

Seq. No.	193969
Contig ID	11568_1.R1039
5'-most EST	LIB3120-018-Q1-K2-D3

Seq. No.	193970
Contig ID	11570_1.R1039
5'-most EST	LIB3120-018-Q1-K2-D5
Method	BLASTX
NCBI GI	g3785983
BLAST score	191
E value	2.0e-14
Match length	70
% identity	49
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193971
Contig ID	11574_1.R1039
5'-most EST	uC-gsflnu33B060a12b1
Method	BLASTX
NCBI GI	g1657948
BLAST score	1227
E value	1.0e-135
Match length	291
% identity	81
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	193972
Contig ID	11577_1.R1039
5'-most EST	LIB3120-018-Q1-K1-E11

Seq. No.	193973
Contig ID	11581_2.R1039
5'-most EST	uC-gsflmaxxa014a08b1
Method	BLASTX
NCBI GI	g3738306
BLAST score	207
E value	4.0e-16
Match length	56
% identity	70
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	193974
Contig ID	11584_1.R1039
5'-most EST	LIB3197-020-Q1-M1-E5

Seq. No. 193975

Contig ID	11586_1.R1039
5'-most EST	LIB3120-018-Q1-K1-F1
Seq. No.	193976
Contig ID	11588_1.R1039
5'-most EST	LIB3165-055-P1-K1-E4
Seq. No.	193977
Contig ID	11591_1.R1039
5'-most EST	LIB3120-018-Q1-K2-F3
Seq. No.	193978
Contig ID	11592_1.R1039
5'-most EST	LIB3148-059-Q1-K1-C4
Method	BLASTX
NCBI GI	g3875463
BLAST score	476
E value	2.0e-47
Match length	234
% identity	46
NCBI Description	(Z68341) predicted using Genefinder; Similarity to Human SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26681 comes from this gene; cDNA EST EMBL:D26680 comes from this gene; ... >gi|3879468|emb|CAA92978| (Z68751) predicted using Genefinder; Similarity to Human SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26681 comes from this gene; cDNA EST EMBL:D26680 comes from this gene;
Seq. No.	193979
Contig ID	11594_1.R1039
5'-most EST	LIB3120-018-Q1-K2-F2
Seq. No.	193980
Contig ID	11595_1.R1039
5'-most EST	LIB3145-047-Q1-K1-C10
Method	BLASTX
NCBI GI	g2583135
BLAST score	661
E value	3.0e-69
Match length	204
% identity	65
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi|3822216 (AF074948) FIL [Arabidopsis thaliana] >gi|4322477|gb|AAD16053| (AF087015) abnormal floral organs protein [Arabidopsis thaliana]
Seq. No.	193981
Contig ID	11595_2.R1039
5'-most EST	LIB3120-018-Q1-K1-F7
Seq. No.	193982
Contig ID	11597_1.R1039
5'-most EST	LIB3120-018-Q1-K1-F9
Method	BLASTX
NCBI GI	g267120

BLAST score	434
E value	8.0e-43
Match length	132
% identity	67
NCBI Description	THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi|100070|pir||S20929 thioredoxin f precursor - garden pea >gi|20907|emb|CAA45098| (X63537) thioredoxin F [Pisum sativum] >gi|1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No.	193983
Contig ID	11598_1.R1039
5'-most EST	LIB3120-018-Q1-K2-G1

Seq. No.	193984
Contig ID	11599_1.R1039
5'-most EST	LIB3135-047-Q1-K1-G1
Method	BLASTX
NCBI GI	g136707
BLAST score	788
E value	3.0e-84
Match length	198
% identity	75
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi|280397|pir||S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi|20832|emb|CAA45151| (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	193985
Contig ID	11602_1.R1039
5'-most EST	LIB3197-034-Q1-M1-C9

Seq. No.	193986
Contig ID	11602_2.R1039
5'-most EST	LIB3166-043-P1-K1-C2

Seq. No.	193987
Contig ID	11603_1.R1039
5'-most EST	LIB3120-018-Q1-K2-G3
Method	BLASTX
NCBI GI	g4151117
BLAST score	255
E value	5.0e-22
Match length	123
% identity	46
NCBI Description	(AJ224926) kco2 [Solanum tuberosum]

Seq. No.	193988
Contig ID	11608_1.R1039
5'-most EST	LIB3120-018-Q1-K1-G9

Seq. No.	193989
Contig ID	11614_1.R1039
5'-most EST	LIB3197-037-Q1-M1-E7
Method	BLASTX
NCBI GI	g2129471

BLAST score	513
E value	6.0e-52
Match length	137
% identity	67
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi|1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	193990
Contig ID	11614_2.R1039
5'-most EST	LIB3196-054-P1-M1-F1

Seq. No.	193991
Contig ID	11615_1.R1039
5'-most EST	LIB3120-018-Q1-K2-H6
Method	BLASTX
NCBI GI	g3785974
BLAST score	256
E value	4.0e-22
Match length	102
% identity	52
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	193992
Contig ID	11687_1.R1039
5'-most EST	LIB3120-019-Q1-K1-B11
Method	BLASTX
NCBI GI	g2347189
BLAST score	271
E value	1.0e-23
Match length	90
% identity	57
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana] >gi|3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	193993
Contig ID	11689_1.R1039
5'-most EST	LIB3166-001-Q1-K1-F6

Seq. No.	193994
Contig ID	11691_1.R1039
5'-most EST	LIB3189-043-P1-K1-C3
Method	BLASTX
NCBI GI	g4105269
BLAST score	326
E value	5.0e-30
Match length	205
% identity	40
NCBI Description	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]

Seq. No.	193995
Contig ID	11693_1.R1039
5'-most EST	LIB3120-019-Q1-K1-B7
Method	BLASTX
NCBI GI	g4558556

BLAST score 273
E value 5.0e-24
Match length 142
% identity 42
NCBI Description (AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 193996
Contig ID 11694_1.R1039
5'-most EST LIB3120-024-Q1-K1-G3
Method BLASTX
NCBI GI g3292817
BLAST score 246
E value 1.0e-20
Match length 95
% identity 57
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 193997
Contig ID 11695_1.R1039
5'-most EST LIB3120-019-Q1-K1-B9
Method BLASTX
NCBI GI g1362152
BLAST score 984
E value 1.0e-107
Match length 231
% identity 76
NCBI Description ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi|871986|emb|CAA56313| (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No. 193998
Contig ID 11697_1.R1039
5'-most EST uC-gsflmaxxa047c08b1

Seq. No. 193999
Contig ID 11698_1.R1039
5'-most EST LIB3196-024-P1-M1-D12

Seq. No. 194000
Contig ID 11699_1.R1039
5'-most EST LIB3120-019-Q1-K1-C12
Method BLASTX
NCBI GI g421813
BLAST score 165
E value 3.0e-11
Match length 87
% identity 36
NCBI Description storage protein, bark - cottonwood >gi|20465|emb|CAA49669| (X70064) bark storage protein [Populus deltoides]

Seq. No. 194001
Contig ID 11700_1.R1039
5'-most EST LIB3120-019-Q1-K1-C2
Method BLASTX
NCBI GI g2501460
BLAST score 239

E value	1.0e-19
Match length	256
% identity	31
NCBI Description	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi|1545952|emb|CAA96580| (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens] >gi|4507857|ref|NP_003461.1|pUSP7| Herpes virus-associated ubiquitin-specific protease

Seq. No.	194002
Contig ID	11706_1.R1039
5'-most EST	LIB3120-019-Q1-K1-C8
Method	BLASTX
NCBI GI	g2191175
BLAST score	163
E value	3.0e-11
Match length	118
% identity	43
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	194003
Contig ID	11709_1.R1039
5'-most EST	LIB3120-019-Q1-K1-D10
Method	BLASTX
NCBI GI	g3135611
BLAST score	525
E value	2.0e-53
Match length	125
% identity	77
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	194004
Contig ID	11711_1.R1039
5'-most EST	LIB3165-043-Q1-K1-B2
Method	BLASTX
NCBI GI	g1173347
BLAST score	587
E value	8.0e-61
Match length	126
% identity	90
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi|100803|pir||S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi|14265|emb|CAA46507| (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	194005
Contig ID	11712_1.R1039
5'-most EST	LIB3272-052-P1-K1-F10
Method	BLASTX
NCBI GI	g3168840
BLAST score	313

E value	2.0e-28
Match length	78
% identity	74
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	194006
Contig ID	11712_2.R1039
5'-most EST	uC-gsflmaxxa028f02b1
Method	BLASTX
NCBI GI	g3168840
BLAST score	330
E value	1.0e-30
Match length	97
% identity	67
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	194007
Contig ID	11712_3.R1039
5'-most EST	uC-gsronu33B061g04b1
Method	BLASTX
NCBI GI	g3168840
BLAST score	306
E value	5.0e-28
Match length	79
% identity	75
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	194008
Contig ID	11712_4.R1039
5'-most EST	LIB3120-019-Q1-K1-D2
Method	BLASTX
NCBI GI	g4432821
BLAST score	256
E value	1.0e-21
Match length	137
% identity	43
NCBI Description	(AC006593) putative transmembrane protein [Arabidopsis thaliana]

Seq. No.	194009
Contig ID	11713_1.R1039
5'-most EST	LIB3165-049-Q1-K1-A6

Seq. No.	194010
Contig ID	11714_1.R1039
5'-most EST	g5045603
Method	BLASTX
NCBI GI	g3953471
BLAST score	280
E value	1.0e-24
Match length	120
% identity	53
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	194011
Contig ID	11717_1.R1039
5'-most EST	LIB3120-019-Q1-K1-D8

Method	BLASTX
NCBI GI	g1814407
BLAST score	817
E value	1.0e-122
Match length	244
% identity	91
NCBI Description	(U84891) H+-transporting ATPase [Mesembryanthemum crystallinum]

Seq. No.	194012
Contig ID	11723_1.R1039
5'-most EST	LIB3120-019-Q1-K1-E2
Method	BLASTN
NCBI GI	g2605910
BLAST score	328
E value	0.0e+00
Match length	584
% identity	89
NCBI Description	Kosteletzkya virginica clone KVATP3 plasma membrane H+-ATPase mRNA, partial cds

Seq. No.	194013
Contig ID	11725_1.R1039
5'-most EST	LIB3166-008-P1-K1-D4
Method	BLASTX
NCBI GI	g2911043
BLAST score	233
E value	3.0e-19
Match length	130
% identity	45
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	194014
Contig ID	11726_1.R1039
5'-most EST	LIB3147-031-Q1-K1-C7

Seq. No.	194015
Contig ID	11730_1.R1039
5'-most EST	LIB3120-019-Q1-K1-F1
Method	BLASTX
NCBI GI	g1200205
BLAST score	360
E value	6.0e-34
Match length	145
% identity	50
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	194016
Contig ID	11731_1.R1039
5'-most EST	LIB3120-019-Q1-K1-F10
Method	BLASTX
NCBI GI	g4454044
BLAST score	145
E value	5.0e-09
Match length	34
% identity	76
NCBI Description	(AL035394) putative Ap2 domain protein [Arabidopsis

thaliana]

Seq. No.	194017
Contig ID	11741_1.R1039
5'-most EST	LIB3120-019-Q1-K1-G10
Method	BLASTX
NCBI GI	g4220521
BLAST score	526
E value	3.0e-53
Match length	315
% identity	45
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	194018
Contig ID	11742_1.R1039
5'-most EST	LIB3189-028-P1-K1-H2
Method	BLASTX
NCBI GI	g4325338
BLAST score	735
E value	6.0e-78
Match length	220
% identity	65
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	194019
Contig ID	11752_1.R1039
5'-most EST	LIB3120-032-Q1-K1-B5
Method	BLASTX
NCBI GI	g2499966
BLAST score	244
E value	4.0e-21
Match length	87
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi|632722|bbs|151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 141 aa] [Nicotiana sylvestris]

Seq. No.	194020
Contig ID	11752_2.R1039
5'-most EST	LIB3146-001-P1-K2-E9
Method	BLASTX
NCBI GI	g2499966
BLAST score	168
E value	1.0e-11
Match length	35
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi|632722|bbs|151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 141 aa] [Nicotiana sylvestris]

Seq. No.	194021
Contig ID	11752_3.R1039
5'-most EST	LIB3165-039-Q1-K1-F3
Method	BLASTX
NCBI GI	g2499966

BLAST score	169
E value	9.0e-12
Match length	111
% identity	42
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi|632722|bbs|151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 141 aa] [Nicotiana sylvestris]

Seq. No.	194022
Contig ID	11752_4.R1039
5'-most EST	LIB3120-027-Q1-K1-B3
Method	BLASTX
NCBI GI	g4512709
BLAST score	257
E value	3.0e-22
Match length	58
% identity	83
NCBI Description	(AC006569) putative photosystem I reaction center subunit IV precursor [Arabidopsis thaliana]

Seq. No.	194023
Contig ID	11757_1.R1039
5'-most EST	LIB3165-047-Q1-K1-F10
Method	BLASTX
NCBI GI	g3892058
BLAST score	324
E value	5.0e-30
Match length	123
% identity	54
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	194024
Contig ID	11761_1.R1039
5'-most EST	LIB3120-019-Q1-K1-H8

Seq. No.	194025
Contig ID	11767_1.R1039
5'-most EST	LIB3165-020-P1-K1-H4
Method	BLASTX
NCBI GI	g2467274
BLAST score	386
E value	5.0e-37
Match length	146
% identity	58
NCBI Description	(Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	194026
Contig ID	11771_1.R1039
5'-most EST	LIB3189-052-P1-K1-E10
Method	BLASTX
NCBI GI	g1916807
BLAST score	635
E value	4.0e-66
Match length	180
% identity	69

NCBI Description	(U81162) auxin-binding protein [Prunus persica]
Seq. No.	194027
Contig ID	11776_1.R1039
5'-most EST	g5049251
Method	BLASTX
NCBI GI	g1729927
BLAST score	435
E value	7.0e-43
Match length	174
% identity	49
NCBI Description	QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi|940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
Seq. No.	194028
Contig ID	11777_1.R1039
5'-most EST	uC-gsflnu33B064b05b1
Method	BLASTX
NCBI GI	g1458245
BLAST score	502
E value	2.0e-50
Match length	367
% identity	35
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]
Seq. No.	194029
Contig ID	11777_2.R1039
5'-most EST	LIB3145-046-Q1-K1-E3
Method	BLASTX
NCBI GI	g1055130
BLAST score	245
E value	2.0e-20
Match length	124
% identity	39
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3
Seq. No.	194030
Contig ID	11780_1.R1039
5'-most EST	uC-gsronu33B167c11b1
Method	BLASTX
NCBI GI	g1532168
BLAST score	260
E value	1.0e-22
Match length	67
% identity	69
NCBI Description	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No.	194031
Contig ID	11781_1.R1039
5'-most EST	LIB3120-020-Q1-K1-B5
Method	BLASTX
NCBI GI	g2708314
BLAST score	272
E value	1.0e-23
Match length	121
% identity	28
NCBI Description	(AF027727) protein disulfide isomerase RB60 [Chlamydomonas reinhardtii] >gi|4104541 (AF036939) protein disulfide isomerase [Chlamydomonas reinhardtii]

Seq. No.	194032
Contig ID	11782_1.R1039
5'-most EST	LIB3166-050-P1-K1-E5
Method	BLASTX
NCBI GI	g3334323
BLAST score	899
E value	4.0e-97
Match length	193
% identity	88
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi|1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi|2104532|gb|AAC78700.1| (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi|2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	194033
Contig ID	11782_2.R1039
5'-most EST	LIB3120-020-Q1-K1-B6
Method	BLASTX
NCBI GI	g3334323
BLAST score	850
E value	2.0e-91
Match length	192
% identity	85
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi|1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi|2104532|gb|AAC78700.1| (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi|2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	194034
Contig ID	11783_1.R1039
5'-most EST	uC-gsronu33B178a12b1
Method	BLASTX
NCBI GI	g2388575
BLAST score	279
E value	2.0e-24
Match length	152
% identity	40
NCBI Description	(AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 194035

Contig ID	11784_1.R1039
5'-most EST	LIB3146-032-Q1-K1-F12
Method	BLASTX
NCBI GI	g3914658
BLAST score	674
E value	9.0e-71
Match length	168
% identity	77
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi|1694974|emb|CAA70851| (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	194036
Contig ID	11786_1.R1039
5'-most EST	LIB3120-036-Q1-K1-C8
Method	BLASTX
NCBI GI	g1084336
BLAST score	392
E value	6.0e-38
Match length	93
% identity	76
NCBI Description	chlorophyll a/b-binding protein type II - Arabidopsis thaliana >gi|541565 (U03395) PSI type II chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	194037
Contig ID	11788_1.R1039
5'-most EST	LIB3120-020-Q1-K1-C11
Method	BLASTX
NCBI GI	g3451463
BLAST score	364
E value	2.0e-34
Match length	185
% identity	43
NCBI Description	(AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	194038
Contig ID	11792_1.R1039
5'-most EST	LIB3165-040-Q1-K1-G3
Method	BLASTX
NCBI GI	g1946367
BLAST score	664
E value	9.0e-70
Match length	162
% identity	79
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	194039
Contig ID	11798_1.R1039
5'-most EST	LIB3197-011-P1-M1-B11
Method	BLASTX
NCBI GI	g2702281
BLAST score	1595
E value	1.0e-178
Match length	434
% identity	70
NCBI Description	(AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No.	194040
Contig ID	11801_1.R1039
5'-most EST	g5049254
Method	BLASTX
NCBI GI	g4538961
BLAST score	1320
E value	1.0e-147
Match length	388
% identity	70
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	194041
Contig ID	11806_1.R1039
5'-most EST	LIB3165-053-Q1-K1-A4
Method	BLASTX
NCBI GI	g3860264
BLAST score	967
E value	1.0e-105
Match length	202
% identity	88
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	194042
Contig ID	11807_1.R1039
5'-most EST	LIB3165-024-P1-K1-A9
Method	BLASTX
NCBI GI	g4417271
BLAST score	760
E value	5.0e-81
Match length	189
% identity	74
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	194043
Contig ID	11809_1.R1039
5'-most EST	g5047641
Method	BLASTN
NCBI GI	g2827140
BLAST score	64
E value	3.0e-27
Match length	308
% identity	82
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds

Seq. No.	194044
Contig ID	11818_1.R1039
5'-most EST	g5046359
Method	BLASTX
NCBI GI	g4091080
BLAST score	685
E value	5.0e-72
Match length	228

% identity	58
NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.	194045
Contig ID	11820_1.R1039
5'-most EST	g5045459
Method	BLASTX
NCBI GI	g3193298
BLAST score	212
E value	1.0e-16
Match length	107
% identity	38
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	194046
Contig ID	11825_1.R1039
5'-most EST	LIB3120-020-Q1-K1-F3
Method	BLASTX
NCBI GI	g3599968
BLAST score	883
E value	3.0e-95
Match length	233
% identity	76
NCBI Description	(AF032123) clp protease [Arabidopsis thaliana]

Seq. No.	194047
Contig ID	11828_1.R1039
5'-most EST	LIB3120-020-Q1-K1-F6
Method	BLASTX
NCBI GI	g1076264
BLAST score	248
E value	5.0e-21
Match length	184
% identity	39
NCBI Description	carboxyl-terminal processing proteinase D1 precursor - spinach >gi|2129489|pir||S65146 photosystem II D1 protein processing enzyme precursor - spinach >gi|999435|dbj|BAA09134| (D50585) C-terminal protease precursor [Spinacia oleracea]

Seq. No.	194048
Contig ID	11831_1.R1039
5'-most EST	LIB3165-046-Q1-K1-E12
Method	BLASTX
NCBI GI	g508304
BLAST score	367
E value	5.0e-35
Match length	82
% identity	79
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	194049
Contig ID	11849_1.R1039
5'-most EST	LIB3166-024-P1-K1-H4
Method	BLASTX
NCBI GI	g3894190
BLAST score	471

E value	8.0e-47
Match length	204
% identity	49
NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No.	194050
Contig ID	11850_1.R1039
5'-most EST	LIB3120-020-Q1-K1-H9
Method	BLASTX
NCBI GI	g2388578
BLAST score	660
E value	3.0e-69
Match length	184
% identity	70
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb|Z84395). ESTs gb|T75785,gb|R30580,gb|T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	194051
Contig ID	11851_1.R1039
5'-most EST	LIB3120-021-Q1-K1-A1

Seq. No.	194052
Contig ID	11852_1.R1039
5'-most EST	LIB3120-021-Q1-K1-A11

Seq. No.	194053
Contig ID	11862_1.R1039
5'-most EST	LIB3197-046-Q1-M1-B3
Method	BLASTX
NCBI GI	g2911073
BLAST score	762
E value	6.0e-81
Match length	228
% identity	68
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	194054
Contig ID	11871_1.R1039
5'-most EST	LIB3272-028-P1-K1-D5
Method	BLASTX
NCBI GI	g1944319
BLAST score	682
E value	2.0e-71
Match length	206
% identity	65
NCBI Description	(D31700) cysteine proteinase inhibitor [Glycine max] >gi|1944342|dbj|BAA19610| (D64115) cysteine proteinase inhibitor [Glycine max]

Seq. No.	194055
Contig ID	11879_1.R1039
5'-most EST	LIB3120-021-Q1-K1-C8
Method	BLASTX
NCBI GI	g2494119
BLAST score	510
E value	1.0e-51

Match length	151
% identity	66
NCBI Description	(AC002376) EST gb|T04104 comes from this gene. [Arabidopsis thaliana]

Seq. No.	194056
Contig ID	11885_1.R1039
5'-most EST	LIB3120-021-Q1-K1-D5
Method	BLASTX
NCBI GI	g3785991
BLAST score	318
E value	2.0e-29
Match length	130
% identity	59
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	194057
Contig ID	11889_1.R1039
5'-most EST	LIB3120-021-Q1-K1-D7
Method	BLASTX
NCBI GI	g4417288
BLAST score	172
E value	3.0e-12
Match length	65
% identity	57
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	194058
Contig ID	11893_1.R1039
5'-most EST	LIB3166-018-P1-K1-E2
Method	BLASTX
NCBI GI	g4469011
BLAST score	1044
E value	1.0e-114
Match length	224
% identity	87
NCBI Description	(AL035602) carbohydrate kinase-like protein [Arabidopsis thaliana]

Seq. No.	194059
Contig ID	11902_1.R1039
5'-most EST	LIB3120-021-Q1-K1-F10
Method	BLASTN
NCBI GI	g4469002
BLAST score	57
E value	5.0e-23
Match length	415
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	194060
Contig ID	11912_1.R1039
5'-most EST	g3326460
Method	BLASTX
NCBI GI	g3775993
BLAST score	1044

E value 1.0e-114
Match length 286
% identity 75
NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 194061
Contig ID 11916_1.R1039
5'-most EST LIB3120-021-Q1-K1-G7
Method BLASTX
NCBI GI g231660
BLAST score 572
E value 4.0e-67
Match length 256
% identity 58
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 194062
Contig ID 11927_1.R1039
5'-most EST LIB3120-022-Q1-K1-A1
Method BLASTX
NCBI GI g2565305
BLAST score 482
E value 1.0e-48
Match length 119
% identity 81
NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No. 194063
Contig ID 11932_1.R1039
5'-most EST uC-gsflnu33B095c07b1
Method BLASTX
NCBI GI g4191785
BLAST score 336
E value 2.0e-32
Match length 123
% identity 59
NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No. 194064
Contig ID 11933_1.R1039
5'-most EST uC-gsflnu33B027b05b1

Seq. No. 194065
Contig ID 11934_1.R1039
5'-most EST LIB3120-024-Q1-K1-G5
Method BLASTX
NCBI GI g4262236
BLAST score 321
E value 1.0e-29
Match length 89
% identity 73
NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 194066
Contig ID 11935_1.R1039

5'-most EST	LIB3149-060-Q1-K1-D4
Method	BLASTX
NCBI GI	g1173198
BLAST score	718
E value	6.0e-76
Match length	151
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi|480095|pir||S36423 ribosomal protein S13.e - garden pea >gi|396639|emb|CAA80974| (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	194067
Contig ID	11946_1.R1039
5'-most EST	LIB3120-022-Q1-K1-B6
Method	BLASTX
NCBI GI	g2129753
BLAST score	1500
E value	1.0e-167
Match length	321
% identity	90
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi|1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	194068
Contig ID	11953_1.R1039
5'-most EST	LIB3165-011-P1-K1-E3
Method	BLASTX
NCBI GI	g3023281
BLAST score	462
E value	3.0e-46
Match length	141
% identity	64
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi|2065194|emb|CAA64475| (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No.	194069
Contig ID	11975_3.R1039
5'-most EST	LIB3189-025-P1-K1-B9
Method	BLASTN
NCBI GI	g2924257
BLAST score	266
E value	1.0e-148
Match length	493
% identity	89
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	194070
Contig ID	11976_1.R1039
5'-most EST	LIB3146-037-P1-K1-F10
Method	BLASTX
NCBI GI	g2828267
BLAST score	1144
E value	1.0e-126
Match length	229
% identity	93

NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
Seq. No.	194071
Contig ID	11978_1.R1039
5'-most EST	LIB3148-003-P1-K1-D4
Method	BLASTX
NCBI GI	g3036796
BLAST score	676
E value	4.0e-71
Match length	225
% identity	61
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi|3805858|emb|CAA21478| (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	194072
Contig ID	11979_1.R1039
5'-most EST	LIB3165-052-Q1-K1-A9
Method	BLASTX
NCBI GI	g4467098
BLAST score	355
E value	1.0e-33
Match length	134
% identity	60
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]
Seq. No.	194073
Contig ID	11993_1.R1039
5'-most EST	LIB3120-022-Q1-K1-G1
Method	BLASTX
NCBI GI	g2194125
BLAST score	1337
E value	1.0e-148
Match length	282
% identity	85
NCBI Description	(AC002062) ESTs gb|R30459,gb|N38441 come from this gene. [Arabidopsis thaliana]
Seq. No.	194074
Contig ID	11996_1.R1039
5'-most EST	LIB3120-022-Q1-K1-G12
Method	BLASTX
NCBI GI	g132901
BLAST score	312
E value	2.0e-28
Match length	66
% identity	86
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi|71356|pir||R5NT33 ribosomal protein L33 - common tobacco chloroplast >gi|11850|emb|CAA77370| (Z00044) ribosomal protein L33 [Nicotiana tabacum] >gi|225219|prf||1211235BA ribosomal protein L33 [Nicotiana tabacum]
Seq. No.	194075
Contig ID	11999_1.R1039
5'-most EST	LIB3165-044-Q1-K1-B4
Method	BLASTX

NCBI GI	g3242704
BLAST score	384
E value	9.0e-37
Match length	141
% identity	53
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194076
Contig ID	12004_1.R1039
5'-most EST	LIB3120-022-Q1-K1-G9
Method	BLASTX
NCBI GI	g400992
BLAST score	363
E value	1.0e-34
Match length	94
% identity	74
NCBI Description	50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR (CL28) >gi|279656|pir||R5NT28 ribosomal protein L28 precursor, chloroplast - tobacco >gi|20016|emb|CAA48211| (X68078) ribosomal protein CL28 [Nicotiana tabacum]

Seq. No.	194077
Contig ID	12014_1.R1039
5'-most EST	LIB3165-014-P1-K1-A12
Method	BLASTX
NCBI GI	g3913651
BLAST score	560
E value	2.0e-57
Match length	127
% identity	82
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi|2225993|emb|CAA74359| (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	194078
Contig ID	12019_1.R1039
5'-most EST	LIB3120-023-Q1-K1-A2
Method	BLASTX
NCBI GI	g3128177
BLAST score	510
E value	1.0e-51
Match length	121
% identity	82
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	194079
Contig ID	12024_1.R1039
5'-most EST	LIB3148-026-Q1-K1-B1

Seq. No.	194080
Contig ID	12025_1.R1039
5'-most EST	LIB3165-018-P1-K1-E6
Method	BLASTX
NCBI GI	g132866
BLAST score	909
E value	3.0e-98
Match length	199

% identity	88
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi|71086|pir||R5NT2 ribosomal protein L2 - common tobacco chloroplast >gi|435269|emb|CAA77384| (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi|1223691|emb|CAA77409| (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi|225238|prf||1211235BW ribosomal protein L2 [Nicotiana tabacum]

Seq. No.	194081
Contig ID	12025_2.R1039
5'-most EST	LIB3148-039-Q1-K1-C1
Method	BLASTX
NCBI GI	g82519
BLAST score	215
E value	4.0e-17
Match length	68
% identity	69
NCBI Description	hypothetical 15K protein (trnH-trnV intergenic region) - rice chloroplast >gi|12029|emb|CAA33937| (X15901) ORF137 [Oryza sativa] >gi|12073|emb|CAA33925| (X15901) ORF137 [Oryza sativa] >gi|226651|prf||1603356CB ORF 137 [Oryza sativa]

Seq. No.	194082
Contig ID	12027_1.R1039
5'-most EST	LIB3120-023-Q1-K1-B1
Method	BLASTX
NCBI GI	g4457221
BLAST score	330
E value	2.0e-30
Match length	87
% identity	78
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	194083
Contig ID	12039_1.R1039
5'-most EST	uC-gsflnu33B071d11b1
Method	BLASTX
NCBI GI	g3063448
BLAST score	774
E value	2.0e-82
Match length	229
% identity	61
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	194084
Contig ID	12041_1.R1039
5'-most EST	LIB3165-038-Q1-K1-C5
Method	BLASTX
NCBI GI	g2739375
BLAST score	226
E value	2.0e-18
Match length	128
% identity	45
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	194085
Contig ID	12051_1.R1039
5'-most EST	LIB3120-023-Q1-K1-H4

Seq. No.	194086
Contig ID	12066_1.R1039
5'-most EST	LIB3189-011-P1-K1-C9

Seq. No.	194087
Contig ID	12079_1.R1039
5'-most EST	g3326831
Method	BLASTX
NCBI GI	g3928760
BLAST score	494
E value	1.0e-49
Match length	183
% identity	58
NCBI Description	(AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No.	194088
Contig ID	12081_1.R1039
5'-most EST	g5049336
Method	BLASTN
NCBI GI	g3928759
BLAST score	57
E value	6.0e-23
Match length	209
% identity	82
NCBI Description	Citrus unshiu CitPAP mRNA for homolog to plastid-lipid-associated protein, complete cds

Seq. No.	194089
Contig ID	12082_1.R1039
5'-most EST	LIB3197-014-P1-M1-G11
Method	BLASTX
NCBI GI	g2739168
BLAST score	419
E value	5.0e-41
Match length	168
% identity	51
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	194090
Contig ID	12097_1.R1039
5'-most EST	LIB3120-024-Q1-K1-A1
Method	BLASTX
NCBI GI	g289920
BLAST score	379
E value	9.0e-37
Match length	79
% identity	92
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	194091
Contig ID	12098_1.R1039
5'-most EST	LIB3165-051-Q1-K1-H6
Method	BLASTX
NCBI GI	g2895188
BLAST score	153
E value	5.0e-10
Match length	69
% identity	27
NCBI Description	(AF016011) CONSTANS homolog [Brassica napus]

Seq. No.	194092
Contig ID	12100_1.R1039
5'-most EST	LIB3165-023-P1-K1-A5

Seq. No.	194093
Contig ID	12101_1.R1039
5'-most EST	uC-gsflmaxxa043h09b1

Seq. No.	194094
Contig ID	12102_1.R1039
5'-most EST	LIB3120-043-P1-K1-E7

Seq. No.	194095
Contig ID	12104_1.R1039
5'-most EST	LIB3145-038-Q1-K1-G5
Method	BLASTX
NCBI GI	g3641252
BLAST score	242
E value	4.0e-20
Match length	61
% identity	79
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	194096
Contig ID	12111_1.R1039
5'-most EST	LIB3120-024-Q1-K1-B12
Method	BLASTX
NCBI GI	g531096
BLAST score	411
E value	5.0e-63
Match length	167
% identity	72
NCBI Description	(D30800) TED2 [Zinnia elegans]

Seq. No.	194097
Contig ID	12113_1.R1039
5'-most EST	LIB3120-024-Q1-K1-B3
Method	BLASTN
NCBI GI	g1617035
BLAST score	87
E value	5.0e-41
Match length	227
% identity	85
NCBI Description	V.unguiculata mRNA for Ted2 protein

Seq. No.	194098
Contig ID	12115_1.R1039
5'-most EST	LIB3272-046-P1-K1-C5
Method	BLASTX
NCBI GI	g3096949
BLAST score	428
E value	2.0e-57
Match length	250
% identity	51
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi|3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	194099
Contig ID	12124_1.R1039
5'-most EST	LIB3120-027-Q1-K1-A8

Seq. No.	194100
Contig ID	12126_1.R1039
5'-most EST	g5045947
Method	BLASTX
NCBI GI	g4056457
BLAST score	571
E value	8.0e-59
Match length	135
% identity	81
NCBI Description	(AC005990) ESTs gb|234051 and gb|F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	194101
Contig ID	12131_1.R1039
5'-most EST	LIB3120-024-Q1-K1-D12
Method	BLASTX
NCBI GI	g2828290
BLAST score	213
E value	9.0e-17
Match length	88
% identity	48
NCBI Description	(AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	194102
Contig ID	12137_1.R1039
5'-most EST	LIB3165-020-P1-K1-B9

Seq. No.	194103
Contig ID	12153_1.R1039
5'-most EST	LIB3165-056-P1-K1-D10
Method	BLASTX
NCBI GI	g121353
BLAST score	1813
E value	0.0e+00
Match length	431
% identity	79
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA) (GLUTAMATE-AMMONIA LIGASE) >gi|68596|pir||AJFBQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - kidney bean >gi|21005|emb|CAA31234| (X12738)

GS precursor protein [Phaseolus vulgaris]

Seq. No.	194104
Contig ID	12160_1.R1039
5'-most EST	LIB3120-033-P1-K1-E4
Method	BLASTX
NCBI GI	g115473
BLAST score	523
E value	3.0e-53
Match length	136
% identity	70
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi|170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi|445610|prf||1909357A carbonic anhydrase [Nicotiana tabacum]

Seq. No.	194105
Contig ID	12161_1.R1039
5'-most EST	LIB3147-008-Q1-K1-A3
Method	BLASTX
NCBI GI	g3885884
BLAST score	824
E value	3.0e-88
Match length	164
% identity	91
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	194106
Contig ID	12161_2.R1039
5'-most EST	LIB3148-048-Q1-K1-D9
Method	BLASTX
NCBI GI	g3885884
BLAST score	802
E value	8.0e-86
Match length	164
% identity	90
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	194107
Contig ID	12161_3.R1039
5'-most EST	LIB3166-047-P1-K1-C4
Method	BLASTX
NCBI GI	g3885884
BLAST score	438
E value	3.0e-58
Match length	133
% identity	80
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	194108
Contig ID	12172_1.R1039
5'-most EST	LIB3120-024-Q1-K1-G9
Method	BLASTX
NCBI GI	g3024127
BLAST score	1919
E value	0.0e+00
Match length	393

% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi|1655578|emb|CAA95857| (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No.	194109
Contig ID	12176_1.R1039
5'-most EST	LIB3146-049-Q1-K1-H3
Method	BLASTN
NCBI GI	g497899
BLAST score	394
E value	0.0e+00
Match length	1166
% identity	83
NCBI Description	Populus trichocarpa * Populus deltoides (clone sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA, complete cds

Seq. No.	194110
Contig ID	12186_1.R1039
5'-most EST	LIB3120-025-Q1-K1-A7
Method	BLASTX
NCBI GI	g3608147
BLAST score	345
E value	2.0e-32
Match length	118
% identity	38
NCBI Description	(AC005314) putative chloroplast 31 kDa ribonucleoprotein precursor [Arabidopsis thaliana]

Seq. No.	194111
Contig ID	12196_1.R1039
5'-most EST	LIB3120-025-Q1-K1-B12
Method	BLASTX
NCBI GI	g3169182
BLAST score	344
E value	2.0e-32
Match length	77
% identity	84
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	194112
Contig ID	12198_1.R1039
5'-most EST	LIB3120-025-Q1-K1-B3
Method	BLASTX
NCBI GI	g4539452
BLAST score	623
E value	5.0e-65
Match length	155
% identity	75
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	194113
Contig ID	12199_1.R1039
5'-most EST	LIB3120-025-Q1-K1-B5

Method	BLASTX
NCBI GI	g1871182
BLAST score	3569
E value	0.0e+00
Match length	829
% identity	79
NCBI Description	(U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No.	194114
Contig ID	12200_1.R1039
5'-most EST	uC-gsflnu33B066f10b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	670
E value	2.0e-70
Match length	200
% identity	61
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	194115
Contig ID	12200_2.R1039
5'-most EST	uC-gsronu33B126e01b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	217
E value	3.0e-17
Match length	78
% identity	54
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	194116
Contig ID	12209_1.R1039
5'-most EST	uC-gsflmaxxa096d06b1

Seq. No.	194117
Contig ID	12213_1.R1039
5'-most EST	LIB3120-025-Q1-K1-C8
Method	BLASTX
NCBI GI	g2191135
BLAST score	197
E value	4.0e-15
Match length	92
% identity	38
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	194118
Contig ID	12221_1.R1039
5'-most EST	LIB3147-042-Q1-K1-A8

Seq. No.	194119
Contig ID	12226_1.R1039
5'-most EST	LIB3189-033-P1-K1-A10

Seq. No.	194120

Contig ID	12231_1.R1039
5'-most EST	LIB3166-017-P1-K1-G10
Method	BLASTX
NCBI GI	g4115563
BLAST score	643
E value	3.0e-67
Match length	207
% identity	60
NCBI Description	(AB013598) UDP-glucose:anthocyanin 5-O-glucosyltransferase [Verbena x hybrida]

Seq. No.	194121
Contig ID	12237_1.R1039
5'-most EST	uC-gsronu33B015d07b1
Method	BLASTX
NCBI GI	g3024362
BLAST score	417
E value	6.0e-41
Match length	109
% identity	74
NCBI Description	PHENYLALANINE AMMONIA-LYASE G2B >gi|2118317|pir||S60042 phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese aspen x large-toothed aspen >gi|1109641|dbj|BAA07860| (D43802) phenylalanine ammonia-lyase [Populus kitakamiensis]

Seq. No.	194122
Contig ID	12247_1.R1039
5'-most EST	LIB3120-025-Q1-K1-F8
Method	BLASTX
NCBI GI	g4309738
BLAST score	433
E value	1.0e-42
Match length	103
% identity	80
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	194123
Contig ID	12247_2.R1039
5'-most EST	g5050556
Method	BLASTX
NCBI GI	g4309738
BLAST score	372
E value	3.0e-35
Match length	83
% identity	82
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	194124
Contig ID	12253_1.R1039
5'-most EST	LIB3120-025-Q1-K1-G2

Seq. No.	194125
Contig ID	12256_1.R1039
5'-most EST	LIB3272-029-P1-K1-E7

Seq. No. 194126

Contig ID	12257_1.R1039
5'-most EST	LIB3120-060-Q1-K1-D9

Seq. No.	194127
Contig ID	12262_1.R1039
5'-most EST	LIB3120-025-Q1-K1-H11

Seq. No.	194128
Contig ID	12263_1.R1039
5'-most EST	LIB3165-013-P1-K1-H6
Method	BLASTX
NCBI GI	g1071913
BLAST score	999
E value	1.0e-109
Match length	284
% identity	73
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi|1066153|dbj|BAA07177| (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	194129
Contig ID	12276_1.R1039
5'-most EST	LIB3120-026-Q1-K1-A3
Method	BLASTX
NCBI GI	g3650033
BLAST score	435
E value	4.0e-46
Match length	179
% identity	42
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	194130
Contig ID	12279_2.R1039
5'-most EST	g5049924
Method	BLASTX
NCBI GI	g4220512
BLAST score	1488
E value	0.0e+00
Match length	373
% identity	85
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	194131
Contig ID	12285_1.R1039
5'-most EST	LIB3165-055-P1-K1-H9
Method	BLASTX
NCBI GI	g1684851
BLAST score	332
E value	1.0e-30
Match length	118
% identity	61
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	194132
Contig ID	12289_1.R1039
5'-most EST	LIB3197-027-Q1-M1-H11
Method	BLASTX

NCBI GI	g2244979
BLAST score	812
E value	1.0e-86
Match length	232
% identity	69
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	194133
Contig ID	12289_2.R1039
5'-most EST	LIB3148-016-Q1-K1-C2
Method	BLASTX
NCBI GI	g2244979
BLAST score	196
E value	5.0e-15
Match length	66
% identity	61
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	194134
Contig ID	12290_1.R1039
5'-most EST	LIB3272-001-P1-K1-E3
Method	BLASTX
NCBI GI	g4220534
BLAST score	954
E value	1.0e-103
Match length	297
% identity	65
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	194135
Contig ID	12300_1.R1039
5'-most EST	LIB3165-047-Q1-K1-B5

Seq. No.	194136
Contig ID	12312_1.R1039
5'-most EST	LIB3146-024-Q1-K1-A9
Method	BLASTX
NCBI GI	g543565
BLAST score	288
E value	1.0e-25
Match length	90
% identity	58
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi|493721|dbj|BAA06462| (D30802) TED4 [Zinnia elegans] >gi|641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	194137
Contig ID	12314_1.R1039
5'-most EST	LIB3165-001-Q1-K1-C4
Method	BLASTX
NCBI GI	g4204267
BLAST score	292
E value	3.0e-26
Match length	146

% identity	50
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	194138
Contig ID	12335_1.R1039
5'-most EST	uC-gsflnu33B129g02b1
Method	BLASTX
NCBI GI	g2384671
BLAST score	963
E value	1.0e-104
Match length	231
% identity	80
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	194139
Contig ID	12336_1.R1039
5'-most EST	uC-gsflmaxxa012a02b1

Seq. No.	194140
Contig ID	12342_1.R1039
5'-most EST	LIB3146-023-Q1-K1-E3
Method	BLASTX
NCBI GI	g3947719
BLAST score	249
E value	3.0e-21
Match length	53
% identity	92
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi|3947721|emb|CAA10102| (AJ012654) ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103| (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	194141
Contig ID	12342_2.R1039
5'-most EST	LIB3149-049-Q1-K1-D9
Method	BLASTX
NCBI GI	g3947719
BLAST score	240
E value	3.0e-20
Match length	51
% identity	92
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi|3947721|emb|CAA10102| (AJ012654) ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103| (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	194142
Contig ID	12370_1.R1039
5'-most EST	uC-gsflnu33B046f11b1

Seq. No.	194143
Contig ID	12373_1.R1039
5'-most EST	LIB3147-046-Q1-K1-D11
Method	BLASTX
NCBI GI	g126896
BLAST score	1404

E value	1.0e-156
Match length	343
% identity	82
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi|319831|pir||DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi|18297|emb|CAA35239| (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	194144
Contig ID	12373_2.R1039
5'-most EST	LIB3147-027-Q1-K1-E7
Method	BLASTX
NCBI GI	g126896
BLAST score	800
E value	1.0e-85
Match length	183
% identity	87
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi|319831|pir||DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi|18297|emb|CAA35239| (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	194145
Contig ID	12373_5.R1039
5'-most EST	uC-gsflmaxxa070b09b1

Seq. No.	194146
Contig ID	12376_1.R1039
5'-most EST	LIB3165-021-P1-K1-F8
Method	BLASTX
NCBI GI	g285317
BLAST score	463
E value	3.0e-46
Match length	141
% identity	70
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	194147
Contig ID	12380_1.R1039
5'-most EST	LIB3120-027-Q1-K1-C5
Method	BLASTX
NCBI GI	g2244840
BLAST score	209
E value	2.0e-16
Match length	77
% identity	60
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194148
Contig ID	12383_1.R1039
5'-most EST	g5044839
Method	BLASTX
NCBI GI	g730922
BLAST score	865
E value	4.0e-93

Match length	279
% identity	61
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (TCP20) (HTR3) >gi|627402|pir||S48087 chaperonin TCP20 - human >gi|517065 (L27706) chaperonin-like protein [Homo sapiens] >gi|4502643|ref|NP_001753.1|pCCT6| chaperonin containing T-complex subunit

Seq. No.	194149
Contig ID	12386_1.R1039
5'-most EST	LIB3165-025-P1-K1-E2
Method	BLASTX
NCBI GI	g3337435
BLAST score	201
E value	2.0e-15
Match length	176
% identity	33
NCBI Description	(AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	194150
Contig ID	12389_1.R1039
5'-most EST	LIB3165-002-Q1-K1-F12
Method	BLASTX
NCBI GI	g3901268
BLAST score	442
E value	2.0e-43
Match length	296
% identity	32
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]

Seq. No.	194151
Contig ID	12396_1.R1039
5'-most EST	LIB3272-058-P1-K1-D4

Seq. No.	194152
Contig ID	12398_1.R1039
5'-most EST	LIB3165-012-P1-K1-A5

Seq. No.	194153
Contig ID	12400_1.R1039
5'-most EST	g5045066
Method	BLASTX
NCBI GI	g3063643
BLAST score	805
E value	5.0e-86
Match length	180
% identity	87
NCBI Description	(AF056622) putative Cu/Zn superoxide dismutase precursor [Vitis vinifera]

Seq. No.	194154
Contig ID	12401_1.R1039
5'-most EST	g5047390
Method	BLASTX
NCBI GI	g1351612
BLAST score	293

E value	3.0e-26
Match length	187
% identity	38
NCBI Description	HYPOTHETICAL OXIDOREDUCTASE C23D3.11 IN CHROMOSOME I >gi|2130343|pir||S62502 hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe)

Seq. No.	194155
Contig ID	12402_1.R1039
5'-most EST	LIB3120-027-Q1-K1-F3

Seq. No.	194156
Contig ID	12413_1.R1039
5'-most EST	LIB3120-027-Q1-K1-G6
Method	BLASTX
NCBI GI	g470373
BLAST score	224
E value	4.0e-18
Match length	136
% identity	38
NCBI Description	(U00047) ZK418.5 gene product [Caenorhabditis elegans]

Seq. No.	194157
Contig ID	12413_2.R1039
5'-most EST	LIB3165-044-Q1-K1-B3
Method	BLASTX
NCBI GI	g470373
BLAST score	174
E value	2.0e-12
Match length	112
% identity	35
NCBI Description	(U00047) ZK418.5 gene product [Caenorhabditis elegans]

Seq. No.	194158
Contig ID	12432_1.R1039
5'-most EST	LIB3120-028-Q1-K1-B2
Method	BLASTX
NCBI GI	g1788928
BLAST score	288
E value	7.0e-26
Match length	137
% identity	44
NCBI Description	(AE000344) quinolinate synthetase, B protein [Escherichia coli]

Seq. No.	194159
Contig ID	12439_1.R1039
5'-most EST	LIB3120-028-Q1-K1-C11
Method	BLASTX
NCBI GI	g4539324
BLAST score	242
E value	2.0e-20
Match length	157
% identity	45
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	194160

Contig ID	12449_1.R1039
5'-most EST	LIB3120-031-Q1-K1-D8
Method	BLASTN
NCBI GI	g12216
BLAST score	88
E value	1.0e-41
Match length	250
% identity	92
NCBI Description	Sinapis alba chloroplast rps16 gene

Seq. No.	194161
Contig ID	12457_1.R1039
5'-most EST	LIB3120-028-Q1-K1-E5
Method	BLASTX
NCBI GI	g4235430
BLAST score	384
E value	7.0e-37
Match length	149
% identity	52
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	194162
Contig ID	12468_1.R1039
5'-most EST	LIB3272-019-P1-K1-F11

Seq. No.	194163
Contig ID	12470_1.R1039
5'-most EST	LIB3120-028-Q1-K1-G1

Seq. No.	194164
Contig ID	12471_1.R1039
5'-most EST	uC-gsflnu33B115d03b1
Method	BLASTX
NCBI GI	g2257531
BLAST score	179
E value	1.0e-12
Match length	181
% identity	26
NCBI Description	(AB004537) WEB1 PROTEIN [Schizosaccharomyces pombe] >gi|2950507|emb|CAA17835| (AL022072) web1 homolog; protein transport protein; WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	194165
Contig ID	12474_1.R1039
5'-most EST	LIB3120-028-Q1-K1-G5

Seq. No.	194166
Contig ID	12476_1.R1039
5'-most EST	LIB3120-028-Q1-K1-H1
Method	BLASTX
NCBI GI	g2880047
BLAST score	150
E value	1.0e-09
Match length	67
% identity	49
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194167
Contig ID	12484_1.R1039
5'-most EST	LIB3120-028-Q1-K1-H8
Method	BLASTX
NCBI GI	g1363479
BLAST score	484
E value	9.0e-49
Match length	125
% identity	78
NCBI Description	photosystem I protein psaL - cucumber >gi|801740|dbj|BAA09047| (D50456) PsaL [Cucumis sativus]

Seq. No.	194168
Contig ID	12485_1.R1039
5'-most EST	LIB3120-060-Q1-K1-H7
Method	BLASTX
NCBI GI	g1877482
BLAST score	187
E value	5.0e-14
Match length	66
% identity	59
NCBI Description	(U89271) short-chain alcohol dehydrogenase [Tripsacum dactyloides]

Seq. No.	194169
Contig ID	12498_1.R1039
5'-most EST	g5046426
Method	BLASTX
NCBI GI	g3128175
BLAST score	197
E value	4.0e-15
Match length	109
% identity	41
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	194170
Contig ID	12509_1.R1039
5'-most EST	LIB3165-021-P1-K1-F1

Seq. No.	194171
Contig ID	12511_1.R1039
5'-most EST	LIB3146-058-Q1-K1-D7
Method	BLASTX
NCBI GI	g3850587
BLAST score	348
E value	9.0e-33
Match length	150
% identity	51
NCBI Description	(AC005278) Strong similarity to gi|2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb|Z97335. [Arabidopsis thaliana]

Seq. No.	194172
Contig ID	12513_1.R1039
5'-most EST	LIB3272-043-P1-K1-F9
Method	BLASTX

NCBI GI	g4572671
BLAST score	538
E value	6.0e-55
Match length	186
% identity	57
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	194173
Contig ID	12514_1.R1039
5'-most EST	g5048505

Seq. No.	194174
Contig ID	12521_1.R1039
5'-most EST	LIB3120-036-Q1-K1-B1

Seq. No.	194175
Contig ID	12523_1.R1039
5'-most EST	LIB3196-028-P1-M1-A11
Method	BLASTX
NCBI GI	g3063392
BLAST score	853
E value	1.0e-91
Match length	247
% identity	69
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	194176
Contig ID	12525_1.R1039
5'-most EST	LIB3120-030-Q1-K1-D11
Method	BLASTX
NCBI GI	g2541876
BLAST score	399
E value	6.0e-39
Match length	152
% identity	59
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	194177
Contig ID	12530_1.R1039
5'-most EST	LIB3120-030-Q1-K1-D8
Method	BLASTX
NCBI GI	g1001355
BLAST score	259
E value	3.0e-22
Match length	135
% identity	40
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	194178
Contig ID	12533_1.R1039
5'-most EST	LIB3165-001-Q1-K1-C7
Method	BLASTX
NCBI GI	g266936
BLAST score	545
E value	7.0e-56

Match length	149
% identity	75
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi|282960|pir||A42840 ribosomal protein L27 - common tobacco >gi|170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi|170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	194179
Contig ID	12542_1.R1039
5'-most EST	LIB3120-030-Q1-K1-F4
Method	BLASTX
NCBI GI	g4468984
BLAST score	263
E value	3.0e-23
Match length	98
% identity	51
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	194180
Contig ID	12561_1.R1039
5'-most EST	LIB3146-057-Q1-K1-B6

Seq. No.	194181
Contig ID	12566_1.R1039
5'-most EST	LIB3120-031-Q1-K1-A5
Method	BLASTX
NCBI GI	g4063760
BLAST score	243
E value	2.0e-20
Match length	81
% identity	53
NCBI Description	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No.	194182
Contig ID	12581_1.R1039
5'-most EST	LIB3165-038-Q1-K1-B10
Method	BLASTX
NCBI GI	g2765081
BLAST score	512
E value	5.0e-52
Match length	139
% identity	73
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	194183
Contig ID	12592_1.R1039
5'-most EST	LIB3120-031-Q1-K1-D11
Method	BLASTX
NCBI GI	g3643607
BLAST score	449
E value	2.0e-44
Match length	94
% identity	89
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	194184

Contig ID	12603_1.R1039
5'-most EST	LIB3196-042-P1-M1-C2
Method	BLASTX
NCBI GI	g2708532
BLAST score	1037
E value	1.0e-113
Match length	301
% identity	41
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No.	194185
Contig ID	12607_1.R1039
5'-most EST	LIB3120-031-Q1-K1-E7
Method	BLASTX
NCBI GI	g3169180
BLAST score	633
E value	5.0e-66
Match length	159
% identity	75
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	194186
Contig ID	12608_1.R1039
5'-most EST	LIB3120-031-Q1-K1-E8
Method	BLASTX
NCBI GI	g418401
BLAST score	147
E value	4.0e-09
Match length	66
% identity	42
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN IN GLY1-GDA1 INTERGENIC REGION >gi|320707|pir||S30833 hypothetical protein YEL044w - yeast (Saccharomyces cerevisiae) >gi|603635 (U18779) Yel044wp [Saccharomyces cerevisiae]

Seq. No.	194187
Contig ID	12610_1.R1039
5'-most EST	uC-gsronu33B051b01b1
Method	BLASTX
NCBI GI	g4105696
BLAST score	421
E value	1.0e-41
Match length	99
% identity	75
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	194188
Contig ID	12614_1.R1039
5'-most EST	LIB3197-002-P1-M1-H6
Method	BLASTX
NCBI GI	g2493046
BLAST score	807
E value	3.0e-86
Match length	201
% identity	77
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi|82297|pir||A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato
>gi|217938|dbj|BAA01511| (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	194189
Contig ID	12620_1.R1039
5'-most EST	LIB3165-039-Q1-K1-B4
Method	BLASTX
NCBI GI	g1050916
BLAST score	192
E value	1.0e-20
Match length	98
% identity	59
NCBI Description	(X92646) homologous to early light induced protein [Helianthus annuus]

Seq. No.	194190
Contig ID	12621_1.R1039
5'-most EST	LIB3165-025-P1-K1-A7
Method	BLASTX
NCBI GI	g4468813
BLAST score	277
E value	1.0e-24
Match length	68
% identity	75
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	194191
Contig ID	12627_1.R1039
5'-most EST	LIB3189-037-P1-K1-A4
Method	BLASTX
NCBI GI	g627468
BLAST score	321
E value	1.0e-29
Match length	124
% identity	54
NCBI Description	hypothetical protein 1 - human >gi|285983|dbj|BAA02799| (D13635) KIAA0010 [Homo sapiens]

Seq. No.	194192
Contig ID	12640_1.R1039
5'-most EST	LIB3120-032-Q1-K1-A6

Seq. No.	194193
Contig ID	12643_1.R1039
5'-most EST	LIB3120-032-Q1-K1-B1

Seq. No.	194194
Contig ID	12653_1.R1039
5'-most EST	LIB3165-016-P1-K1-E4
Method	BLASTX
NCBI GI	g3980238
BLAST score	185
E value	1.0e-13
Match length	56
% identity	61

NCBI Description	(Z21677) ribosomal protein L18 [Thermotoga maritima]

Seq. No.	194195
Contig ID	12657_1.R1039
5'-most EST	LIB3120-032-Q1-K1-D4
Method	BLASTX
NCBI GI	g2498291
BLAST score	256
E value	3.0e-22
Match length	126
% identity	45
NCBI Description	DIHYDRODIPICOLINATE REDUCTASE >gi|1651716|dbj|BAA16644| (D90899) dihydrodipicolinate reductase [Synechocystis sp.]

Seq. No.	194196
Contig ID	12658_1.R1039
5'-most EST	LIB3146-040-Q1-K1-F1
Method	BLASTX
NCBI GI	g3294491
BLAST score	253
E value	2.0e-21
Match length	158
% identity	38
NCBI Description	(AF016421) Similar to nitrophenylphosphatase; coded for by C. elegans cDNA yk312h2.5; coded for by C. elegans cDNA yk267e8.5; coded for by C. elegans cDNA yk312h2.3 [Caenorhabditis elegans]

Seq. No.	194197
Contig ID	12663_1.R1039
5'-most EST	LIB3120-032-Q1-K1-E4
Method	BLASTX
NCBI GI	g2462749
BLAST score	196
E value	6.0e-15
Match length	60
% identity	55
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	194198
Contig ID	12701_1.R1039
5'-most EST	LIB3120-033-P1-K1-D7
Method	BLASTX
NCBI GI	g115581
BLAST score	455
E value	2.0e-45
Match length	139
% identity	68
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) >gi|68031|pir||QYIX2 phosphoenolpyruvate carboxylase (EC 4.1.1.31) 2 - common ice plant >gi|4469271|emb|CAA32728| (X14588) phosphoenolpyruvate carboxylase [Mesembryanthemum crystallinum]

Seq. No.	194199
Contig ID	12702_1.R1039

5'-most EST	LIB3146-006-Q1-K1-G3
Method	BLASTX
NCBI GI	g3892052
BLAST score	174
E value	4.0e-12
Match length	258
% identity	24
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	194200
Contig ID	12731_1.R1039
5'-most EST	LIB3165-041-Q1-K1-F10

Seq. No.	194201
Contig ID	12734_1.R1039
5'-most EST	g5046859
Method	BLASTX
NCBI GI	g484656
BLAST score	399
E value	1.0e-38
Match length	129
% identity	57
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi|452165|dbj|BAA05408| (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	194202
Contig ID	12735_1.R1039
5'-most EST	LIB3120-034-Q1-K1-A7

Seq. No.	194203
Contig ID	12742_1.R1039
5'-most EST	LIB3196-018-P1-M1-B3
Method	BLASTN
NCBI GI	g4455189
BLAST score	34
E value	2.0e-09
Match length	110
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSAII project)

Seq. No.	194204
Contig ID	12743_1.R1039
5'-most EST	LIB3166-030-P1-K1-H4
Method	BLASTX
NCBI GI	g1076316
BLAST score	311
E value	3.0e-28
Match length	123
% identity	46
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi|469110|emb|CAA55321| (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	194205

Contig ID	12743_2.R1039
5'-most EST	g5049856
Method	BLASTX
NCBI GI	g1076316
BLAST score	391
E value	2.0e-37
Match length	115
% identity	61
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi|469110|emb|CAA55321| (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	194206
Contig ID	12743_3.R1039
5'-most EST	LIB3166-058-P1-K1-H7
Method	BLASTX
NCBI GI	g1076316
BLAST score	258
E value	3.0e-22
Match length	71
% identity	58
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi|469110|emb|CAA55321| (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	194207
Contig ID	12744_1.R1039
5'-most EST	LIB3146-042-Q1-K1-E2

Seq. No.	194208
Contig ID	12746_1.R1039
5'-most EST	LIB3165-051-Q1-K1-C7
Method	BLASTX
NCBI GI	g416681
BLAST score	377
E value	4.0e-36
Match length	177
% identity	53
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi|280404|pir||S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi|19787|emb|CAA45153| (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	194209
Contig ID	12752_1.R1039
5'-most EST	LIB3120-034-Q1-K1-C7

Seq. No.	194210
Contig ID	12760_1.R1039
5'-most EST	LIB3146-018-Q1-K1-G10
Method	BLASTX
NCBI GI	g4049346
BLAST score	327
E value	5.0e-30
Match length	133
% identity	47

NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	194211
Contig ID	12762_1.R1039
5'-most EST	LIB3120-034-Q1-K1-G2
Method	BLASTX
NCBI GI	g4127688
BLAST score	240
E value	3.0e-20
Match length	71
% identity	63
NCBI Description	(AJ006065) isochorismate synthase [Catharanthus roseus]
Seq. No.	194212
Contig ID	12766_1.R1039
5'-most EST	g5048084
Method	BLASTX
NCBI GI	g2956717
BLAST score	478
E value	6.0e-48
Match length	158
% identity	63
NCBI Description	(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
Seq. No.	194213
Contig ID	12770_1.R1039
5'-most EST	uC-gsronu33B049h09b1
Seq. No.	194214
Contig ID	12777_2.R1039
5'-most EST	uC-gsronu33B163d05b2
Seq. No.	194215
Contig ID	12790_1.R1039
5'-most EST	LIB3120-034-Q1-K1-F9
Method	BLASTX
NCBI GI	g2244811
BLAST score	261
E value	4.0e-46
Match length	166
% identity	67
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]
Seq. No.	194216
Contig ID	12796_2.R1039
5'-most EST	LIB3120-034-Q1-K1-G3
Method	BLASTX
NCBI GI	g2894598
BLAST score	565
E value	3.0e-58
Match length	116
% identity	87
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	194217
Contig ID	12798_1.R1039
5'-most EST	uC-gsronu33B168b03b1

Method	BLASTN
NCBI GI	g4150964
BLAST score	144
E value	6.0e-75
Match length	383
% identity	87
NCBI Description	Asparagus officinalis mRNA for glutamate dehydrogenase

Seq. No.	194218
Contig ID	12801_1.R1039
5'-most EST	LIB3165-040-Q1-K1-E6

Seq. No.	194219
Contig ID	12809_1.R1039
5'-most EST	LIB3189-033-P1-K1-D12
Method	BLASTX
NCBI GI	g2511594
BLAST score	1096
E value	1.0e-120
Match length	231
% identity	89
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi|2827525|emb|CAA16533| (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi|3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	194220
Contig ID	12809_2.R1039
5'-most EST	LIB3149-001-P1-K1-G12
Method	BLASTX
NCBI GI	g2511594
BLAST score	527
E value	1.0e-53
Match length	124
% identity	81
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi|2827525|emb|CAA16533| (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi|3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	194221
Contig ID	12818_1.R1039
5'-most EST	LIB3135-051-Q1-K1-D8

Seq. No.	194222
Contig ID	12820_1.R1039
5'-most EST	LIB3120-036-Q1-K1-A5
Method	BLASTX
NCBI GI	g2465773
BLAST score	148
E value	7.0e-12
Match length	92
% identity	33

NCBI Description	(AF022186) homologous to orf238 in Porphyra purpurea [Cyanidium caldarium]

Seq. No.	194223
Contig ID	12822_1.R1039
5'-most EST	LIB3189-037-P1-K1-H1

Seq. No.	194224
Contig ID	12831_1.R1039
5'-most EST	LIB3120-036-Q1-K1-B5
Method	BLASTX
NCBI GI	g3924594
BLAST score	1458
E value	1.0e-162
Match length	435
% identity	67
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi|4262139|gb|AAD14439| (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	194225
Contig ID	12851_1.R1039
5'-most EST	LIB3272-033-P1-K1-A4
Method	BLASTX
NCBI GI	g2583108
BLAST score	378
E value	3.0e-36
Match length	142
% identity	56
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	194226
Contig ID	12856_1.R1039
5'-most EST	LIB3146-024-Q1-K1-E2
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	6.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat >gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	194227
Contig ID	12856_2.R1039
5'-most EST	LIB3146-030-Q1-K1-B3
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	6.0e-61
Match length	136

% identity	88
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat >gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	194228
Contig ID	12856_3.R1039
5'-most EST	LIB3147-060-Q1-K1-B7
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	7.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat >gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	194229
Contig ID	12856_4.R1039
5'-most EST	LIB3196-004-P1-M1-D10
Method	BLASTX
NCBI GI	g122087
BLAST score	581
E value	5.0e-60
Match length	136
% identity	86
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat >gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	194230
Contig ID	12856_5.R1039
5'-most EST	LIB3147-052-Q1-K1-H9
Method	BLASTX
NCBI GI	g122087
BLAST score	582
E value	4.0e-60
Match length	136
% identity	87
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat

>gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	194231
Contig ID	12859_1.R1039
5'-most EST	LIB3120-036-Q1-K1-E11
Method	BLASTX
NCBI GI	g4335772
BLAST score	170
E value	6.0e-12
Match length	88
% identity	42
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	194232
Contig ID	12863_1.R1039
5'-most EST	LIB3120-036-Q1-K1-E4

Seq. No.	194233
Contig ID	12879_1.R1039
5'-most EST	LIB3120-036-Q1-K1-G1
Method	BLASTX
NCBI GI	g1363484
BLAST score	263
E value	6.0e-23
Match length	74
% identity	65
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi|972929 (U18415) IAA13 [Arabidopsis thaliana] >gi|2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	194234
Contig ID	12885_1.R1039
5'-most EST	LIB3120-036-Q1-K1-G6

Seq. No.	194235
Contig ID	12892_1.R1039
5'-most EST	LIB3120-036-Q1-K1-H12
Method	BLASTX
NCBI GI	g2191128
BLAST score	384
E value	5.0e-37
Match length	135
% identity	64
NCBI Description	(AF007269) belongs to the L5P family of ribosomal proteins [Arabidopsis thaliana]

Seq. No.	194236
Contig ID	12904_1.R1039
5'-most EST	LIB3120-037-P1-K1-A8

Seq. No.	194237
Contig ID	12908_1.R1039

5'-most EST	LIB3166-004-P1-K1-F11
Seq. No.	194238
Contig ID	12909_1.R1039
5'-most EST	LIB3120-037-P1-K1-C2
Method	BLASTX
NCBI GI	g2190012
BLAST score	337
E value	2.0e-31
Match length	108
% identity	63
NCBI Description	(AB004242) din1 [Raphanus sativus]
Seq. No.	194239
Contig ID	12909_2.R1039
5'-most EST	LIB3165-012-P1-K1-G2
Seq. No.	194240
Contig ID	12915_1.R1039
5'-most EST	uC-gsflnu33B144f01b1
Method	BLASTX
NCBI GI	g3769673
BLAST score	406
E value	2.0e-39
Match length	116
% identity	59
NCBI Description	(AF095285) Tic20 [Pisum sativum]
Seq. No.	194241
Contig ID	12931_1.R1039
5'-most EST	LIB3272-017-P1-K1-C12
Method	BLASTX
NCBI GI	g485514
BLAST score	390
E value	2.0e-37
Match length	79
% identity	91
NCBI Description	ADR11-2 protein - soybean (fragment) >gi|296443|emb|CAA49341| (X69640) auxin down regulated [Glycine max]
Seq. No.	194242
Contig ID	12936_2.R1039
5'-most EST	LIB3165-060-Q1-K1-E4
Method	BLASTX
NCBI GI	g3023752
BLAST score	272
E value	4.0e-24
Match length	82
% identity	66
NCBI Description	FERREDOXIN I PRECURSOR >gi|1418982|emb|CAA99756| (Z75520) ferredoxin-I [Lycopersicon esculentum]
Seq. No.	194243
Contig ID	12958_1.R1039
5'-most EST	uC-gsflnu33B107f04b1
Method	BLASTX

NCBI GI	g4417280
BLAST score	870
E value	2.0e-93
Match length	240
% identity	70
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	194244
Contig ID	12958_2.R1039
5'-most EST	LIB3197-010-P1-M1-H1
Method	BLASTX
NCBI GI	g4417280
BLAST score	787
E value	6.0e-84
Match length	241
% identity	66
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	194245
Contig ID	12960_1.R1039
5'-most EST	LIB3146-015-Q1-K1-E3
Method	BLASTX
NCBI GI	g1769887
BLAST score	724
E value	8.0e-77
Match length	169
% identity	83
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	194246
Contig ID	12981_1.R1039
5'-most EST	LIB3120-039-P1-K1-F3
Method	BLASTX
NCBI GI	g4262234
BLAST score	515
E value	2.0e-66
Match length	210
% identity	65
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	194247
Contig ID	12995_1.R1039
5'-most EST	LIB3120-039-P1-K1-H4
Method	BLASTX
NCBI GI	g547911
BLAST score	170
E value	7.0e-12
Match length	155
% identity	33
NCBI Description	MO25 PROTEIN >gi|2143483|pir||I57997 hypothetical calcium-binding protein - mouse >gi|262934|bbs|121784 (S51858) putative Ca2+ binding protein [mice, embryos, Peptide, 341 aa] [Mus sp.]

Seq. No.	194248
Contig ID	13016_1.R1039
5'-most EST	LIB3120-043-P1-K1-B3

Method	BLASTX
NCBI GI	g2131751
BLAST score	333
E value	5.0e-31
Match length	130
% identity	46
NCBI Description	hypothetical protein YLR019w - yeast (Saccharomyces cerevisiae) >gi|1360322|emb|CAA97541| (Z73191) ORF YLR019w [Saccharomyces cerevisiae]

Seq. No.	194249
Contig ID	13032_1.R1039
5'-most EST	LIB3272-038-P1-K1-B5
Method	BLASTX
NCBI GI	g4406767
BLAST score	362
E value	2.0e-34
Match length	153
% identity	49
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	194250
Contig ID	13033_1.R1039
5'-most EST	LIB3120-043-P1-K1-C9
Method	BLASTX
NCBI GI	g3075488
BLAST score	321
E value	9.0e-30
Match length	110
% identity	57
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	194251
Contig ID	13036_1.R1039
5'-most EST	uC-gsronu33B178c08b1

Seq. No.	194252
Contig ID	13037_1.R1039
5'-most EST	uC-gsronu33B116b03b1
Method	BLASTX
NCBI GI	g2795809
BLAST score	1200
E value	1.0e-132
Match length	241
% identity	88
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	194253
Contig ID	13046_1.R1039
5'-most EST	uC-gsronu33B017d12b1
Method	BLASTX
NCBI GI	g285286
BLAST score	501
E value	2.0e-50
Match length	176
% identity	51

NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.	194254
Contig ID	13051_1.R1039
5'-most EST	LIB3166-022-P1-K1-A6
Method	BLASTX
NCBI GI	g1711355
BLAST score	605
E value	2.0e-62
Match length	240
% identity	53
NCBI Description	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE >gi|421786|pir||S34678 short-chain alcohol dehydrogenase - Norway spruce >gi|395223|emb|CAA52213| (X74115) short-chain alcohol dehydrogenase [Picea abies]
Seq. No.	194255
Contig ID	13063_1.R1039
5'-most EST	g5049457
Method	BLASTX
NCBI GI	g1170714
BLAST score	1247
E value	1.0e-137
Match length	241
% identity	94
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi|541850|pir||S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi|456509|emb|CAA53180| (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi|2059329|emb|CAA73247| (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.	194256
Contig ID	13065_1.R1039
5'-most EST	LIB3146-010-Q1-K1-B5
Seq. No.	194257
Contig ID	13070_1.R1039
5'-most EST	LIB3120-043-P1-K1-G12
Method	BLASTX
NCBI GI	g4454014
BLAST score	320
E value	3.0e-29
Match length	150
% identity	49
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	194258
Contig ID	13080_1.R1039
5'-most EST	LIB3166-034-P1-K1-G5
Seq. No.	194259
Contig ID	13087_1.R1039
5'-most EST	LIB3120-044-P1-K1-A10
Method	BLASTX
NCBI GI	g3885344
BLAST score	152

E value	5.0e-10
Match length	92
% identity	33
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana] >gi|4557057|gb|AAD22497.1|AC007154_1 (AC007154) unknown protein [Arabidopsis thaliana]

Seq. No.	194260
Contig ID	13091_1.R1039
5'-most EST	LIB3120-044-P1-K1-A4

Seq. No.	194261
Contig ID	13097_1.R1039
5'-most EST	LIB3135-034-Q1-K1-D3

Seq. No.	194262
Contig ID	13106_1.R1039
5'-most EST	LIB3165-060-Q1-K1-C7
Method	BLASTN
NCBI GI	g1130681
BLAST score	833
E value	0.0e+00
Match length	857
% identity	99
NCBI Description	G.hirsutum gene for acetohydroxyacid synthase (3231 bp)

Seq. No.	194263
Contig ID	13136_1.R1039
5'-most EST	LIB3120-044-P1-K1-E8
Method	BLASTX
NCBI GI	g1170567
BLAST score	358
E value	2.0e-34
Match length	74
% identity	85
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi|1085960|pir||S52648 INO1 protein - Citrus paradisi >gi|602565|emb|CAA83565| (Z32632) INO1 [Citrus x paradisi]

Seq. No.	194264
Contig ID	13142_1.R1039
5'-most EST	LIB3120-044-P1-K1-F6

Seq. No.	194265
Contig ID	13145_1.R1039
5'-most EST	LIB3196-022-P1-M1-E7

Seq. No.	194266
Contig ID	13146_1.R1039
5'-most EST	LIB3166-014-P1-K1-B5
Method	BLASTX
NCBI GI	g3059095
BLAST score	1066
E value	1.0e-116
Match length	217
% identity	94
NCBI Description	(AJ001091) magnesium chelatase subunit [Glycine max]

Seq. No.	194267
Contig ID	13147_1.R1039
5'-most EST	LIB3120-044-P1-K1-G6
Method	BLASTX
NCBI GI	g3128195
BLAST score	231
E value	6.0e-24
Match length	65
% identity	87
NCBI Description	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No.	194268
Contig ID	13156_1.R1039
5'-most EST	LIB3146-050-Q1-K1-H5
Method	BLASTX
NCBI GI	g3643090
BLAST score	468
E value	5.0e-48
Match length	132
% identity	71
NCBI Description	(AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	194269
Contig ID	13164_1.R1039
5'-most EST	LIB3120-045-P1-K1-A6
Method	BLASTX
NCBI GI	g4127688
BLAST score	421
E value	3.0e-43
Match length	128
% identity	71
NCBI Description	(AJ006065) isochorismate synthase [Catharanthus roseus]

Seq. No.	194270
Contig ID	13165_1.R1039
5'-most EST	LIB3120-045-P1-K1-B5

Seq. No.	194271
Contig ID	13169_1.R1039
5'-most EST	LIB3120-045-P1-K1-B6

Seq. No.	194272
Contig ID	13176_1.R1039
5'-most EST	uC-gsronu33b025a07b1
Method	BLASTX
NCBI GI	g2583108
BLAST score	654
E value	4.0e-68
Match length	318
% identity	42
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	194273
Contig ID	13176_2.R1039
5'-most EST	LIB3149-020-Q1-K1-F1
Method	BLASTX
NCBI GI	g4006877
BLAST score	401
E value	7.0e-39
Match length	159
% identity	37
NCBI Description	(Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No.	194274
Contig ID	13183_1.R1039
5'-most EST	LIB3166-003-P1-K1-C4
Method	BLASTX
NCBI GI	g3600031
BLAST score	243
E value	1.0e-20
Match length	108
% identity	56
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	194275
Contig ID	13190_1.R1039
5'-most EST	LIB3147-009-Q1-K1-D4

Seq. No.	194276
Contig ID	13192_1.R1039
5'-most EST	LIB3165-020-P1-K1-B8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	194277
Contig ID	13193_1.R1039
5'-most EST	uC-gsflmaxxa098g04b1
Method	BLASTX
NCBI GI	g3875112
BLAST score	603
E value	3.0e-62
Match length	241
% identity	51
NCBI Description	(Z68882) Similarity to Bovine inorganic pyrophosphatase (SW:IPYR_BOVIN); cDNA EST EMBL:D66533 comes from this gene; cDNA EST EMBL:D70345 comes from this gene; cDNA EST yk338a8.3 comes from this gene; cDNA EST yk338a8.5 comes fr

Seq. No.	194278
Contig ID	13218_1.R1039
5'-most EST	uC-gsronu33B038b11b1
Method	BLASTX
NCBI GI	g1931655

BLAST score	321
E value	1.0e-29
Match length	109
% identity	62
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	194279
Contig ID	13221_1.R1039
5'-most EST	LIB3120-046-P1-K1-B7
Method	BLASTN
NCBI GI	g3985931
BLAST score	39
E value	2.0e-12
Match length	67
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	194280
Contig ID	13226_1.R1039
5'-most EST	LIB3120-046-P1-K1-C11
Method	BLASTX
NCBI GI	g4263710
BLAST score	281
E value	5.0e-25
Match length	63
% identity	51
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	194281
Contig ID	13230_1.R1039
5'-most EST	LIB3120-046-P1-K1-C4
Method	BLASTX
NCBI GI	g225282
BLAST score	166
E value	2.0e-11
Match length	46
% identity	72
NCBI Description	RNA polymerase beta [Nicotiana tabacum]

Seq. No.	194282
Contig ID	13244_1.R1039
5'-most EST	LIB3165-045-Q1-K1-G7
Method	BLASTX
NCBI GI	g2191152
BLAST score	495
E value	3.0e-50
Match length	122
% identity	76
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	194283
Contig ID	13249_1.R1039
5'-most EST	uC-gsflnu33B112h03b1
Method	BLASTX

NCBI GI	g4455192
BLAST score	368
E value	3.0e-35
Match length	126
% identity	55
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	194284
Contig ID	13268_1.R1039
5'-most EST	LIB3120-046-P1-K1-G10
Method	BLASTN
NCBI GI	g1150931
BLAST score	55
E value	5.0e-22
Match length	251
% identity	80
NCBI Description	M.sativa mRNA for cyclin protein

Seq. No.	194285
Contig ID	13272_1.R1039
5'-most EST	LIB3197-034-Q1-M1-C11
Method	BLASTX
NCBI GI	g2739046
BLAST score	305
E value	1.0e-27
Match length	169
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	194286
Contig ID	13274_1.R1039
5'-most EST	uC-gsronu33B164d01b2
Method	BLASTX
NCBI GI	g3080439
BLAST score	525
E value	1.0e-53
Match length	140
% identity	72
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	194287
Contig ID	13274_2.R1039
5'-most EST	LIB3148-006-Q1-K1-D1
Method	BLASTX
NCBI GI	g3080439
BLAST score	400
E value	2.0e-54
Match length	161
% identity	68
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	194288
Contig ID	13287_1.R1039
5'-most EST	LIB3189-041-P1-K1-A8
Method	BLASTX
NCBI GI	g2326812

BLAST score 149
E value 2.0e-09
Match length 97
% identity 43
NCBI Description (Z74955) ORF YOR046c [Saccharomyces cerevisiae]

Seq. No. 194289
Contig ID 13296_1.R1039
5'-most EST LIB3135-040-Q1-K1-H7
Method BLASTX
NCBI GI g2407802
BLAST score 181
E value 2.0e-13
Match length 38
% identity 95
NCBI Description (Y12576) histone H2B [Arabidopsis thaliana]

Seq. No. 194290
Contig ID 13301_1.R1039
5'-most EST uC-gsflnu33B012e12b1
Method BLASTX
NCBI GI g1835260
BLAST score 956
E value 1.0e-103
Match length 284
% identity 65
NCBI Description (Z75660) mitotic cyclin [Sesbania rostrata]

Seq. No. 194291
Contig ID 13303_1.R1039
5'-most EST LIB3120-048-P1-K1-C2
Method BLASTX
NCBI GI g3128168
BLAST score 625
E value 7.0e-65
Match length 189
% identity 59
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 194292
Contig ID 13304_1.R1039
5'-most EST LIB3120-048-P1-K1-C3
Method BLASTX
NCBI GI g3451072
BLAST score 581
E value 6.0e-60
Match length 153
% identity 69
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 194293
Contig ID 13310_1.R1039
5'-most EST LIB3120-048-P1-K1-D1

Seq. No. 194294
Contig ID 13311_1.R1039

5'-most EST	LIB3120-048-P1-K1-D6
Seq. No.	194295
Contig ID	13331_1.R1039
5'-most EST	uC-gsflnu33B025c12b1
Seq. No.	194296
Contig ID	13346_1.R1039
5'-most EST	LIB3120-053-P1-K1-A10
Method	BLASTX
NCBI GI	g1705651
BLAST score	230
E value	4.0e-19
Match length	70
% identity	63
NCBI Description	20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT) (CBP20) >gi|984139|emb|CAA58962| (X84157) subunit of the dimeric cap binding complex CBC [Homo sapiens] >gi|1582342|prf||2118330A cap-binding protein [Homo sapiens]
Seq. No.	194297
Contig ID	13349_1.R1039
5'-most EST	LIB3165-019-P1-K1-H9
Method	BLASTX
NCBI GI	g82263
BLAST score	368
E value	3.0e-35
Match length	119
% identity	69
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato
Seq. No.	194298
Contig ID	13357_1.R1039
5'-most EST	g5048252
Method	BLASTX
NCBI GI	g3924613
BLAST score	342
E value	1.0e-31
Match length	132
% identity	54
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana] >gi|4263512|gb|AAD15338| (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194299
Contig ID	13367_1.R1039
5'-most EST	LIB3165-049-Q1-K1-D2
Seq. No.	194300
Contig ID	13368_1.R1039
5'-most EST	LIB3120-053-P1-K1-C10
Seq. No.	194301
Contig ID	13382_1.R1039
5'-most EST	g5048158

Method	BLASTX
NCBI GI	g4101626
BLAST score	1767
E value	0.0e+00
Match length	447
% identity	71
NCBI Description	(AF005096) desaturase/cytochrome b5 protein [Ricinus communis]

Seq. No.	194302
Contig ID	13383_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A12
Method	BLASTX
NCBI GI	g2499542
BLAST score	538
E value	4.0e-55
Match length	156
% identity	64
NCBI Description	IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP) >gi|1218042 (U48448) secreted purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	194303
Contig ID	13399_1.R1039
5'-most EST	LIB3135-044-Q1-K1-E2
Method	BLASTX
NCBI GI	g1707640
BLAST score	165
E value	3.0e-11
Match length	123
% identity	35
NCBI Description	(X98355) transcription factor GAMyb [Oryza sativa]

Seq. No.	194304
Contig ID	13403_1.R1039
5'-most EST	LIB3120-053-P1-K1-G6

Seq. No.	194305
Contig ID	13419_1.R1039
5'-most EST	LIB3120-054-P1-K1-A10
Method	BLASTN
NCBI GI	g3510339
BLAST score	33
E value	5.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	194306
Contig ID	13422_1.R1039
5'-most EST	g3325803

Seq. No.	194307
Contig ID	13429_1.R1039
5'-most EST	LIB3145-044-Q1-K1-F3
Method	BLASTX

NCBI GI	g1931647
BLAST score	1146
E value	1.0e-126
Match length	255
% identity	82
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	194308
Contig ID	13442_1.R1039
5'-most EST	LIB3165-028-P1-K1-B6

Seq. No.	194309
Contig ID	13450_1.R1039
5'-most EST	uC-gsronu33B089a03b1
Method	BLASTX
NCBI GI	g3355480
BLAST score	327
E value	6.0e-30
Match length	146
% identity	42
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	194310
Contig ID	13451_1.R1039
5'-most EST	LIB3165-053-Q1-K1-H3
Method	BLASTX
NCBI GI	g3128199
BLAST score	229
E value	1.0e-18
Match length	101
% identity	49
NCBI Description	(AC004521) putative proteinase [Arabidopsis thaliana]

Seq. No.	194311
Contig ID	13486_1.R1039
5'-most EST	LIB3165-025-P1-K1-B3
Method	BLASTN
NCBI GI	g2564045
BLAST score	39
E value	2.0e-12
Match length	155
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	194312
Contig ID	13490_1.R1039
5'-most EST	LIB3120-057-Q1-K1-A11
Method	BLASTX
NCBI GI	g3915826
BLAST score	1069
E value	1.0e-117
Match length	260
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	194313
Contig ID	13490_9.R1039
5'-most EST	LIB3120-057-Q1-K1-E10

Seq. No.	194314
Contig ID	13520_1.R1039
5'-most EST	LIB3120-060-Q1-K1-A1
Method	BLASTX
NCBI GI	g3334441
BLAST score	342
E value	6.0e-32
Match length	214
% identity	26
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN T5I7.9 IN CHROMOSOME II >gi|2642161 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194315
Contig ID	13523_1.R1039
5'-most EST	LIB3120-060-Q1-K1-A12
Method	BLASTX
NCBI GI	g2494275
BLAST score	562
E value	1.0e-57
Match length	169
% identity	58
NCBI Description	ELONGATION FACTOR P (EF-P) >gi|1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No.	194316
Contig ID	13527_1.R1039
5'-most EST	LIB3149-015-Q1-K1-A2
Method	BLASTX
NCBI GI	g2459420
BLAST score	716
E value	1.0e-75
Match length	140
% identity	98
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	194317
Contig ID	13527_2.R1039
5'-most EST	uC-gsflnu33B013d12b1
Method	BLASTX
NCBI GI	g2459420
BLAST score	716
E value	7.0e-76
Match length	140
% identity	98
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	194318
Contig ID	13527_3.R1039
5'-most EST	LIB3149-001-P1-K1-H7

Method	BLASTX
NCBI GI	g2982289
BLAST score	402
E value	3.0e-39
Match length	82
% identity	94
NCBI Description	(AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No.	194319
Contig ID	13527_4.R1039
5'-most EST	LIB3135-055-Q1-K1-C12
Method	BLASTX
NCBI GI	g2341028
BLAST score	201
E value	7.0e-16
Match length	39
% identity	100
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb|X01694). EST gb|AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	194320
Contig ID	13528_1.R1039
5'-most EST	LIB3120-060-Q1-K1-A6
Method	BLASTN
NCBI GI	g12139
BLAST score	36
E value	2.0e-10
Match length	52
% identity	92
NCBI Description	Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No.	194321
Contig ID	13529_1.R1039
5'-most EST	LIB3120-060-Q1-K1-A7
Method	BLASTX
NCBI GI	g4567302
BLAST score	333
E value	3.0e-39
Match length	166
% identity	60
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	194322
Contig ID	13529_3.R1039
5'-most EST	LIB3148-006-Q1-K1-H3

Seq. No.	194323
Contig ID	13530_1.R1039
5'-most EST	uC-gsflmaxxa006b09b1
Method	BLASTX
NCBI GI	g1707939
BLAST score	1118
E value	1.0e-122
Match length	269

% identity	79
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi|1076256|pir||S51943 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small chain B1 precursor - beet (fragment) >gi|556622|emb|CAA55515| (X78899) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No.	194324
Contig ID	13531_1.R1039
5'-most EST	LIB3120-060-Q1-K1-A9
Method	BLASTX
NCBI GI	g3023436
BLAST score	969
E value	1.0e-130
Match length	247
% identity	92
NCBI Description	CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi|857578 (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus tremuloides]

Seq. No.	194325
Contig ID	13536_1.R1039
5'-most EST	uC-gsflnu33B111g11b1
Method	BLASTN
NCBI GI	g2960357
BLAST score	267
E value	1.0e-148
Match length	707
% identity	85
NCBI Description	Populus balsamifera subsp. trichocarpa mRNA for caffeoyl-CoA 3-O-methyltransferase, clone PtCCoAOMT2a

Seq. No.	194326
Contig ID	13540_1.R1039
5'-most EST	LIB3146-010-Q1-K1-G11
Method	BLASTX
NCBI GI	g2581785
BLAST score	596
E value	9.0e-62
Match length	153
% identity	75
NCBI Description	(U94999) class 2 non-symbiotic hemoglobin [Arabidopsis thaliana]

Seq. No.	194327
Contig ID	13561_1.R1039
5'-most EST	LIB3165-057-P1-K1-B6
Method	BLASTX
NCBI GI	g3660471
BLAST score	1456
E value	1.0e-162
Match length	326
% identity	84

NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
Seq. No.	194328
Contig ID	13570_1.R1039
5'-most EST	LIB3272-014-P1-K1-H10
Seq. No.	194329
Contig ID	13604_1.R1039
5'-most EST	LIB3120-060-Q1-K1-H8
Seq. No.	194330
Contig ID	13611_1.R1039
5'-most EST	LIB3135-002-Q1-K1-A6
Method	BLASTX
NCBI GI	g3885327
BLAST score	303
E value	1.0e-27
Match length	83
% identity	66
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194331
Contig ID	13612_1.R1039
5'-most EST	LIB3148-017-Q1-K1-D12
Method	BLASTX
NCBI GI	g2245107
BLAST score	257
E value	5.0e-22
Match length	120
% identity	23
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]
Seq. No.	194332
Contig ID	13614_1.R1039
5'-most EST	LIB3135-002-Q1-K1-A9
Method	BLASTX
NCBI GI	g2980795
BLAST score	804
E value	5.0e-86
Match length	177
% identity	88
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	194333
Contig ID	13616_1.R1039
5'-most EST	LIB3145-056-Q1-K1-C8
Seq. No.	194334
Contig ID	13633_1.R1039
5'-most EST	g5049380
Method	BLASTX
NCBI GI	g2982266
BLAST score	524
E value	3.0e-53
Match length	112
% identity	89

NCBI Description	(AF051216) probable fibrillarin [Picea mariana]
Seq. No.	194335
Contig ID	13645_1.R1039
5'-most EST	LIB3135-002-Q1-K1-D6
Method	BLASTN
NCBI GI	g2564048
BLAST score	38
E value	6.0e-12
Match length	271
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.	194336
Contig ID	13646_1.R1039
5'-most EST	uC-gsflmaxxa098e08b1
Method	BLASTX
NCBI GI	g3341687
BLAST score	155
E value	8.0e-10
Match length	58
% identity	57
NCBI Description	(AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.	194337
Contig ID	13648_1.R1039
5'-most EST	LIB3148-006-Q1-K1-A4
Seq. No.	194338
Contig ID	13649_1.R1039
5'-most EST	LIB3135-002-Q1-K1-E1
Method	BLASTX
NCBI GI	g2827536
BLAST score	219
E value	1.0e-17
Match length	74
% identity	53
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194339
Contig ID	13650_1.R1039
5'-most EST	g5046570
Method	BLASTX
NCBI GI	g2947060
BLAST score	1310
E value	1.0e-145
Match length	276
% identity	87
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]
Seq. No.	194340
Contig ID	13654_1.R1039
5'-most EST	LIB3148-035-Q1-K1-E7
Seq. No.	194341
Contig ID	13662_1.R1039

5'-most EST	g5049609
Method	BLASTX
NCBI GI	g629858
BLAST score	565
E value	4.0e-58
Match length	129
% identity	82
NCBI Description	protein kinase C inhibitor - maize

Seq. No.	194342
Contig ID	13662_2.R1039
5'-most EST	LIB3146-058-Q1-K1-E10

Seq. No.	194343
Contig ID	13663_1.R1039
5'-most EST	LIB3146-003-P1-K1-E4
Method	BLASTX
NCBI GI	g2980770
BLAST score	360
E value	6.0e-34
Match length	121
% identity	64
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	194344
Contig ID	13666_1.R1039
5'-most EST	LIB3197-048-Q1-M1-B6
Method	BLASTX
NCBI GI	g3522929
BLAST score	754
E value	1.0e-148
Match length	273
% identity	93
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi|3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	194345
Contig ID	13666_2.R1039
5'-most EST	LIB3197-034-Q1-M1-H4
Method	BLASTX
NCBI GI	g2760326
BLAST score	541
E value	4.0e-55
Match length	227
% identity	48
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	194346
Contig ID	13666_3.R1039
5'-most EST	g5046201
Method	BLASTX
NCBI GI	g2760326
BLAST score	596
E value	2.0e-61
Match length	294
% identity	46

NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.	194347
Contig ID	13668_1.R1039
5'-most EST	LIB3135-002-Q1-K1-F6
Method	BLASTX
NCBI GI	g2827548
BLAST score	676
E value	7.0e-71
Match length	297
% identity	42
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]
Seq. No.	194348
Contig ID	13670_1.R1039
5'-most EST	LIB3135-002-Q1-K1-F8
Method	BLASTX
NCBI GI	g2911059
BLAST score	296
E value	7.0e-27
Match length	70
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]
Seq. No.	194349
Contig ID	13674_1.R1039
5'-most EST	LIB3166-036-P1-K1-A10
Method	BLASTX
NCBI GI	g4538911
BLAST score	928
E value	1.0e-100
Match length	250
% identity	73
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194350
Contig ID	13675_2.R1039
5'-most EST	LIB3135-045-Q1-K1-C12
Seq. No.	194351
Contig ID	13676_1.R1039
5'-most EST	uC-gsflnu33B085f12b1
Method	BLASTX
NCBI GI	g4105798
BLAST score	904
E value	2.0e-97
Match length	247
% identity	57
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	194352
Contig ID	13677_1.R1039
5'-most EST	LIB3165-011-P1-K1-H1
Seq. No.	194353
Contig ID	13680_1.R1039

5'-most EST	uC-gsflnu33B128f07b1
Method	BLASTX
NCBI GI	g3293547
BLAST score	158
E value	6.0e-19
Match length	191
% identity	37
NCBI Description	(AF072709) putative oxidoreductase [Streptomyces lividans]

Seq. No.	194354
Contig ID	13680_2.R1039
5'-most EST	LIB3272-016-P1-K1-F3
Method	BLASTX
NCBI GI	g117549
BLAST score	180
E value	4.0e-13
Match length	107
% identity	39
NCBI Description	QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) >gi|65895|pir||CYGPZ zeta-crystallin / quinone reductase (NADPH) (EC 1.6.-.-) - guinea pig >gi|305333 (M26936) zeta-crystallin [Cavia porcellus]

Seq. No.	194355
Contig ID	13686_1.R1039
5'-most EST	uC-gsronu33B114h07b1
Method	BLASTX
NCBI GI	g1421730
BLAST score	453
E value	6.0e-45
Match length	219
% identity	50
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	194356
Contig ID	13687_1.R1039
5'-most EST	LIB3272-015-P1-K1-D6
Method	BLASTX
NCBI GI	g416649
BLAST score	480
E value	4.0e-48
Match length	168
% identity	57
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT1/PCNT110) >gi|100303|pir||S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi|19789|emb|CAA39709| (X56268) auxin-induced protein [Nicotiana tabacum] >gi|19795|emb|CAA39705| (X56264) auxin-induced protein [Nicotiana tabacum]

Seq. No.	194357
Contig ID	13688_1.R1039
5'-most EST	LIB3272-039-P1-K1-G1

Seq. No.	194358
Contig ID	13690_1.R1039
5'-most EST	LIB3135-002-Q1-K1-H9

Seq. No.	194359
Contig ID	13692_1.R1039
5'-most EST	g3326349
Method	BLASTX
NCBI GI	g2274915
BLAST score	651
E value	5.0e-68
Match length	197
% identity	66
NCBI Description	(AJ000081) beta-1,3-glucanase [Citrus sinensis]

Seq. No.	194360
Contig ID	13696_1.R1039
5'-most EST	LIB3135-003-Q1-K1-A3
Method	BLASTX
NCBI GI	g4455326
BLAST score	511
E value	5.0e-52
Match length	136
% identity	67
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	194361
Contig ID	13698_1.R1039
5'-most EST	uC-gsflmaxxa004g11b1
Method	BLASTX
NCBI GI	g1296816
BLAST score	764
E value	3.0e-81
Match length	171
% identity	87
NCBI Description	(X94995) naringenin-chalcone synthase [Juglans sp.]

Seq. No.	194362
Contig ID	13704_1.R1039
5'-most EST	LIB3135-003-Q1-K1-B10

Seq. No.	194363
Contig ID	13705_1.R1039
5'-most EST	LIB3189-016-P1-K1-B7
Method	BLASTX
NCBI GI	g3915826
BLAST score	1197
E value	1.0e-132
Match length	286
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	194364
Contig ID	13706_1.R1039
5'-most EST	LIB3147-027-Q1-K1-D3
Method	BLASTX
NCBI GI	g4531444
BLAST score	242
E value	6.0e-36
Match length	130

% identity	61
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	194365
Contig ID	13708_1.R1039
5'-most EST	LIB3135-003-Q1-K1-B3
Method	BLASTX
NCBI GI	g2832681
BLAST score	497
E value	4.0e-50
Match length	97
% identity	91
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	194366
Contig ID	13709_1.R1039
5'-most EST	LIB3145-008-Q1-K1-D5
Method	BLASTX
NCBI GI	g4262149
BLAST score	1155
E value	1.0e-127
Match length	271
% identity	75
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	194367
Contig ID	13709_2.R1039
5'-most EST	LIB3149-029-Q1-K1-E9
Method	BLASTX
NCBI GI	g4262149
BLAST score	164
E value	3.0e-11
Match length	71
% identity	77
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	194368
Contig ID	13709_3.R1039
5'-most EST	uC-gsflnu33B023g06b1
Method	BLASTX
NCBI GI	g4262149
BLAST score	151
E value	8.0e-21
Match length	67
% identity	73
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	194369
Contig ID	13715_1.R1039
5'-most EST	uC-gsronu33B038c11b1

Seq. No.	194370
Contig ID	13716_1.R1039
5'-most EST	LIB3135-003-Q1-K1-C2

Seq. No.	194371
Contig ID	13717_1.R1039
5'-most EST	LIB3147-049-Q1-K1-G12
Method	BLASTX
NCBI GI	g4539417
BLAST score	488
E value	5.0e-49
Match length	105
% identity	82
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	194372
Contig ID	13718_1.R1039
5'-most EST	uC-gsronu33B169c07b1
Method	BLASTX
NCBI GI	g3367576
BLAST score	362
E value	4.0e-34
Match length	134
% identity	50
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	194373
Contig ID	13721_1.R1039
5'-most EST	uC-gsflnu33B088e12b1
Method	BLASTX
NCBI GI	g1169009
BLAST score	1687
E value	0.0e+00
Match length	364
% identity	86
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi|542009|pir||S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi|437777|emb|CAA52814| (X74814) 0-Methyltransferase [Eucalyptus gunnii]

Seq. No.	194374
Contig ID	13721_2.R1039
5'-most EST	LIB3145-041-Q1-K1-F7
Method	BLASTX
NCBI GI	g729274
BLAST score	169
E value	7.0e-12
Match length	93
% identity	40
NCBI Description	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) >gi|422797|pir||A45981 peptidylprolyl isomerase (EC 5.2.1.8) CyP-40 - human >gi|348910 (L11667) cyclophilin-40 [Homo sapiens] >gi|1769812|dbj|BAA09923| (D63861) cyclophilin 40 [Homo sapiens]

Seq. No.	194375
Contig ID	13721_3.R1039

5'-most EST	uC-gsflnu33B111f02b1
Method	BLASTX
NCBI GI	g3913295
BLAST score	509
E value	9.0e-52
Match length	113
% identity	90
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi|602588|emb|CAA58218| (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No.	194376
Contig ID	13721_4.R1039
5'-most EST	uC-gsronu33B145h08b1
Method	BLASTX
NCBI GI	g1169009
BLAST score	670
E value	5.0e-78
Match length	183
% identity	77
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi|542009|pir||S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi|437777|emb|CAA52814| (X74814) O-Methyltransferase [Eucalyptus gunnii]

Seq. No.	194377
Contig ID	13724_1.R1039
5'-most EST	LIB3135-003-Q1-K1-D10

Seq. No.	194378
Contig ID	13725_1.R1039
5'-most EST	uC-gsflnu33B064d05b1
Method	BLASTX
NCBI GI	g4454466
BLAST score	197
E value	4.0e-15
Match length	52
% identity	69
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	194379
Contig ID	13725_3.R1039
5'-most EST	LIB3272-020-P1-K1-D10
Method	BLASTX
NCBI GI	g4454466
BLAST score	190
E value	3.0e-14
Match length	52
% identity	65
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	194380
Contig ID	13729_1.R1039
5'-most EST	LIB3197-050-Q1-M1-H11

Method	BLASTX
NCBI GI	g1346675
BLAST score	717
E value	9.0e-76
Match length	148
% identity	91
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) >gi|499112 (U10283) nucleoside diphosphate kinase [Flaveria bidentis]

Seq. No.	194381
Contig ID	13735_1.R1039
5'-most EST	uC-gsflmaxxa094e12b1
Method	BLASTX
NCBI GI	g4204695
BLAST score	461
E value	6.0e-46
Match length	237
% identity	49
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No.	194382
Contig ID	13738_1.R1039
5'-most EST	LIB3135-003-Q1-K1-E5

Seq. No.	194383
Contig ID	13747_1.R1039
5'-most EST	LIB3135-034-Q1-K1-B5
Method	BLASTX
NCBI GI	g1710077
BLAST score	643
E value	2.0e-67
Match length	162
% identity	73
NCBI Description	PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C) >gi|2130029|pir||S60285 B15C protein - barley >gi|471321|emb|CAA54066| (X76605) HvB15C [Hordeum vulgare] >gi|1694833|emb|CAA65387| (X96551) peroxiredoxin [Hordeum vulgare]

Seq. No.	194384
Contig ID	13748_1.R1039
5'-most EST	LIB3135-003-Q1-K1-F5
Method	BLASTX
NCBI GI	g3915847
BLAST score	1028
E value	1.0e-112
Match length	214
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi|2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	194385
Contig ID	13748_2.R1039
5'-most EST	uC-gsronu33b112h10b1
Method	BLASTX

NCBI GI	g3915847
BLAST score	292
E value	2.0e-26
Match length	173
% identity	38
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi|2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	194386
Contig ID	13748_3.R1039
5'-most EST	LIB3189-008-P1-K1-A1
Method	BLASTX
NCBI GI	g3915847
BLAST score	191
E value	4.0e-14
Match length	129
% identity	42
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi|2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	194387
Contig ID	13753_1.R1039
5'-most EST	uC-gsflnu33B022e12b1
Method	BLASTX
NCBI GI	g1632831
BLAST score	596
E value	1.0e-61
Match length	131
% identity	89
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	194388
Contig ID	13754_1.R1039
5'-most EST	LIB3135-042-Q1-K1-F5
Method	BLASTX
NCBI GI	g100351
BLAST score	499
E value	2.0e-50
Match length	140
% identity	67
NCBI Description	pathogenesis-related protein 4A - common tobacco >gi|19962|emb|CAA41437| (X58546) pathogenesis-related protein 4A [Nicotiana tabacum]

Seq. No.	194389
Contig ID	13755_1.R1039
5'-most EST	LIB3135-003-Q1-K1-G2
Method	BLASTX
NCBI GI	g3779024
BLAST score	693
E value	4.0e-73
Match length	160
% identity	86
NCBI Description	(AC005171) unknown protein [Arabidopsis thaliana]

Seq. No.	194390
Contig ID	13764_2.R1039

5'-most EST	LIB3148-004-Q1-K1-F6
Seq. No.	194391
Contig ID	13765_1.R1039
5'-most EST	LIB3135-003-Q1-K1-H12
Method	BLASTX
NCBI GI	g3319774
BLAST score	201
E value	2.0e-15
Match length	44
% identity	84
NCBI Description	(Y16228) TOM7 protein [Solanum tuberosum]
Seq. No.	194392
Contig ID	13766_1.R1039
5'-most EST	LIB3272-017-P1-K1-F10
Method	BLASTX
NCBI GI	g4150974
BLAST score	369
E value	4.0e-35
Match length	95
% identity	69
NCBI Description	(AJ224331) cystatin [Castanea sativa]
Seq. No.	194393
Contig ID	13769_1.R1039
5'-most EST	LIB3135-025-Q1-K1-H12
Seq. No.	194394
Contig ID	13769_3.R1039
5'-most EST	uC-gsflmaxxa028e01b1
Seq. No.	194395
Contig ID	13774_1.R1039
5'-most EST	LIB3197-028-Q1-M1-D5
Method	BLASTX
NCBI GI	g1888485
BLAST score	1452
E value	1.0e-161
Match length	329
% identity	82
NCBI Description	(Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
Seq. No.	194396
Contig ID	13774_2.R1039
5'-most EST	uC-gsflnu33B057a03b1
Method	BLASTN
NCBI GI	g530848
BLAST score	367
E value	0.0e+00
Match length	371
% identity	100
NCBI Description	Gossypium davidsonii 5.8S rRNA gene and internal transcribed spacer 1 and
Seq. No.	194397
Contig ID	13774_3.R1039

5'-most EST	LIB3272-016-P1-K1-H4
Method	BLASTX
NCBI GI	g4033467
BLAST score	532
E value	2.0e-75
Match length	265
% identity	64
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi|1707366|emb|CAA67798| (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	194398
Contig ID	13774_6.R1039
5'-most EST	LIB3148-038-Q1-K1-F5
Method	BLASTX
NCBI GI	g3785991
BLAST score	432
E value	3.0e-42
Match length	192
% identity	56
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	194399
Contig ID	13776_1.R1039
5'-most EST	uC-gsflnu33B071c08b1

Seq. No.	194400
Contig ID	13779_1.R1039
5'-most EST	LIB3135-052-Q1-K1-C2
Method	BLASTX
NCBI GI	g1706547
BLAST score	337
E value	1.0e-31
Match length	99
% identity	67
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi|2129912|pir||S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi|1184668 (U22147) beta-1,3-glucanase [Hevea brasiliensis]

Seq. No.	194401
Contig ID	13786_1.R1039
5'-most EST	LIB3135-004-Q1-K1-B12

Seq. No.	194402
Contig ID	13787_3.R1039
5'-most EST	LIB3196-007-P1-M1-A1

Seq. No.	194403
Contig ID	13789_1.R1039
5'-most EST	LIB3135-004-Q1-K1-B4
Method	BLASTX
NCBI GI	g3928543
BLAST score	164
E value	2.0e-11

Match length	124
% identity	38
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	194404
Contig ID	13792_1.R1039
5'-most EST	g5049922
Method	BLASTX
NCBI GI	g3928086
BLAST score	549
E value	4.0e-56
Match length	178
% identity	63
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	194405
Contig ID	13801_1.R1039
5'-most EST	LIB3135-004-Q1-K1-C7
Method	BLASTX
NCBI GI	g4559382
BLAST score	224
E value	3.0e-18
Match length	92
% identity	43
NCBI Description	(AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	194406
Contig ID	13807_1.R1039
5'-most EST	LIB3135-025-Q1-K1-H2
Method	BLASTX
NCBI GI	g3183088
BLAST score	209
E value	2.0e-16
Match length	71
% identity	56
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi|629658|pir||S47084 lipid transfer like protein - cowpea >gi|499034|emb|CAA56113| (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	194407
Contig ID	13810_1.R1039
5'-most EST	LIB3166-058-P1-K1-B5

Seq. No.	194408
Contig ID	13813_1.R1039
5'-most EST	LIB3165-005-P1-K1-D2

Seq. No.	194409
Contig ID	13816_1.R1039
5'-most EST	g5049824
Method	BLASTX
NCBI GI	g2997684
BLAST score	325
E value	8.0e-30

Match length	108
% identity	62
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

Seq. No.	194410
Contig ID	13819_1.R1039
5'-most EST	LIB3135-004-Q1-K1-E6
Method	BLASTX
NCBI GI	g4376650
BLAST score	282
E value	1.0e-24
Match length	166
% identity	39
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	194411
Contig ID	13821_1.R1039
5'-most EST	LIB3272-058-P1-K1-D9

Seq. No.	194412
Contig ID	13823_1.R1039
5'-most EST	LIB3135-004-Q1-K1-F1
Method	BLASTX
NCBI GI	g4539660
BLAST score	408
E value	7.0e-41
Match length	158
% identity	57
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	194413
Contig ID	13835_1.R1039
5'-most EST	LIB3135-052-Q1-K1-A12
Method	BLASTX
NCBI GI	g2497752
BLAST score	294
E value	4.0e-26
Match length	96
% identity	59
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi|1321911|emb|CAA65475| (X96714) lipid transfer protein [Prunus dulcis]

Seq. No.	194414
Contig ID	13835_2.R1039
5'-most EST	LIB3147-054-Q1-K1-F12
Method	BLASTX
NCBI GI	g2497752
BLAST score	211
E value	1.0e-16
Match length	67
% identity	60
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi|1321911|emb|CAA65475| (X96714) lipid transfer protein [Prunus dulcis]

Seq. No.	194415
Contig ID	13842_1.R1039
5'-most EST	LIB3135-004-Q1-K1-H12

Seq. No.	194416
Contig ID	13847_1.R1039
5'-most EST	LIB3135-004-Q1-K1-H6
Method	BLASTX
NCBI GI	g2809326
BLAST score	487
E value	4.0e-49
Match length	127
% identity	75
NCBI Description	(U72663) uricase II [Phaseolus vulgaris]

Seq. No.	194417
Contig ID	13859_1.R1039
5'-most EST	LIB3165-004-P1-K1-E3

Seq. No.	194418
Contig ID	13859_2.R1039
5'-most EST	LIB3272-016-P1-K1-G8

Seq. No.	194419
Contig ID	13863_1.R1039
5'-most EST	LIB3135-005-Q1-K1-B3
Method	BLASTX
NCBI GI	g4512698
BLAST score	154
E value	2.0e-12
Match length	93
% identity	47
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194420
Contig ID	13865_1.R1039
5'-most EST	LIB3135-005-Q1-K1-B6
Method	BLASTX
NCBI GI	g3738320
BLAST score	676
E value	5.0e-71
Match length	188
% identity	70
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	194421
Contig ID	13867_1.R1039
5'-most EST	LIB3272-020-P1-K1-H8
Method	BLASTX
NCBI GI	g3913182
BLAST score	312
E value	1.0e-28
Match length	114
% identity	48
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi|2239258|emb|CAA74070| (Y13733) cinnamyl alcohol

dehydrogenase [Zea mays]

Seq. No.	194422
Contig ID	13868_1.R1039
5'-most EST	LIB3145-030-Q1-K1-F12

Seq. No.	194423
Contig ID	13871_1.R1039
5'-most EST	LIB3135-060-Q1-K1-B11

Seq. No.	194424
Contig ID	13874_1.R1039
5'-most EST	uC-gsflnu33B031a05b1
Method	BLASTX
NCBI GI	g3421102
BLAST score	767
E value	1.0e-81
Match length	216
% identity	68
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	194425
Contig ID	13874_2.R1039
5'-most EST	uC-gsflmaxxa057d07b1
Method	BLASTX
NCBI GI	g2511578
BLAST score	716
E value	9.0e-76
Match length	159
% identity	85
NCBI Description	(Y13178) multicatalytic endopeptidase [Arabidopsis thaliana]

Seq. No.	194426
Contig ID	13879_1.R1039
5'-most EST	LIB3189-012-P1-K1-D9
Method	BLASTX
NCBI GI	g462013
BLAST score	523
E value	3.0e-53
Match length	151
% identity	72
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi|542022|pir||S39558 HSP90 homolog - Madagascar periwinkle >gi|348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	194427
Contig ID	13882_1.R1039
5'-most EST	LIB3166-027-P1-K1-D11
Method	BLASTX
NCBI GI	g2827528
BLAST score	792
E value	1.0e-84
Match length	217
% identity	72

NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.	194428
Contig ID	13889_1.R1039
5'-most EST	uC-gsronu33B046f10b1
Method	BLASTX
NCBI GI	g417148
BLAST score	554
E value	1.0e-56
Match length	217
% identity	51
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi|99912|pir||A33654 heat shock protein 26A - soybean >gi|169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.	194429
Contig ID	13890_2.R1039
5'-most EST	LIB3147-006-Q1-K1-A9
Method	BLASTX
NCBI GI	g3242704
BLAST score	399
E value	1.0e-38
Match length	142
% identity	52
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194430
Contig ID	13894_1.R1039
5'-most EST	uC-gsronu33B147f08b1
Method	BLASTX
NCBI GI	g3850571
BLAST score	439
E value	2.0e-43
Match length	94
% identity	89
NCBI Description	(AC005278) Similar to gb|U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb|AA612141 comes from this gene. [Arabidopsis thaliana]
Seq. No.	194431
Contig ID	13895_1.R1039
5'-most EST	LIB3135-005-Q1-K1-E5
Seq. No.	194432
Contig ID	13898_1.R1039
5'-most EST	LIB3147-038-Q1-K2-G7
Seq. No.	194433
Contig ID	13899_1.R1039
5'-most EST	g5049141
Method	BLASTX
NCBI GI	g3540194
BLAST score	330
E value	2.0e-30
Match length	77
% identity	82
NCBI Description	(AC004260) AtVPS45p [Arabidopsis thaliana]

Seq. No.	194434
Contig ID	13911_1.R1039
5'-most EST	LIB3166-018-P1-K1-E4

Seq. No.	194435
Contig ID	13914_1.R1039
5'-most EST	LIB3135-005-Q1-K1-G8
Method	BLASTX
NCBI GI	g2267567
BLAST score	394
E value	4.0e-38
Match length	86
% identity	90
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi|2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	194436
Contig ID	13915_1.R1039
5'-most EST	uC-gsronu33B132c12b1
Method	BLASTN
NCBI GI	g2267566
BLAST score	57
E value	4.0e-23
Match length	289
% identity	82
NCBI Description	Pelargonium x hortorum glycine-rich RNA binding protein 1 (GRP1) mRNA, complete cds

Seq. No.	194437
Contig ID	13919_1.R1039
5'-most EST	LIB3135-005-Q1-K1-G9
Method	BLASTX
NCBI GI	g2132388
BLAST score	164
E value	3.0e-11
Match length	112
% identity	37
NCBI Description	PHO85 protein - yeast (Saccharomyces cerevisiae) >gi|1163103 (U43503) Lph16p [Saccharomyces cerevisiae]

Seq. No.	194438
Contig ID	13928_1.R1039
5'-most EST	LIB3149-036-Q1-K1-E9
Method	BLASTX
NCBI GI	g2760334
BLAST score	416
E value	1.0e-40
Match length	91
% identity	80
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No.	194439
Contig ID	13935_1.R1039
5'-most EST	LIB3146-011-Q1-K1-G10
Method	BLASTX

NCBI GI	g2764941
BLAST score	415
E value	2.0e-40
Match length	101
% identity	70
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	194440
Contig ID	13942_1.R1039
5'-most EST	LIB3135-046-Q1-K1-H4

Seq. No.	194441
Contig ID	13942_2.R1039
5'-most EST	LIB3146-054-Q1-K1-F10

Seq. No.	194442
Contig ID	13945_1.R1039
5'-most EST	LIB3135-045-Q1-K1-D2
Method	BLASTX
NCBI GI	g122770
BLAST score	693
E value	5.0e-73
Match length	160
% identity	84
NCBI Description	HEMOGLOBIN II >gi|99509|pir||S13378 hemoglobin II - swamp oak >gi|18015|emb|CAA37898| (X53950) hemoglobin [Casuarina glauca]

Seq. No.	194443
Contig ID	13957_1.R1039
5'-most EST	LIB3135-031-Q1-K1-D4

Seq. No.	194444
Contig ID	13957_2.R1039
5'-most EST	uC-gsronu33B150d07b1

Seq. No.	194445
Contig ID	13959_1.R1039
5'-most EST	g5047411
Method	BLASTX
NCBI GI	g499693
BLAST score	725
E value	1.0e-76
Match length	255
% identity	59
NCBI Description	(L32095) cyclophilin [Vicia faba]

Seq. No.	194446
Contig ID	13966_1.R1039
5'-most EST	LIB3135-018-Q1-K1-D10
Method	BLASTN
NCBI GI	g434990
BLAST score	45
E value	4.0e-16
Match length	120

% identity	93
NCBI Description	O.berteriana mitochondrial trnI gene

Seq. No.	194447
Contig ID	13970_1.R1039
5'-most EST	LIB3135-034-Q1-K1-E7

Seq. No.	194448
Contig ID	13973_1.R1039
5'-most EST	LIB3272-003-P1-K1-H3
Method	BLASTX
NCBI GI	g2459417
BLAST score	963
E value	1.0e-104
Match length	292
% identity	66
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	194449
Contig ID	13975_1.R1039
5'-most EST	LIB3135-007-Q1-K1-A5

Seq. No.	194450
Contig ID	13978_1.R1039
5'-most EST	LIB3148-046-Q1-K1-F11
Method	BLASTX
NCBI GI	g131015
BLAST score	801
E value	2.0e-85
Match length	198
% identity	71
NCBI Description	PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR (THAUMATIN-LIKE PROTEIN E22) >gi|100385|pir||JH0230 pathogenesis-related protein R precursor - common tobacco >gi|19855|emb|CAA33293| (X15224) thaumatin-like protein [Nicotiana tabacum] >gi|19980|emb|CAA31235| (X12739) pathogenesis-related protein R (AA 1 - 226) [Nicotiana tabacum]

Seq. No.	194451
Contig ID	13982_1.R1039
5'-most EST	uC-gsronu33B019f01b1

Seq. No.	194452
Contig ID	13988_1.R1039
5'-most EST	LIB3166-013-P1-K1-C6
Method	BLASTX
NCBI GI	g3122388
BLAST score	619
E value	2.0e-64
Match length	131
% identity	31
NCBI Description	WD-40 REPEAT PROTEIN MSI2 >gi|2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	194453

Contig ID 13994_1.R1039
5'-most EST LIB3135-007-Q1-K1-C5

Seq. No. 194454
Contig ID 13998_1.R1039
5'-most EST LIB3196-017-P1-M1-E8

Seq. No. 194455
Contig ID 14012_1.R1039
5'-most EST LIB3135-007-Q1-K1-E11
Method BLASTX
NCBI GI g2829923
BLAST score 438
E value 1.0e-43
Match length 117
% identity 42
NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No. 194456
Contig ID 14017_1.R1039
5'-most EST LIB3166-051-P1-K1-E4

Seq. No. 194457
Contig ID 14019_1.R1039
5'-most EST LIB3166-020-P1-K1-G1
Method BLASTX
NCBI GI g3600061
BLAST score 410
E value 5.0e-44
Match length 220
% identity 50
NCBI Description (AF080120) contains similarity to DNA binding proteins [Arabidopsis thaliana]

Seq. No. 194458
Contig ID 14034_1.R1039
5'-most EST uC-gsronu33B124f09b1

Seq. No. 194459
Contig ID 14037_1.R1039
5'-most EST LIB3135-007-Q1-K1-H12
Method BLASTX
NCBI GI g1001755
BLAST score 148
E value 2.0e-09
Match length 79
% identity 11
NCBI Description (D64004) hypothetical protein [Synechocystis sp.]

Seq. No. 194460
Contig ID 14041_1.R1039
5'-most EST LIB3135-058-Q1-K1-A5

Seq. No. 194461
Contig ID 14051_1.R1039
5'-most EST LIB3166-027-P1-K1-G6

Method	BLASTX
NCBI GI	g2493318
BLAST score	273
E value	8.0e-24
Match length	100
% identity	51
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi|562779|emb|CAA80963| (Z25471) blue copper protein [Pisum sativum] >gi|1098264|prf||2115352A blue Cu protein [Pisum sativum]

Seq. No.	194462
Contig ID	14051_2.R1039
5'-most EST	uC-gsflmaxxa042g11b1
Method	BLASTX
NCBI GI	g728949
BLAST score	236
E value	2.0e-19
Match length	103
% identity	46
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi|99665|pir||S25555 blue copper protein - Arabidopsis thaliana >gi|2147156|pir||I39698 blue copper-binding protein - Arabidopsis thaliana >gi|16203|emb|CAA78771| (Z15058) blue copper-binding protein [unidentified bacterium] >gi|739987|prf||2004275A blue copper-binding protein [Arabidopsis thaliana]

Seq. No.	194463
Contig ID	14053_1.R1039
5'-most EST	LIB3189-012-P1-K1-H2
Method	BLASTX
NCBI GI	g3080402
BLAST score	1265
E value	1.0e-140
Match length	323
% identity	76
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi|4455266|emb|CAB36802.1| (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	194464
Contig ID	14055_1.R1039
5'-most EST	LIB3148-039-Q1-K1-G5
Method	BLASTX
NCBI GI	g4325342
BLAST score	152
E value	1.0e-09
Match length	33
% identity	88
NCBI Description	(AF128393) No definition line found [Arabidopsis thaliana]

Seq. No.	194465
Contig ID	14058_1.R1039
5'-most EST	LIB3135-008-Q1-K1-B4
Method	BLASTX
NCBI GI	g1103318

BLAST score 219
E value 2.0e-17
Match length 145
% identity 39
NCBI Description (X78818) casein kinase I [Arabidopsis thaliana] >gi|2244791|emb|CAB10213.1| (Z97336) casein kinase I [Arabidopsis thaliana]

Seq. No. 194466
Contig ID 14059_1.R1039
5'-most EST LIB3135-008-Q1-K1-B6

Seq. No. 194467
Contig ID 14061_1.R1039
5'-most EST LIB3165-051-Q1-K1-A4
Method BLASTX
NCBI GI g4455246
BLAST score 233
E value 3.0e-19
Match length 94
% identity 50
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 194468
Contig ID 14071_1.R1039
5'-most EST LIB3135-008-Q1-K1-D1
Method BLASTX
NCBI GI g2832677
BLAST score 192
E value 1.0e-14
Match length 87
% identity 45
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 194469
Contig ID 14073_1.R1039
5'-most EST LIB3166-013-P1-K1-E5
Method BLASTX
NCBI GI g3193292
BLAST score 881
E value 5.0e-95
Match length 218
% identity 80
NCBI Description (AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No. 194470
Contig ID 14079_1.R1039
5'-most EST LIB3146-041-Q1-K1-G6

Seq. No. 194471
Contig ID 14084_1.R1039
5'-most EST LIB3135-008-Q1-K1-E2
Method BLASTX
NCBI GI g4106538
BLAST score 515

E value	2.0e-52
Match length	141
% identity	72
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	194472
Contig ID	14093_1.R1039
5'-most EST	uC-gsflnu33B126e02b1
Method	BLASTX
NCBI GI	g1703108
BLAST score	1034
E value	1.0e-113
Match length	208
% identity	97
NCBI Description	ACTIN 2/7 >gi|2129525|pir||S71210 actin 2 - Arabidopsis thaliana >gi|2129528|pir||S68107 actin 7 - Arabidopsis thaliana >gi|1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi|1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	194473
Contig ID	14098_1.R1039
5'-most EST	LIB3146-053-Q1-K1-E4

Seq. No.	194474
Contig ID	14098_2.R1039
5'-most EST	LIB3145-008-Q1-K1-A3

Seq. No.	194475
Contig ID	14098_3.R1039
5'-most EST	LIB3146-015-Q1-K1-C4
Method	BLASTN
NCBI GI	g2687434
BLAST score	49
E value	2.0e-18
Match length	89
% identity	89
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	194476
Contig ID	14100_1.R1039
5'-most EST	LIB3189-016-P1-K1-H4
Method	BLASTX
NCBI GI	g2673868
BLAST score	584
E value	3.0e-60
Match length	152
% identity	78
NCBI Description	(Y14856) fimbriata-associated protein [Antirrhinum majus]

Seq. No.	194477
Contig ID	14106_1.R1039
5'-most EST	LIB3135-008-Q1-K1-G4
Method	BLASTX
NCBI GI	g2345148

BLAST score	144
E value	6.0e-09
Match length	56
% identity	52
NCBI Description	(AF014821) developmentally regulated GTP binding protein [Pisum sativum]

Seq. No.	194478
Contig ID	14129_1.R1039
5'-most EST	uC-gsflnu33B001h05b1
Method	BLASTX
NCBI GI	g1323704
BLAST score	240
E value	7.0e-20
Match length	185
% identity	38
NCBI Description	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]

Seq. No.	194479
Contig ID	14129_2.R1039
5'-most EST	LIB3146-039-Q1-K1-A5

Seq. No.	194480
Contig ID	14129_3.R1039
5'-most EST	LIB3146-018-Q1-K1-F5

Seq. No.	194481
Contig ID	14132_1.R1039
5'-most EST	uC-gsflnu33B081a07b1
Method	BLASTX
NCBI GI	g3881724
BLAST score	284
E value	4.0e-25
Match length	90
% identity	57
NCBI Description	(Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No. S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST yk290e3.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	194482
Contig ID	14153_1.R1039
5'-most EST	g3326772
Method	BLASTX
NCBI GI	g136644
BLAST score	395
E value	2.0e-48
Match length	158
% identity	72
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|100765|pir||A34506 23K ubiquitin carrier protein E2 - wheat >gi|170782 (M28059) ubiquitin carrier protein [Triticum vulgare]

Seq. No.	194483
Contig ID	14153_2.R1039
5'-most EST	LIB3147-036-Q1-K1-A5

Method	BLASTX
NCBI GI	g1174850
BLAST score	296
E value	3.0e-45
Match length	150
% identity	67
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No.	194484
Contig ID	14160_1.R1039
5'-most EST	LIB3145-046-Q1-K1-B4

Seq. No.	194485
Contig ID	14163_1.R1039
5'-most EST	uC-gsflnu33B091f05b1
Method	BLASTX
NCBI GI	g2370595
BLAST score	497
E value	7.0e-50
Match length	231
% identity	46
NCBI Description	(AJ001414) GTPase activating protein [Yarrowia lipolytica]

Seq. No.	194486
Contig ID	14165_1.R1039
5'-most EST	uC-gsflmaxxa045d08b1
Method	BLASTX
NCBI GI	g3158476
BLAST score	1136
E value	1.0e-125
Match length	253
% identity	87
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	194487
Contig ID	14166_1.R1039
5'-most EST	LIB3135-009-Q1-K1-F9

Seq. No.	194488
Contig ID	14168_1.R1039
5'-most EST	LIB3135-027-Q1-K1-D9
Method	BLASTX
NCBI GI	g3928099
BLAST score	768
E value	1.0e-81
Match length	280
% identity	36
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	194489
Contig ID	14169_1.R1039
5'-most EST	LIB3272-016-P1-K1-H6
Method	BLASTX
NCBI GI	g2792297
BLAST score	261
E value	2.0e-22

Match length 77
% identity 58
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 194490
Contig ID 14171_1.R1039
5'-most EST LIB3189-030-P1-K1-G4
Method BLASTX
NCBI GI g1220453
BLAST score 476
E value 2.0e-47
Match length 168
% identity 54
NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. No. 194491
Contig ID 14172_1.R1039
5'-most EST LIB3147-028-Q1-K1-E6
Method BLASTX
NCBI GI g2465923
BLAST score 604
E value 1.0e-62
Match length 181
% identity 66
NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 194492
Contig ID 14188_1.R1039
5'-most EST LIB3135-051-Q1-K1-A7

Seq. No. 194493
Contig ID 14190_1.R1039
5'-most EST LIB3165-033-P1-K1-E3

Seq. No. 194494
Contig ID 14196_1.R1039
5'-most EST LIB3135-010-Q1-K1-A3
Method BLASTX
NCBI GI g3928079
BLAST score 284
E value 2.0e-25
Match length 144
% identity 45
NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No. 194495
Contig ID 14204_1.R1039
5'-most EST LIB3135-010-Q1-K1-B2

Seq. No. 194496
Contig ID 14205_2.R1039
5'-most EST LIB3146-017-Q1-K1-C5

Seq. No. 194497
Contig ID 14205_3.R1039
5'-most EST uC-gsflnu33B129e07b1

Method	BLASTX
NCBI GI	g3298546
BLAST score	247
E value	1.0e-20
Match length	92
% identity	57
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	194498
Contig ID	14205_4.R1039
5'-most EST	LIB3149-028-Q1-K1-H5

Seq. No.	194499
Contig ID	14209_1.R1039
5'-most EST	LIB3135-010-Q1-K1-B8

Seq. No.	194500
Contig ID	14216_1.R1039
5'-most EST	uC-gsronu33B171a04b1

Seq. No.	194501
Contig ID	14217_1.R1039
5'-most EST	LIB3135-010-Q1-K1-D11

Seq. No.	194502
Contig ID	14220_1.R1039
5'-most EST	g5050250
Method	BLASTX
NCBI GI	g4512698
BLAST score	2162
E value	0.0e+00
Match length	460
% identity	86
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194503
Contig ID	14227_1.R1039
5'-most EST	LIB3149-063-Q1-K1-F8

Seq. No.	194504
Contig ID	14241_1.R1039
5'-most EST	LIB3135-010-Q1-K1-G2

Seq. No.	194505
Contig ID	14268_1.R1039
5'-most EST	uC-gsronu33B150e08b1

Seq. No.	194506
Contig ID	14276_1.R1039
5'-most EST	LIB3135-011-Q1-K1-B7
Method	BLASTN
NCBI GI	g2760172
BLAST score	37
E value	3.0e-11
Match length	73
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	194507
Contig ID	14282_1.R1039
5'-most EST	uC-gsflnu33B083h11b1
Method	BLASTX
NCBI GI	g2979549
BLAST score	398
E value	1.0e-38
Match length	138
% identity	54
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	194508
Contig ID	14285_1.R1039
5'-most EST	LIB3135-011-Q1-K1-C5
Method	BLASTX
NCBI GI	g4314355
BLAST score	188
E value	4.0e-14
Match length	125
% identity	38
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	194509
Contig ID	14288_1.R1039
5'-most EST	uC-gsflnu33B128e09b1
Method	BLASTX
NCBI GI	g2462761
BLAST score	229
E value	9.0e-19
Match length	96
% identity	52
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	194510
Contig ID	14290_1.R1039
5'-most EST	LIB3145-011-Q1-K1-G10
Method	BLASTX
NCBI GI	g4557078
BLAST score	162
E value	1.0e-10
Match length	283
% identity	23
NCBI Description	(AC007045) putative Ta11-1 pol polyprotein, 5' partial [Arabidopsis thaliana]

Seq. No.	194511
Contig ID	14297_1.R1039
5'-most EST	LIB3197-045-Q1-M1-B11
Method	BLASTX
NCBI GI	g4406816
BLAST score	879
E value	6.0e-95
Match length	185

% identity	89
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	194512
Contig ID	14304_1.R1039
5'-most EST	LIB3135-021-Q1-K1-D11
Method	BLASTX
NCBI GI	g3128195
BLAST score	515
E value	1.0e-52
Match length	111
% identity	93
NCBI Description	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No.	194513
Contig ID	14305_1.R1039
5'-most EST	uC-gsronu33B036b09b1
Method	BLASTX
NCBI GI	g2959370
BLAST score	269
E value	2.0e-23
Match length	129
% identity	36
NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	194514
Contig ID	14311_1.R1039
5'-most EST	g3326718
Method	BLASTX
NCBI GI	g1877480
BLAST score	441
E value	2.0e-43
Match length	161
% identity	60
NCBI Description	(U89270) short-chain alcohol dehydrogenase [Tripsacum dactyloides]

Seq. No.	194515
Contig ID	14316_1.R1039
5'-most EST	LIB3165-003-P1-K1-A3
Method	BLASTX
NCBI GI	g1168728
BLAST score	1360
E value	1.0e-151
Match length	358
% identity	71
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi|598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	194516
Contig ID	14316_3.R1039
5'-most EST	LIB3146-037-P1-K1-D5
Method	BLASTX
NCBI GI	g1168728

BLAST score 239
E value 4.0e-20
Match length 76
% identity 84
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi|598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 194517
Contig ID 14324_1.R1039
5'-most EST LIB3145-012-Q1-K1-A10
Method BLASTX
NCBI GI g3915037
BLAST score 1010
E value 1.0e-110
Match length 215
% identity 86
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi|2570067|emb|CAA04512| (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No. 194518
Contig ID 14326_1.R1039
5'-most EST LIB3135-011-Q1-K1-H6

Seq. No. 194519
Contig ID 14327_1.R1039
5'-most EST uC-gsronu33B154h08b2
Method BLASTX
NCBI GI g3169182
BLAST score 360
E value 4.0e-34
Match length 78
% identity 85
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 194520
Contig ID 14327_2.R1039
5'-most EST LIB3135-011-Q1-K1-H7
Method BLASTX
NCBI GI g3860323
BLAST score 372
E value 2.0e-35
Match length 78
% identity 87
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 194521
Contig ID 14327_5.R1039
5'-most EST LIB3146-010-Q1-K1-A3
Method BLASTX
NCBI GI g3169182
BLAST score 167
E value 1.0e-11
Match length 35
% identity 83
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	194522
Contig ID	14330_1.R1039
5'-most EST	LIB3189-018-P1-K1-B11
Method	BLASTX
NCBI GI	g4559384
BLAST score	842
E value	2.0e-90
Match length	222
% identity	74
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	194523
Contig ID	14337_1.R1039
5'-most EST	LIB3135-012-Q1-K1-B11
Method	BLASTX
NCBI GI	g3599491
BLAST score	1078
E value	1.0e-118
Match length	256
% identity	76
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	194524
Contig ID	14341_1.R1039
5'-most EST	LIB3272-033-P1-K1-E10
Method	BLASTX
NCBI GI	g2664210
BLAST score	724
E value	4.0e-90
Match length	301
% identity	61
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	194525
Contig ID	14347_1.R1039
5'-most EST	LIB3146-050-Q1-K1-F3

Seq. No.	194526
Contig ID	14349_1.R1039
5'-most EST	LIB3272-012-P1-K1-D7
Method	BLASTX
NCBI GI	g1483218
BLAST score	572
E value	6.0e-59
Match length	137
% identity	75
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	194527
Contig ID	14349_3.R1039
5'-most EST	LIB3272-053-P1-K1-H1
Method	BLASTX
NCBI GI	g1483218
BLAST score	271
E value	6.0e-24

Match length	63
% identity	79
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	194528
Contig ID	14355_1.R1039
5'-most EST	LIB3145-054-Q1-K1-E9

Seq. No.	194529
Contig ID	14357_1.R1039
5'-most EST	LIB3135-012-Q1-K1-D7

Seq. No.	194530
Contig ID	14362_1.R1039
5'-most EST	LIB3149-061-Q1-K1-A5
Method	BLASTX
NCBI GI	g462011
BLAST score	560
E value	2.0e-57
Match length	143
% identity	75
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi|349802 (L23324) enolase [Schistosoma japonicum]

Seq. No.	194531
Contig ID	14362_2.R1039
5'-most EST	LIB3149-023-Q1-K1-E3
Method	BLASTX
NCBI GI	g3717946
BLAST score	345
E value	3.0e-32
Match length	110
% identity	65
NCBI Description	(AJ005901) vag1 [Arabidopsis thaliana]

Seq. No.	194532
Contig ID	14364_1.R1039
5'-most EST	LIB3135-012-Q1-K1-F10
Method	BLASTX
NCBI GI	g2565275
BLAST score	184
E value	2.0e-13
Match length	52
% identity	79
NCBI Description	(AF023611) Dim1p homolog [Homo sapiens]

Seq. No.	194533
Contig ID	14367_1.R1039
5'-most EST	LIB3149-007-Q1-K1-C11
Method	BLASTX
NCBI GI	g1808656
BLAST score	518
E value	1.0e-52
Match length	115
% identity	85

NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	194534
Contig ID	14369_1.R1039
5'-most EST	LIB3135-012-Q1-K1-F4
Method	BLASTX
NCBI GI	g3395436
BLAST score	302
E value	1.0e-27
Match length	112
% identity	49
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	194535
Contig ID	14370_1.R1039
5'-most EST	LIB3146-008-Q1-K1-B3

Seq. No.	194536
Contig ID	14371_1.R1039
5'-most EST	uC-gsflmaxxa004b01b1

Seq. No.	194537
Contig ID	14375_1.R1039
5'-most EST	uC-gsronu33B148c09b1
Method	BLASTX
NCBI GI	g3219823
BLAST score	405
E value	2.0e-39
Match length	149
% identity	52
NCBI Description	PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) >gi|2127740|pir||C64362 aconitate hydratase (EC 4.2.1.3) - Methanococcus jannaschii >gi|1591201 (U67499) 3-isopropylmalate dehydratase (leuC) [Methanococcus jannaschii]

Seq. No.	194538
Contig ID	14378_1.R1039
5'-most EST	uC-gsronu33B113a01b1
Method	BLASTX
NCBI GI	g4185819
BLAST score	192
E value	3.0e-14
Match length	47
% identity	68
NCBI Description	(AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No.	194539
Contig ID	14378_2.R1039
5'-most EST	uC-gsflnu33B138f10b1
Method	BLASTN
NCBI GI	g1418705
BLAST score	217
E value	1.0e-118
Match length	481

% identity	93
NCBI Description	G.hirsutum metallothionein-like gene

Seq. No.	194540
Contig ID	14380_1.R1039
5'-most EST	LIB3272-002-P1-K1-D12
Method	BLASTX
NCBI GI	g585165
BLAST score	2144
E value	0.0e+00
Match length	461
% identity	88
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi|2129985|pir||S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi|471345|emb|CAA52442| (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No.	194541
Contig ID	14385_1.R1039
5'-most EST	LIB3135-050-Q1-K1-F10
Method	BLASTX
NCBI GI	g1710076
BLAST score	273
E value	4.0e-24
Match length	71
% identity	75
NCBI Description	REHYDRIN HOMOLOG (DORMANCY-ASSOCIATED PROTEIN PBS128) >gi|82340|pir||S22499 hypothetical protein - chess bromegrass (fragment) >gi|17932|emb|CAA44884| (X63202) ORF [Bromus secalinus]

Seq. No.	194542
Contig ID	14401_1.R1039
5'-most EST	LIB3166-038-P1-K1-G7
Method	BLASTX
NCBI GI	g4567251
BLAST score	600
E value	5.0e-62
Match length	145
% identity	77
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	194543
Contig ID	14410_1.R1039
5'-most EST	LIB3189-048-P1-K1-G11
Method	BLASTX
NCBI GI	g1917019
BLAST score	977
E value	1.0e-106
Match length	248
% identity	78
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	194544
Contig ID	14416_1.R1039
5'-most EST	LIB3135-013-Q1-K1-C5

Method	BLASTX
NCBI GI	g1361019
BLAST score	247
E value	4.0e-21
Match length	125
% identity	43
NCBI Description	probable tagatose 1,6-bisphosphate aldolase gatY - Escherichia coli (strain EC3132) >gi|599738|emb|CAA56226| (X79837) unknown function [Escherichia coli] >gi|1096946|prf||2113201A carbohydrate phosphotransferase II [Escherichia coli]

Seq. No.	194545
Contig ID	14417_1.R1039
5'-most EST	g3326233
Method	BLASTX
NCBI GI	g4490292
BLAST score	627
E value	3.0e-65
Match length	146
% identity	84
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	194546
Contig ID	14417_2.R1039
5'-most EST	g5045176
Method	BLASTX
NCBI GI	g4490292
BLAST score	905
E value	1.0e-97
Match length	228
% identity	78
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	194547
Contig ID	14418_1.R1039
5'-most EST	LIB3272-012-P1-K1-H11
Method	BLASTX
NCBI GI	g2463569
BLAST score	1257
E value	1.0e-139
Match length	275
% identity	86
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	194548
Contig ID	14418_2.R1039
5'-most EST	LIB3166-019-P1-K1-H7
Method	BLASTX
NCBI GI	g2463569
BLAST score	535
E value	1.0e-82
Match length	226
% identity	71
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	194549

Contig ID	14424_1.R1039
5'-most EST	LIB3135-013-Q1-K1-D4
Method	BLASTX
NCBI GI	g2464852
BLAST score	309
E value	3.0e-28
Match length	114
% identity	56
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	194550
Contig ID	14431_1.R1039
5'-most EST	LIB3148-015-Q1-K1-A4

Seq. No.	194551
Contig ID	14432_1.R1039
5'-most EST	LIB3135-032-Q1-K1-C9
Method	BLASTN
NCBI GI	g2695738
BLAST score	146
E value	4.0e-76
Match length	205
% identity	93
NCBI Description	Pisum sativum mitochondrial tRNA-Gly gene and flanking sequences

Seq. No.	194552
Contig ID	14436_1.R1039
5'-most EST	LIB3135-013-Q1-K1-F10
Method	BLASTX
NCBI GI	g4544399
BLAST score	492
E value	1.0e-49
Match length	170
% identity	55
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	194553
Contig ID	14440_1.R1039
5'-most EST	LIB3145-008-Q1-K1-B10
Method	BLASTX
NCBI GI	g927428
BLAST score	1085
E value	1.0e-119
Match length	240
% identity	83
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	194554
Contig ID	14445_1.R1039
5'-most EST	LIB3272-021-P1-K1-H8
Method	BLASTX
NCBI GI	g2827528
BLAST score	215
E value	4.0e-17
Match length	117

% identity	39
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	194555
Contig ID	14447_1.R1039
5'-most EST	LIB3135-013-Q1-K1-G2
Method	BLASTN
NCBI GI	g12614
BLAST score	352
E value	0.0e+00
Match length	571
% identity	91
NCBI Description	L.esculentum genes for tRNA Asn and tRNA Tyr

Seq. No.	194556
Contig ID	14450_1.R1039
5'-most EST	LIB3148-037-Q1-K1-E9
Method	BLASTX
NCBI GI	g3237190
BLAST score	224
E value	4.0e-18
Match length	86
% identity	51
NCBI Description	(AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No.	194557
Contig ID	14451_1.R1039
5'-most EST	LIB3147-019-Q1-K1-G9
Method	BLASTX
NCBI GI	g1351359
BLAST score	291
E value	5.0e-26
Match length	69
% identity	71
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi|1071788|pir||S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi|488712|emb|CAA55860| (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	194558
Contig ID	14451_2.R1039
5'-most EST	g5045052
Method	BLASTX
NCBI GI	g1351359
BLAST score	294
E value	2.0e-26
Match length	69
% identity	74
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi|1071788|pir||S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi|488712|emb|CAA55860| (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	194559
Contig ID	14453_1.R1039

5'-most EST	uC-gsronu33B160c08b1
Seq. No.	194560
Contig ID	14457_1.R1039
5'-most EST	LIB3135-041-Q1-K1-A2
Seq. No.	194561
Contig ID	14478_1.R1039
5'-most EST	uC-gsronu33B155d06b2
Method	BLASTX
NCBI GI	g3334244
BLAST score	724
E value	1.0e-76
Match length	174
% identity	77
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi|2113825|emb|CAA73691| (Y13239) Glyoxalase I [Brassica juncea]
Seq. No.	194562
Contig ID	14478_2.R1039
5'-most EST	LIB3135-028-Q1-K1-F1
Method	BLASTX
NCBI GI	g4127862
BLAST score	325
E value	4.0e-30
Match length	78
% identity	77
NCBI Description	(AJ010423) glyoxalase I [Glycine max]
Seq. No.	194563
Contig ID	14480_1.R1039
5'-most EST	uC-gsflmaxxa076c06b1
Method	BLASTX
NCBI GI	g1653702
BLAST score	199
E value	4.0e-15
Match length	176
% identity	41
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.	194564
Contig ID	14481_1.R1039
5'-most EST	LIB3166-047-P1-K1-D12
Method	BLASTX
NCBI GI	g4558672
BLAST score	188
E value	3.0e-14
Match length	53
% identity	68
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]
Seq. No.	194565

Contig ID	14490_1.R1039
5'-most EST	LIB3135-014-Q1-K1-C9
Method	BLASTX
NCBI GI	g1362078
BLAST score	520
E value	1.0e-52
Match length	157
% identity	59
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi|311835|emb|CAA48324| (X68254) cellulase [Tropaeolum majus]

Seq. No.	194566
Contig ID	14492_1.R1039
5'-most EST	uC-gsflnu33B056g11b1

Seq. No.	194567
Contig ID	14493_1.R1039
5'-most EST	LIB3135-023-Q1-K1-B6
Method	BLASTN
NCBI GI	g871468
BLAST score	97
E value	6.0e-47
Match length	452
% identity	89
NCBI Description	H.annuus mitochondrion genes trnH and trnE

Seq. No.	194568
Contig ID	14494_1.R1039
5'-most EST	uC-gsflnu33B080d06b1

Seq. No.	194569
Contig ID	14496_1.R1039
5'-most EST	LIB3135-014-Q1-K1-D8

Seq. No.	194570
Contig ID	14503_1.R1039
5'-most EST	uC-gsflnu33B142b05b1
Method	BLASTX
NCBI GI	g3738323
BLAST score	384
E value	3.0e-37
Match length	96
% identity	72
NCBI Description	(AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194571
Contig ID	14507_1.R1039
5'-most EST	LIB3146-047-Q1-K1-F2
Method	BLASTX
NCBI GI	g1063684
BLAST score	247
E value	4.0e-21
Match length	75
% identity	65
NCBI Description	(U39072) AtGRP2b [Arabidopsis thaliana]

Seq. No.	194572
Contig ID	14527_1.R1039
5'-most EST	LIB3166-015-P1-K1-F4
Method	BLASTX
NCBI GI	g4210332
BLAST score	922
E value	1.0e-116
Match length	405
% identity	61
NCBI Description	(AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]

Seq. No.	194573
Contig ID	14535_1.R1039
5'-most EST	LIB3146-033-Q1-K1-C5

Seq. No.	194574
Contig ID	14537_1.R1039
5'-most EST	LIB3272-030-P1-K1-D6

Seq. No.	194575
Contig ID	14538_1.R1039
5'-most EST	LIB3135-018-Q1-K1-A12

Seq. No.	194576
Contig ID	14544_1.R1039
5'-most EST	LIB3135-018-Q1-K1-A9
Method	BLASTX
NCBI GI	g1703446
BLAST score	438
E value	2.0e-43
Match length	135
% identity	67
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi|1076292|pir||S53127 asparaginase - Arabidopsis thaliana >gi|735918|emb|CAA84367| (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	194577
Contig ID	14547_1.R1039
5'-most EST	LIB3148-051-Q1-K1-G4

Seq. No.	194578
Contig ID	14548_1.R1039
5'-most EST	LIB3196-006-P1-M1-B3
Method	BLASTX
NCBI GI	g2924781
BLAST score	930
E value	1.0e-100
Match length	229
% identity	74
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	194579
Contig ID	14553_1.R1039
5'-most EST	uC-gsflmaxxa003d12b1

Method	BLASTX
NCBI GI	g4006932
BLAST score	170
E value	7.0e-12
Match length	131
% identity	39
NCBI Description	(AJ011400) NADH:ubiquinone oxidoreductase b17.2 subunit [Bos taurus]

Seq. No.	194580
Contig ID	14556_1.R1039
5'-most EST	LIB3197-026-Q1-M1-C3
Method	BLASTX
NCBI GI	g461812
BLAST score	164
E value	5.0e-14
Match length	101
% identity	46
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi|167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi|445604|prf||1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	194581
Contig ID	14557_1.R1039
5'-most EST	LIB3135-028-Q1-K1-G8
Method	BLASTX
NCBI GI	g3861189
BLAST score	272
E value	8.0e-24
Match length	115
% identity	50
NCBI Description	(AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia prowazekii]

Seq. No.	194582
Contig ID	14564_1.R1039
5'-most EST	LIB3135-018-Q1-K1-D1
Method	BLASTX
NCBI GI	g2708314
BLAST score	371
E value	2.0e-35
Match length	189
% identity	30
NCBI Description	(AF027727) protein disulfide isomerase RB60 [Chlamydomonas reinhardtii] >gi|4104541 (AF036939) protein disulfide isomerase [Chlamydomonas reinhardtii]

Seq. No.	194583
Contig ID	14570_1.R1039
5'-most EST	LIB3135-018-Q1-K1-D4
Method	BLASTX
NCBI GI	g3236253
BLAST score	705
E value	1.0e-74
Match length	155

% identity	85
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	194584
Contig ID	14575_1.R1039
5'-most EST	LIB3135-018-Q1-K1-E11
Method	BLASTX
NCBI GI	g2880051
BLAST score	148
E value	2.0e-09
Match length	44
% identity	64
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	194585
Contig ID	14576_1.R1039
5'-most EST	LIB3135-018-Q1-K1-E12

Seq. No.	194586
Contig ID	14579_2.R1039
5'-most EST	uC-gsronu33B027a04b1

Seq. No.	194587
Contig ID	14590_1.R1039
5'-most EST	g5047794
Method	BLASTX
NCBI GI	g2501494
BLAST score	173
E value	4.0e-21
Match length	147
% identity	40
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi|542015|pir||S41951 UTP-glucose glucosyltransferase - cassava >gi|453249|emb|CAA54612| (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	194588
Contig ID	14592_1.R1039
5'-most EST	LIB3135-018-Q1-K1-F8
Method	BLASTX
NCBI GI	g3128180
BLAST score	447
E value	2.0e-44
Match length	96
% identity	86
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	194589
Contig ID	14594_1.R1039
5'-most EST	g5044658
Method	BLASTX
NCBI GI	g3033396
BLAST score	304
E value	2.0e-27
Match length	99

% identity	55
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	194590
Contig ID	14596_1.R1039
5'-most EST	LIB3135-018-Q1-K1-G12
Method	BLASTX
NCBI GI	g1170949
BLAST score	562
E value	6.0e-58
Match length	149
% identity	68
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi|481207|pir||S38327 protein kinase - Arabidopsis thaliana >gi|166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	194591
Contig ID	14601_1.R1039
5'-most EST	uC-gsronu33B021g04b1

Seq. No.	194592
Contig ID	14602_1.R1039
5'-most EST	LIB3135-018-Q1-K1-G9
Method	BLASTX
NCBI GI	g4580397
BLAST score	155
E value	2.0e-12
Match length	128
% identity	37
NCBI Description	(AC007171) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	194593
Contig ID	14610_1.R1039
5'-most EST	LIB3147-052-Q1-K1-D5
Method	BLASTX
NCBI GI	g3687243
BLAST score	236
E value	9.0e-20
Match length	61
% identity	77
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	194594
Contig ID	14628_1.R1039
5'-most EST	LIB3146-008-Q1-K1-A2

Seq. No.	194595
Contig ID	14632_1.R1039
5'-most EST	LIB3189-015-P1-K1-H3
Method	BLASTX
NCBI GI	g4558665
BLAST score	625
E value	4.0e-65
Match length	213
% identity	66
NCBI Description	(AC007063) putative white protein [Arabidopsis thaliana]

Seq. No. 194596
Contig ID 14635_1.R1039
5'-most EST LIB3135-019-Q1-K1-C9

Seq. No. 194597
Contig ID 14637_1.R1039
5'-most EST LIB3135-019-Q1-K1-D10

Seq. No. 194598
Contig ID 14637_2.R1039
5'-most EST uC-gsronu33B107e12b1
Method BLASTX
NCBI GI g169080
BLAST score 555
E value 6.0e-57
Match length 155
% identity 65
NCBI Description (M18250) disease resistance response protein [Pisum sativum] >gi|226760|prf||1604467C disease response resistance gene [Pisum sativum]

Seq. No. 194599
Contig ID 14639_1.R1039
5'-most EST LIB3166-052-P1-K1-D4
Method BLASTX
NCBI GI g4165323
BLAST score 776
E value 1.0e-82
Match length 160
% identity 91
NCBI Description (AB022442) p-type H+-ATPase [Vicia faba]

Seq. No. 194600
Contig ID 14648_1.R1039
5'-most EST LIB3272-028-P1-K1-E2

Seq. No. 194601
Contig ID 14652_1.R1039
5'-most EST LIB3148-059-Q1-K1-G11
Method BLASTX
NCBI GI g1495251
BLAST score 961
E value 1.0e-104
Match length 272
% identity 69
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 194602
Contig ID 14657_1.R1039
5'-most EST LIB3135-019-Q1-K1-F7

Seq. No. 194603
Contig ID 14658_1.R1039
5'-most EST LIB3147-036-Q1-K1-E5
Method BLASTX
NCBI GI g266972

BLAST score	204
E value	6.0e-16
Match length	54
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi|631884|pir||S30298 ribosomal protein S29 - rat >gi|1362934|pir||S55919 ribosomal protein S29 - human >gi|57133|emb|CAA41778| (X59051) ribosomal protein S29 [Rattus norvegicus] >gi|550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi|1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi|1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi|1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi|1096945|prf||2113200H ribosomal protein S29 [Homo sapiens] >gi|4506717|ref|NP_001023.1|pRPS29| ribosomal protein S29

Seq. No.	194604
Contig ID	14658_3.R1039
5'-most EST	LIB3165-050-Q1-K1-F10
Method	BLASTX
NCBI GI	g266972
BLAST score	204
E value	5.0e-16
Match length	54
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi|631884|pir||S30298 ribosomal protein S29 - rat >gi|1362934|pir||S55919 ribosomal protein S29 - human >gi|57133|emb|CAA41778| (X59051) ribosomal protein S29 [Rattus norvegicus] >gi|550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi|1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi|1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi|1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi|1096945|prf||2113200H ribosomal protein S29 [Homo sapiens] >gi|4506717|ref|NP_001023.1|pRPS29| ribosomal protein S29

Seq. No.	194605
Contig ID	14669_1.R1039
5'-most EST	LIB3135-019-Q1-K1-H1
Method	BLASTX
NCBI GI	g1350930
BLAST score	730
E value	3.0e-77
Match length	150
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	194606
Contig ID	14670_1.R1039
5'-most EST	LIB3135-019-Q1-K1-H12
Method	BLASTX
NCBI GI	g3150407
BLAST score	268
E value	2.0e-23
Match length	73
% identity	75

NCBI Description	(AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194607
Contig ID	14677_1.R1039
5'-most EST	g5045993
Method	BLASTX
NCBI GI	g2982268
BLAST score	488
E value	5.0e-49
Match length	106
% identity	91
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	194608
Contig ID	14685_1.R1039
5'-most EST	LIB3196-041-P1-M1-B11
Method	BLASTX
NCBI GI	g4240116
BLAST score	1154
E value	1.0e-127
Match length	276
% identity	79
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi|4240118|dbj|BAA74838| (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	194609
Contig ID	14688_1.R1039
5'-most EST	LIB3272-029-P1-K1-G11

Seq. No.	194610
Contig ID	14694_1.R1039
5'-most EST	uC-gsronu33B044f11b1
Method	BLASTX
NCBI GI	g1363492
BLAST score	634
E value	4.0e-66
Match length	131
% identity	88
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi|576507 (L36858) outer membrane protein [Pisum sativum] >gi|633607|emb|CAA58720| (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	194611
Contig ID	14696_1.R1039
5'-most EST	LIB3166-047-P1-K1-D2
Method	BLASTX
NCBI GI	g3128228
BLAST score	648
E value	6.0e-68
Match length	134
% identity	90
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi|3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	194612
Contig ID	14699_1.R1039
5'-most EST	LIB3135-020-Q1-K1-C9
Method	BLASTX
NCBI GI	g1429226
BLAST score	229
E value	1.0e-18
Match length	46
% identity	91
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]

Seq. No.	194613
Contig ID	14706_1.R1039
5'-most EST	uC-gsronu33B157c08b1

Seq. No.	194614
Contig ID	14710_1.R1039
5'-most EST	uC-gsronu33B134d06b1
Method	BLASTN
NCBI GI	g3869075
BLAST score	66
E value	2.0e-28
Match length	273
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	194615
Contig ID	14716_1.R1039
5'-most EST	LIB3147-008-Q1-K1-D7

Seq. No.	194616
Contig ID	14730_1.R1039
5'-most EST	LIB3272-044-P1-K1-D2
Method	BLASTX
NCBI GI	g2160166
BLAST score	1302
E value	1.0e-144
Match length	436
% identity	60
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	194617
Contig ID	14731_1.R1039
5'-most EST	g3326101
Method	BLASTX
NCBI GI	g4191788
BLAST score	521
E value	9.0e-54
Match length	191
% identity	60
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	194618
Contig ID	14732_1.R1039

5'-most EST	LIB3272-041-P1-K1-G2
Method	BLASTX
NCBI GI	g3608140
BLAST score	249
E value	5.0e-21
Match length	153
% identity	39
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	194619
Contig ID	14733_1.R1039
5'-most EST	g5048022
Method	BLASTX
NCBI GI	g4539330
BLAST score	558
E value	5.0e-57
Match length	260
% identity	47
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	194620
Contig ID	14735_1.R1039
5'-most EST	LIB3189-003-P1-K1-F8
Method	BLASTX
NCBI GI	g2129581
BLAST score	1132
E value	1.0e-124
Match length	258
% identity	86
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi|471089|dbj|BAA03091| (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi|4165448|emb|CAA49558| (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	194621
Contig ID	14741_1.R1039
5'-most EST	LIB3145-011-Q1-K1-E6
Method	BLASTX
NCBI GI	g2695711
BLAST score	436
E value	7.0e-43
Match length	134
% identity	59
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	194622
Contig ID	14742_1.R1039
5'-most EST	LIB3135-021-Q1-K1-A10
Method	BLASTX
NCBI GI	g2911044
BLAST score	369
E value	4.0e-35
Match length	118
% identity	60
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	194623
Contig ID	14744_1.R1039
5'-most EST	uC-gsflmaxxa069e03b1
Method	BLASTX
NCBI GI	g2852640
BLAST score	214
E value	2.0e-16
Match length	176
% identity	39
NCBI Description	(AF007157) unknown [Homo sapiens]

Seq. No.	194624
Contig ID	14745_1.R1039
5'-most EST	LIB3135-028-Q1-K1-A5
Method	BLASTX
NCBI GI	g3036798
BLAST score	155
E value	3.0e-10
Match length	131
% identity	37
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi|3805860|emb|CAA21480| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	194625
Contig ID	14752_1.R1039
5'-most EST	g3293387

Seq. No.	194626
Contig ID	14754_1.R1039
5'-most EST	uC-gsronu33B103e10b1
Method	BLASTX
NCBI GI	g1173043
BLAST score	251
E value	2.0e-21
Match length	69
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi|479441|pir||S33899 ribosomal protein L38 - tomato (cv. Moneymaker) >gi|313027|emb|CAA49599| (X69979) ribosomal protein L38 [Lycopersicon esculentum]

Seq. No.	194627
Contig ID	14765_1.R1039
5'-most EST	LIB3147-038-Q1-K2-A6
Method	BLASTX
NCBI GI	g4027895
BLAST score	589
E value	7.0e-61
Match length	136
% identity	76
NCBI Description	(AF049352) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	194628
Contig ID	14765_2.R1039
5'-most EST	LIB3149-029-Q1-K1-A1

Method	BLASTX
NCBI GI	g1040877
BLAST score	701
E value	5.0e-74
Match length	156
% identity	80
NCBI Description	(U30460) expansin S2 precursor [Cucumis sativus]

Seq. No.	194629
Contig ID	14767_1.R1039
5'-most EST	g3326659
Method	BLASTX
NCBI GI	g3452263
BLAST score	495
E value	2.0e-85
Match length	203
% identity	83
NCBI Description	(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No.	194630
Contig ID	14769_1.R1039
5'-most EST	LIB3135-021-Q1-K1-C9
Method	BLASTX
NCBI GI	g3850778
BLAST score	445
E value	4.0e-44
Match length	106
% identity	79
NCBI Description	(Y18346) gluaredoxin [Lycopersicon esculentum]

Seq. No.	194631
Contig ID	14774_1.R1039
5'-most EST	LIB3272-018-P1-K1-A2

Seq. No.	194632
Contig ID	14779_1.R1039
5'-most EST	g5048249
Method	BLASTX
NCBI GI	g1620986
BLAST score	291
E value	1.0e-28
Match length	94
% identity	76
NCBI Description	(Y08858) 40S ribosomal protein S17 [Nicotiana plumbaginifolia]

Seq. No.	194633
Contig ID	14784_1.R1039
5'-most EST	uC-gsflnu33B135a05b1
Method	BLASTX
NCBI GI	g1173043
BLAST score	259
E value	2.0e-22
Match length	69
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi|479441|pir||S33899 ribosomal

protein L38 - tomato (cv. Moneymaker)
>gi|313027|emb|CAA49599| (X69979) ribosomal protein L38
[Lycopersicon esculentum]

Seq. No.	194634
Contig ID	14784_2.R1039
5'-most EST	LIB3147-043-Q1-K1-B3
Method	BLASTX
NCBI GI	g1173043
BLAST score	308
E value	5.0e-28
Match length	65
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi|479441|pir||S33899 ribosomal protein L38 - tomato (cv. Moneymaker) >gi|313027|emb|CAA49599| (X69979) ribosomal protein L38 [Lycopersicon esculentum]

Seq. No.	194635
Contig ID	14791_1.R1039
5'-most EST	LIB3146-046-Q1-K1-H10

Seq. No.	194636
Contig ID	14794_1.R1039
5'-most EST	LIB3135-021-Q1-K1-F7

Seq. No.	194637
Contig ID	14803_1.R1039
5'-most EST	LIB3135-021-Q1-K1-G6
Method	BLASTX
NCBI GI	g294668
BLAST score	455
E value	2.0e-45
Match length	93
% identity	95
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	194638
Contig ID	14807_1.R1039
5'-most EST	LIB3135-021-Q1-K1-H12
Method	BLASTX
NCBI GI	g1352461
BLAST score	540
E value	2.0e-55
Match length	130
% identity	80
NCBI Description	IN2-2 PROTEIN

Seq. No.	194639
Contig ID	14817_1.R1039
5'-most EST	LIB3135-022-Q1-K1-A5

Seq. No.	194640
Contig ID	14822_1.R1039
5'-most EST	LIB3135-045-Q1-K1-B12

Seq. No. 194641

Contig ID	14829_1.R1039
5'-most EST	LIB3135-022-Q1-K1-B8
Method	BLASTX
NCBI GI	g3367594
BLAST score	435
E value	4.0e-43
Match length	140
% identity	60
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	194642
Contig ID	14837_1.R1039
5'-most EST	LIB3196-016-P1-M1-F9
Method	BLASTX
NCBI GI	g3176664
BLAST score	191
E value	4.0e-14
Match length	162
% identity	34
NCBI Description	(AC004393) Contains similarity to beta scruin gb|Z47541 from Limulus polyphemus. ESTs gb|T04493 and gb|AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	194643
Contig ID	14839_1.R1039
5'-most EST	LIB3135-052-Q1-K1-D11

Seq. No.	194644
Contig ID	14842_1.R1039
5'-most EST	LIB3146-027-Q1-K1-H2

Seq. No.	194645
Contig ID	14847_1.R1039
5'-most EST	uC-gsronu33B012d10b1

Seq. No.	194646
Contig ID	14851_1.R1039
5'-most EST	g5048078
Method	BLASTX
NCBI GI	g1345975
BLAST score	656
E value	9.0e-69
Match length	132
% identity	87
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi|1084421|pir||JC2555 omega-3 fatty acid desaturase - Common tobacco (cv. SR1) >gi|599592|dbj|BAA05515| (D26509) microsomal omega-3 acid desaturase [Nicotiana tabacum]

Seq. No.	194647
Contig ID	14853_1.R1039
5'-most EST	LIB3135-022-Q1-K1-E4
Method	BLASTX
NCBI GI	g4262250
BLAST score	678
E value	3.0e-71
Match length	148

% identity	86
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.	194648
Contig ID	14857_1.R1039
5'-most EST	LIB3135-022-Q1-K1-E8
Seq. No.	194649
Contig ID	14858_1.R1039
5'-most EST	uC-gsflnu33B109d01b1
Method	BLASTX
NCBI GI	g3738283
BLAST score	402
E value	5.0e-39
Match length	82
% identity	85
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	194650
Contig ID	14877_1.R1039
5'-most EST	uC-gsflmaxxa004h03b1
Seq. No.	194651
Contig ID	14878_1.R1039
5'-most EST	g5046622
Method	BLASTX
NCBI GI	g4455256
BLAST score	834
E value	1.0e-89
Match length	206
% identity	73
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]
Seq. No.	194652
Contig ID	14879_1.R1039
5'-most EST	LIB3272-036-P1-K1-E6
Method	BLASTX
NCBI GI	g4204313
BLAST score	203
E value	2.0e-15
Match length	129
% identity	41
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	194653
Contig ID	14900_1.R1039
5'-most EST	LIB3147-035-Q1-K1-H8
Seq. No.	194654
Contig ID	14902_1.R1039
5'-most EST	LIB3135-023-Q1-K1-B9
Method	BLASTX
NCBI GI	g2511541
BLAST score	629
E value	8.0e-66

Match length	139
% identity	88
NCBI Description	(AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No.	194655
Contig ID	14904_1.R1039
5'-most EST	LIB3165-057-P1-K1-E4
Method	BLASTX
NCBI GI	g134892
BLAST score	284
E value	1.0e-46
Match length	164
% identity	63
NCBI Description	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi|88607|pir||A29440 signal recognition particle receptor - human >gi|30866|emb|CAA29608| (X06272) docking protein [Homo sapiens] >gi|4507223|ref|NP_003130.1|pSRPR| signal recognition particle receptor ('docking protein')

Seq. No.	194656
Contig ID	14904_2.R1039
5'-most EST	LIB3149-035-Q1-K1-G6
Method	BLASTX
NCBI GI	g134892
BLAST score	550
E value	1.0e-58
Match length	219
% identity	58
NCBI Description	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi|88607|pir||A29440 signal recognition particle receptor - human >gi|30866|emb|CAA29608| (X06272) docking protein [Homo sapiens] >gi|4507223|ref|NP_003130.1|pSRPR| signal recognition particle receptor ('docking protein')

Seq. No.	194657
Contig ID	14922_1.R1039
5'-most EST	uC-gsronu33B147f06b1

Seq. No.	194658
Contig ID	14936_1.R1039
5'-most EST	LIB3135-023-Q1-K1-G8

Seq. No.	194659
Contig ID	14943_1.R1039
5'-most EST	LIB3135-023-Q1-K1-H6

Seq. No.	194660
Contig ID	14950_1.R1039
5'-most EST	LIB3135-024-Q1-K1-A2

Seq. No.	194661
Contig ID	14952_1.R1039
5'-most EST	LIB3135-024-Q1-K1-A8

Seq. No. 194662

Contig ID	14958_2.R1039
5'-most EST	LIB3145-035-Q1-K1-C7

Seq. No.	194663
Contig ID	14968_1.R1039
5'-most EST	LIB3135-024-Q1-K1-C10
Method	BLASTX
NCBI GI	g2558654
BLAST score	442
E value	8.0e-44
Match length	157
% identity	57
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	194664
Contig ID	14971_1.R1039
5'-most EST	LIB3146-038-P1-K1-D4

Seq. No.	194665
Contig ID	14978_1.R1039
5'-most EST	uC-gsronu33B116d12b1
Method	BLASTX
NCBI GI	g1890281
BLAST score	440
E value	3.0e-43
Match length	213
% identity	18
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No.	194666
Contig ID	14984_1.R1039
5'-most EST	LIB3135-024-Q1-K1-D6
Method	BLASTX
NCBI GI	g2501231
BLAST score	422
E value	2.0e-61
Match length	187
% identity	62
NCBI Description	HYPOTHETICAL 38.1 KD PROTEIN >gi|99505|pir||S24930 hypothetical protein - pink corydalis >gi|18258|emb|CAA45139| (X63595) protein of unknown function [Corydalis sempervirens] >gi|444333|prf||1906382A pCSC71 protein [Corydalis sempervirens]

Seq. No.	194667
Contig ID	14985_1.R1039
5'-most EST	LIB3272-019-P1-K1-E8

Seq. No.	194668
Contig ID	14990_1.R1039
5'-most EST	LIB3135-024-Q1-K1-E3
Method	BLASTX
NCBI GI	g3297819
BLAST score	546
E value	6.0e-56
Match length	162

% identity	65
NCBI Description	(AL031032) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	194669
Contig ID	14996_1.R1039
5'-most EST	LIB3148-055-Q1-K1-H12
Method	BLASTN
NCBI GI	g2351063
BLAST score	34
E value	2.0e-09
Match length	140
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	194670
Contig ID	14997_1.R1039
5'-most EST	LIB3147-038-Q1-K2-F4
Method	BLASTX
NCBI GI	g3123264
BLAST score	564
E value	6.0e-58
Match length	135
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi|2244857|emb|CAB10279| (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194671
Contig ID	14997_2.R1039
5'-most EST	uC-gsronu33B012d12b1
Method	BLASTX
NCBI GI	g3123264
BLAST score	580
E value	6.0e-60
Match length	131
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi|2244857|emb|CAB10279| (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194672
Contig ID	15002_1.R1039
5'-most EST	LIB3135-024-Q1-K1-F7
Method	BLASTX
NCBI GI	g1362615
BLAST score	256
E value	5.0e-22
Match length	113
% identity	48
NCBI Description	iswi protein - fruit fly (Drosophila melanogaster) >gi|439197 (L27127) ISWI protein [Drosophila melanogaster]

Seq. No.	194673
Contig ID	15008_1.R1039
5'-most EST	LIB3135-024-Q1-K1-G2
Method	BLASTN
NCBI GI	g3821780

BLAST score	33
E value	6.0e-09
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	194674
Contig ID	15009_1.R1039
5'-most EST	LIB3146-061-Q1-K1-A7
Method	BLASTX
NCBI GI	g2511541
BLAST score	437
E value	6.0e-43
Match length	101
% identity	84
NCBI Description	(AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No.	194675
Contig ID	15014_1.R1039
5'-most EST	LIB3135-024-Q1-K1-H2
Method	BLASTX
NCBI GI	g719291
BLAST score	559
E value	1.0e-57
Match length	149
% identity	74
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi|1095007|prf||2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	194676
Contig ID	15018_1.R1039
5'-most EST	LIB3149-006-Q1-K1-H5
Method	BLASTX
NCBI GI	g2431769
BLAST score	270
E value	1.0e-23
Match length	112
% identity	54
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	194677
Contig ID	15032_1.R1039
5'-most EST	LIB3147-032-Q1-K1-H7
Method	BLASTX
NCBI GI	g2924772
BLAST score	704
E value	3.0e-74
Match length	143
% identity	91
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	194678
Contig ID	15035_1.R1039
5'-most EST	LIB3149-015-Q1-K1-E2

Seq. No.	194679
Contig ID	15037_1.R1039

5'-most EST	LIB3135-025-Q1-K1-B4
Method	BLASTX
NCBI GI	g2076884
BLAST score	437
E value	4.0e-43
Match length	149
% identity	59
NCBI Description	(U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]

Seq. No.	194680
Contig ID	15042_1.R1039
5'-most EST	uC-gsronu33B041g01b1
Method	BLASTX
NCBI GI	g2244917
BLAST score	282
E value	9.0e-25
Match length	147
% identity	39
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194681
Contig ID	15046_1.R1039
5'-most EST	LIB3166-021-P1-K1-B4
Method	BLASTX
NCBI GI	g2407639
BLAST score	231
E value	3.0e-19
Match length	126
% identity	38
NCBI Description	(AF018263) protein phosphatase 5; PP5 [Xenopus laevis]

Seq. No.	194682
Contig ID	15049_1.R1039
5'-most EST	LIB3135-025-Q1-K1-D1
Method	BLASTX
NCBI GI	g3914403
BLAST score	283
E value	2.0e-25
Match length	126
% identity	51
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi|2370335|emb|CAA73866| (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi|3929920|dbj|BAA34712| (AB020500) mitochondrial protoporphyrinogen oxidase [Nicotiana tabacum] >gi|4105188 (AF044129) protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No.	194683
Contig ID	15056_1.R1039
5'-most EST	LIB3149-033-Q1-K1-C11
Method	BLASTX
NCBI GI	g285741
BLAST score	751
E value	8.0e-80
Match length	243

% identity	62
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	194684
Contig ID	15058_1.R1039
5'-most EST	g5044808
Method	BLASTX
NCBI GI	g2687726
BLAST score	438
E value	4.0e-43
Match length	135
% identity	61
NCBI Description	(AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine max]

Seq. No.	194685
Contig ID	15061_1.R1039
5'-most EST	LIB3135-025-Q1-K1-E1

Seq. No.	194686
Contig ID	15065_1.R1039
5'-most EST	LIB3135-025-Q1-K1-E10
Method	BLASTX
NCBI GI	g3329368
BLAST score	192
E value	3.0e-22
Match length	141
% identity	40
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	194687
Contig ID	15068_1.R1039
5'-most EST	LIB3146-002-P1-K2-G11
Method	BLASTX
NCBI GI	g3334144
BLAST score	958
E value	1.0e-104
Match length	240
% identity	78
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi|1695698|dbj|BAA13181| (D86925) C-type cyclin [Oryza sativa]

Seq. No.	194688
Contig ID	15072_1.R1039
5'-most EST	uC-gsflnu33B023d12b1

Seq. No.	194689
Contig ID	15079_1.R1039
5'-most EST	uC-gsflnu33B031d02b1
Method	BLASTX
NCBI GI	g3309575
BLAST score	175
E value	1.0e-15
Match length	71
% identity	65
NCBI Description	(AF060553) calcium sensor homolog [Arabidopsis thaliana] >gi|4538989|emb|CAB39731.1| (Y18870) CBL4 protein

[Arabidopsis thaliana]

Seq. No.	194690
Contig ID	15085_1.R1039
5'-most EST	uC-gsflnu33B022c10b1
Method	BLASTX
NCBI GI	g3193298
BLAST score	162
E value	1.0e-10
Match length	126
% identity	30
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	194691
Contig ID	15096_1.R1039
5'-most EST	LIB3135-025-Q1-K1-H3
Method	BLASTX
NCBI GI	g4454014
BLAST score	238
E value	8.0e-20
Match length	96
% identity	54
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	194692
Contig ID	15098_1.R1039
5'-most EST	LIB3272-022-P1-K1-A4
Method	BLASTX
NCBI GI	g231574
BLAST score	552
E value	1.0e-56
Match length	202
% identity	57
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi|81837|pir||S22523 asparaginase (EC 3.5.1.1) - tree lupine (fragment) >gi|19137|emb|CAA36824| (X52588) asparaginase [Lupinus arboreus]

Seq. No.	194693
Contig ID	15106_1.R1039
5'-most EST	LIB3272-036-P1-K1-C10
Method	BLASTX
NCBI GI	g2677830
BLAST score	756
E value	2.0e-80
Match length	166
% identity	89
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	194694
Contig ID	15112_1.R1039
5'-most EST	uC-gsflmaxxa014a10b1
Method	BLASTX
NCBI GI	g2244835
BLAST score	443
E value	8.0e-44
Match length	132

% identity	67
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]
Seq. No.	194695
Contig ID	15118_1.R1039
5'-most EST	uC-gsflmaxxa048f12b1
Method	BLASTX
NCBI GI	g2832672
BLAST score	652
E value	3.0e-68
Match length	161
% identity	80
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.	194696
Contig ID	15118_2.R1039
5'-most EST	g5048348
Method	BLASTX
NCBI GI	g2832672
BLAST score	613
E value	1.0e-63
Match length	137
% identity	85
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.	194697
Contig ID	15119_1.R1039
5'-most EST	uC-gsflnu33B015c09b1
Method	BLASTX
NCBI GI	g1651934
BLAST score	249
E value	6.0e-21
Match length	176
% identity	36
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]
Seq. No.	194698
Contig ID	15119_2.R1039
5'-most EST	uC-gsflnu33B009c02b1
Seq. No.	194699
Contig ID	15120_1.R1039
5'-most EST	LIB3147-019-Q1-K1-G12
Method	BLASTX
NCBI GI	g231660
BLAST score	833
E value	2.0e-89
Match length	294
% identity	58
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.	194700
Contig ID	15129_1.R1039
5'-most EST	LIB3146-002-P1-K2-A12
Method	BLASTX
NCBI GI	g4567304
BLAST score	356

E value	2.0e-33
Match length	160
% identity	54
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	194701
Contig ID	15132_1.R1039
5'-most EST	LIB3272-001-P1-K1-H6

Seq. No.	194702
Contig ID	15142_1.R1039
5'-most EST	LIB3148-030-Q1-K1-A9

Seq. No.	194703
Contig ID	15143_1.R1039
5'-most EST	LIB3147-001-Q1-K2-B2
Method	BLASTX
NCBI GI	g2832898
BLAST score	364
E value	2.0e-34
Match length	141
% identity	66
NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	194704
Contig ID	15144_1.R1039
5'-most EST	LIB3145-017-Q1-K1-C9
Method	BLASTX
NCBI GI	g3402683
BLAST score	267
E value	4.0e-23
Match length	160
% identity	43
NCBI Description	(AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No.	194705
Contig ID	15148_1.R1039
5'-most EST	LIB3189-002-P1-K1-B10
Method	BLASTX
NCBI GI	g732080
BLAST score	142
E value	9.0e-09
Match length	87
% identity	38
NCBI Description	HYPOTHETICAL 32.0 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F284) >gi|1361266|pir||S56578 yjiA protein - Escherichia coli >gi|537194 (U14003) yjiA gene product [Escherichia coli] >gi|1790812 (AE000506) orf, hypothetical protein [Escherichia coli]

Seq. No.	194706
Contig ID	15151_1.R1039
5'-most EST	LIB3135-026-Q1-K1-F12

Seq. No.	194707
Contig ID	15159_1.R1039

5'-most EST	g3325760
Method	BLASTN
NCBI GI	g4567193
BLAST score	106
E value	3.0e-52
Match length	818
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	194708
Contig ID	15160_1.R1039
5'-most EST	LIB3135-026-Q1-K1-G11
Method	BLASTX
NCBI GI	g1079652
BLAST score	220
E value	9.0e-18
Match length	63
% identity	65
NCBI Description	(U38247) late embryogenesis abundant protein [Glycine soja]

Seq. No.	194709
Contig ID	15161_1.R1039
5'-most EST	LIB3135-026-Q1-K1-G12
Method	BLASTX
NCBI GI	g2062173
BLAST score	362
E value	2.0e-34
Match length	99
% identity	68
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	194710
Contig ID	15164_1.R1039
5'-most EST	LIB3135-054-Q1-K1-A4

Seq. No.	194711
Contig ID	15168_1.R1039
5'-most EST	LIB3135-026-Q1-K1-G9
Method	BLASTX
NCBI GI	g3738320
BLAST score	177
E value	1.0e-12
Match length	88
% identity	41
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	194712
Contig ID	15169_1.R1039
5'-most EST	LIB3135-028-Q1-K1-B9
Method	BLASTX
NCBI GI	g3128228
BLAST score	464
E value	2.0e-46
Match length	92

% identity	93
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi|3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	194713
Contig ID	15175_1.R1039
5'-most EST	LIB3135-026-Q1-K1-H7
Seq. No.	194714
Contig ID	15178_1.R1039
5'-most EST	LIB3135-027-Q1-K1-A12
Method	BLASTX
NCBI GI	g1076511
BLAST score	1327
E value	1.0e-147
Match length	313
% identity	82
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi|758250|emb|CAA59799| (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]
Seq. No.	194715
Contig ID	15179_1.R1039
5'-most EST	LIB3147-059-Q1-K1-H10
Method	BLASTX
NCBI GI	g3913791
BLAST score	577
E value	5.0e-69
Match length	148
% identity	88
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi|2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]
Seq. No.	194716
Contig ID	15180_1.R1039
5'-most EST	LIB3135-027-Q1-K1-B10
Method	BLASTX
NCBI GI	g3342211
BLAST score	287
E value	1.0e-25
Match length	105
% identity	59
NCBI Description	(U89255) Pti4 [Lycopersicon esculentum]
Seq. No.	194717
Contig ID	15182_1.R1039
5'-most EST	uC-gsronu33B137d09b1
Method	BLASTN
NCBI GI	g3434966
BLAST score	35
E value	4.0e-10
Match length	43
% identity	95
NCBI Description	Arabidopsis thaliana AtERF-1 mRNA for ethylene responsive

element binding factor 1, complete cds

Seq. No.	194718
Contig ID	15183_1.R1039
5'-most EST	LIB3145-042-Q1-K1-G12

Seq. No.	194719
Contig ID	15184_1.R1039
5'-most EST	LIB3272-054-P1-K1-D5
Method	BLASTX
NCBI GI	g1313968
BLAST score	407
E value	1.0e-39
Match length	138
% identity	59
NCBI Description	(Z72426) major allergen Mal d 1 [Malus domestica]

Seq. No.	194720
Contig ID	15185_1.R1039
5'-most EST	LIB3166-014-P1-K1-G11

Seq. No.	194721
Contig ID	15195_1.R1039
5'-most EST	LIB3135-027-Q1-K1-F9
Method	BLASTX
NCBI GI	g1086651
BLAST score	146
E value	3.0e-09
Match length	66
% identity	45
NCBI Description	(U41015) similar to cystic fibrosis transmembrane conductance regulator and other ABC transporters (MDR subfamily) [Caenorhabditis elegans]

Seq. No.	194722
Contig ID	15201_1.R1039
5'-most EST	LIB3135-028-Q1-K1-A10
Method	BLASTX
NCBI GI	g480450
BLAST score	414
E value	2.0e-40
Match length	89
% identity	90
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi|402552|emb|CAA49506| (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	194723
Contig ID	15220_1.R1039
5'-most EST	LIB3135-028-Q1-K1-B8
Method	BLASTX
NCBI GI	g1369981
BLAST score	193
E value	2.0e-14
Match length	103
% identity	37
NCBI Description	(X95609) mec-8 [Caenorhabditis elegans]

>gi|3874374|emb|CAB02754| (Z81037) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2... >gi|3877217|emb|CAB03111| (Z81084) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2

Seq. No.	194724
Contig ID	15224_1.R1039
5'-most EST	LIB3197-026-Q1-M1-A11
Method	BLASTX
NCBI GI	g4106515
BLAST score	825
E value	3.0e-88
Match length	190
% identity	82
NCBI Description	(AF092743) CAK associated cyclinH homolog [Populus tremula x Populus tremuloides]

Seq. No.	194725
Contig ID	15235_1.R1039
5'-most EST	LIB3166-045-P1-K1-C2
Method	BLASTX
NCBI GI	g2262172
BLAST score	496
E value	2.0e-50
Match length	217
% identity	53
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	194726
Contig ID	15244_1.R1039
5'-most EST	LIB3146-037-P1-K1-C7

Seq. No.	194727
Contig ID	15244_2.R1039
5'-most EST	LIB3145-005-Q1-K1-E5

Seq. No.	194728
Contig ID	15260_1.R1039
5'-most EST	g5049097
Method	BLASTX
NCBI GI	g3337091
BLAST score	809
E value	2.0e-86
Match length	300
% identity	59
NCBI Description	(AB016204) polygalacturonase inhibitor (PGIP) [Citrus unshiu]

Seq. No.	194729
Contig ID	15263_1.R1039
5'-most EST	LIB3166-025-P1-K1-C1

Seq. No.	194730
Contig ID	15264_1.R1039
5'-most EST	uC-gsronu33B166h05b2
Method	BLASTX
NCBI GI	g2853097
BLAST score	177
E value	1.0e-12
Match length	141
% identity	32
NCBI Description	(AL021767) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	194731
Contig ID	15271_1.R1039
5'-most EST	LIB3146-034-Q1-K1-C1
Method	BLASTX
NCBI GI	g1203832
BLAST score	546
E value	8.0e-56
Match length	219
% identity	52
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi|1588407|prf||2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	194732
Contig ID	15276_1.R1039
5'-most EST	uC-gsflmaxxa042f05b1

Seq. No.	194733
Contig ID	15283_1.R1039
5'-most EST	LIB3147-015-Q1-K1-H5
Method	BLASTX
NCBI GI	g231574
BLAST score	385
E value	3.0e-37
Match length	113
% identity	65
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi|81837|pir||S22523 asparaginase (EC 3.5.1.1) - tree lupine (fragment) >gi|19137|emb|CAA36824| (X52588) asparaginase [Lupinus arboreus]

Seq. No.	194734
Contig ID	15285_2.R1039
5'-most EST	uC-gsflnu33B009g07b1
Method	BLASTX
NCBI GI	g1542941
BLAST score	744
E value	7.0e-79
Match length	177
% identity	84
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	194735
Contig ID	15287_1.R1039
5'-most EST	uC-gsflnu33B138b12b1

Method	BLASTX
NCBI GI	g3786008
BLAST score	199
E value	2.0e-15
Match length	100
% identity	52
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	194736
Contig ID	15309_1.R1039
5'-most EST	LIB3272-058-P1-K1-D10

Seq. No.	194737
Contig ID	15309_2.R1039
5'-most EST	g5045337

Seq. No.	194738
Contig ID	15312_1.R1039
5'-most EST	LIB3135-029-Q1-K1-D1

Seq. No.	194739
Contig ID	15314_1.R1039
5'-most EST	LIB3135-029-Q1-K1-D11

Seq. No.	194740
Contig ID	15316_1.R1039
5'-most EST	LIB3135-029-Q1-K1-D2
Method	BLASTX
NCBI GI	g3641868
BLAST score	383
E value	6.0e-37
Match length	105
% identity	70
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	194741
Contig ID	15321_2.R1039
5'-most EST	LIB3149-021-Q1-K1-A8
Method	BLASTX
NCBI GI	g1170745
BLAST score	591
E value	4.0e-61
Match length	151
% identity	74
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi|167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	194742
Contig ID	15329_1.R1039
5'-most EST	LIB3166-025-P1-K1-H6
Method	BLASTX
NCBI GI	g4544443
BLAST score	439
E value	9.0e-95
Match length	289

% identity	67
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	194743
Contig ID	15330_1.R1039
5'-most EST	LIB3145-053-Q1-K1-D4
Method	BLASTX
NCBI GI	g710626
BLAST score	153
E value	6.0e-10
Match length	43
% identity	60
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi|3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi|3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	194744
Contig ID	15331_1.R1039
5'-most EST	uC-gsflmaxxa026c08b1
Method	BLASTX
NCBI GI	g3790252
BLAST score	181
E value	2.0e-13
Match length	95
% identity	42
NCBI Description	(AL031966) putative Zn-protease [Schizosaccharomyces pombe]

Seq. No.	194745
Contig ID	15333_1.R1039
5'-most EST	LIB3197-012-P1-M1-F9

Seq. No.	194746
Contig ID	15346_1.R1039
5'-most EST	LIB3146-014-Q1-K1-C7
Method	BLASTX
NCBI GI	g4455235
BLAST score	255
E value	8.0e-22
Match length	68
% identity	75
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	194747
Contig ID	15347_1.R1039
5'-most EST	LIB3145-015-Q1-K1-H6
Method	BLASTX
NCBI GI	g2244855
BLAST score	377
E value	4.0e-36
Match length	155
% identity	54
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194748

Contig ID 15354_1.R1039
5'-most EST LIB3197-044-Q1-M1-F11
Method BLASTX
NCBI GI g4165861
BLAST score 293
E value 2.0e-26
Match length 136
% identity 24
NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No. 194749
Contig ID 15355_1.R1039
5'-most EST LIB3135-039-Q1-K1-C3
Method BLASTX
NCBI GI g4432859
BLAST score 195
E value 1.0e-14
Match length 85
% identity 46
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 194750
Contig ID 15356_1.R1039
5'-most EST LIB3147-019-Q1-K1-C8

Seq. No. 194751
Contig ID 15365_1.R1039
5'-most EST LIB3135-031-Q1-K1-A7

Seq. No. 194752
Contig ID 15369_1.R1039
5'-most EST LIB3149-026-Q1-K1-E11

Seq. No. 194753
Contig ID 15372_1.R1039
5'-most EST LIB3146-025-Q1-K2-E2
Method BLASTX
NCBI GI g729470
BLAST score 182
E value 3.0e-13
Match length 51
% identity 71
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi|542089|pir||JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi|297798|emb|CAA79702| (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No. 194754
Contig ID 15375_1.R1039
5'-most EST LIB3145-010-Q1-K1-D1

Seq. No. 194755
Contig ID 15384_1.R1039
5'-most EST LIB3272-046-P1-K1-H5
Method BLASTX

NCBI GI	g2529229
BLAST score	479
E value	2.0e-76
Match length	171
% identity	91
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	194756
Contig ID	15384_2.R1039
5'-most EST	LIB3272-027-P1-K1-A2
Method	BLASTX
NCBI GI	g2529229
BLAST score	475
E value	1.0e-47
Match length	101
% identity	91
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	194757
Contig ID	15388_1.R1039
5'-most EST	LIB3135-031-Q1-K1-D1
Method	BLASTX
NCBI GI	g3075402
BLAST score	165
E value	3.0e-11
Match length	91
% identity	42
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	194758
Contig ID	15389_1.R1039
5'-most EST	LIB3135-031-Q1-K1-D10

Seq. No.	194759
Contig ID	15390_1.R1039
5'-most EST	LIB3135-031-Q1-K1-D11

Seq. No.	194760
Contig ID	15395_1.R1039
5'-most EST	LIB3146-059-Q1-K1-C3

Seq. No.	194761
Contig ID	15397_1.R1039
5'-most EST	uC-gsflnu33B081a04b1

Seq. No.	194762
Contig ID	15398_1.R1039
5'-most EST	LIB3135-031-Q1-K1-E1

Seq. No.	194763
Contig ID	15400_1.R1039
5'-most EST	LIB3135-031-Q1-K1-E10
Method	BLASTX
NCBI GI	g1172584
BLAST score	457
E value	3.0e-45
Match length	250

% identity	41
NCBI Description	POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE) >gi|1076478|pir||S52984 catechol oxidase (EC 1.10.3.1) precursor - apple tree >gi|507280 (L29450) polyphenol oxidase [Malus domestica]
Seq. No.	194764
Contig ID	15404_1.R1039
5'-most EST	LIB3147-051-Q1-K1-B2
Method	BLASTX
NCBI GI	g1617002
BLAST score	909
E value	3.0e-98
Match length	213
% identity	83
NCBI Description	(X99552) asparagine synthetase [Asparagus officinalis]
Seq. No.	194765
Contig ID	15406_1.R1039
5'-most EST	LIB3135-031-Q1-K1-E5
Method	BLASTX
NCBI GI	g2500376
BLAST score	472
E value	4.0e-47
Match length	95
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi|4262177|gb|AAD14494| (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.	194766
Contig ID	15411_1.R1039
5'-most EST	LIB3147-026-Q1-K1-C11
Method	BLASTX
NCBI GI	g336392
BLAST score	391
E value	1.0e-37
Match length	143
% identity	62
NCBI Description	(J05215) ribosomal protein S17 [Arabidopsis thaliana]
Seq. No.	194767
Contig ID	15424_1.R1039
5'-most EST	g5045731
Method	BLASTX
NCBI GI	g100487
BLAST score	129
E value	1.0e-10
Match length	120
% identity	33
NCBI Description	TNP1 protein - garden snapdragon >gi|16057|emb|CAA40554| (X57297) TNP1 [Antirrhinum majus]
Seq. No.	194768
Contig ID	15425_1.R1039
5'-most EST	LIB3146-006-Q1-K1-C12
Seq. No.	194769

Contig ID 15426_1.R1039
5'-most EST uC-gsronu33B101c06b1
Method BLASTX
NCBI GI g4455365
BLAST score 374
E value 9.0e-36
Match length 74
% identity 88
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 194770
Contig ID 15428_1.R1039
5'-most EST LIB3135-031-Q1-K1-G8

Seq. No. 194771
Contig ID 15429_1.R1039
5'-most EST LIB3135-031-Q1-K1-G9
Method BLASTX
NCBI GI g3874214
BLAST score 389
E value 2.0e-37
Match length 198
% identity 47
NCBI Description (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W (SW:YED1_YEAST); cDNA EST EMBL:D27574 comes from this gene; cDNA EST EMBL:D33757 comes from this gene; cDNA EST EMBL:D34256 comes from this gene; cDNA EST EMBL:D37288 comes from

Seq. No. 194772
Contig ID 15432_1.R1039
5'-most EST LIB3135-031-Q1-K1-H11

Seq. No. 194773
Contig ID 15435_1.R1039
5'-most EST LIB3196-015-P1-M1-E1
Method BLASTX
NCBI GI g1352681
BLAST score 814
E value 5.0e-87
Match length 303
% identity 57
NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi|1076391|pir||S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi|633028|dbj|BAA07287| (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 194774
Contig ID 15439_1.R1039
5'-most EST LIB3272-022-P1-K1-D10

Seq. No. 194775
Contig ID 15440_1.R1039
5'-most EST LIB3196-025-P1-M1-A8
Method BLASTX
NCBI GI g633890
BLAST score 630

E value	1.0e-65
Match length	168
% identity	72
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No.	194776
Contig ID	15441_1.R1039
5'-most EST	LIB3135-032-Q1-K1-A1

Seq. No.	194777
Contig ID	15455_1.R1039
5'-most EST	LIB3135-032-Q1-K1-B2

Seq. No.	194778
Contig ID	15457_1.R1039
5'-most EST	g5044923
Method	BLASTX
NCBI GI	g2244939
BLAST score	326
E value	5.0e-30
Match length	149
% identity	44
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194779
Contig ID	15459_1.R1039
5'-most EST	g5048676
Method	BLASTX
NCBI GI	g1841870
BLAST score	720
E value	5.0e-76
Match length	230
% identity	63
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	194780
Contig ID	15459_2.R1039
5'-most EST	LIB3165-050-Q1-K1-A1
Method	BLASTX
NCBI GI	g1841870
BLAST score	328
E value	3.0e-30
Match length	128
% identity	77
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	194781
Contig ID	15459_3.R1039
5'-most EST	LIB3135-032-Q1-K1-B7
Method	BLASTX
NCBI GI	g1352347
BLAST score	248
E value	3.0e-21
Match length	57
% identity	84
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)

>gi|480620|pir||S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
>gi|398608|emb|CAA52751| (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	194782
Contig ID	15464_1.R1039
5'-most EST	LIB3197-029-Q1-M1-A10
Method	BLASTX
NCBI GI	g4056488
BLAST score	477
E value	1.0e-47
Match length	105
% identity	78
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	194783
Contig ID	15464_2.R1039
5'-most EST	LIB3189-041-P1-K1-H2
Method	BLASTX
NCBI GI	g4056488
BLAST score	319
E value	2.0e-29
Match length	76
% identity	74
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	194784
Contig ID	15466_1.R1039
5'-most EST	LIB3135-032-Q1-K1-C3

Seq. No.	194785
Contig ID	15468_1.R1039
5'-most EST	LIB3135-032-Q1-K1-C4

Seq. No.	194786
Contig ID	15469_1.R1039
5'-most EST	LIB3147-059-Q1-K1-F6
Method	BLASTX
NCBI GI	g4337210
BLAST score	193
E value	2.0e-14
Match length	86
% identity	45
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194787
Contig ID	15469_2.R1039
5'-most EST	LIB3148-025-Q1-K1-D10
Method	BLASTX
NCBI GI	g4337210
BLAST score	247
E value	6.0e-21
Match length	107
% identity	46
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194788
Contig ID	15471_1.R1039
5'-most EST	LIB3148-006-Q1-K1-E7
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	3.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	194789
Contig ID	15473_1.R1039
5'-most EST	LIB3197-021-Q1-M1-H12
Method	BLASTX
NCBI GI	g3860272
BLAST score	1221
E value	1.0e-140
Match length	293
% identity	83
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi|4314399|gb|AAD15609| (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	194790
Contig ID	15475_1.R1039
5'-most EST	LIB3135-032-Q1-K1-D11
Method	BLASTX
NCBI GI	g2832898
BLAST score	1120
E value	1.0e-123
Match length	246
% identity	85
NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	194791
Contig ID	15480_2.R1039
5'-most EST	LIB3135-032-Q1-K1-D5

Seq. No.	194792
Contig ID	15484_1.R1039
5'-most EST	uC-gsronu33B147f10b1
Method	BLASTX
NCBI GI	g1370194
BLAST score	417
E value	9.0e-41
Match length	86
% identity	95
NCBI Description	(Z73946) RAB8C [Lotus japonicus]

Seq. No.	194793
Contig ID	15509_1.R1039
5'-most EST	uC-gsronu33B044g04b1
Method	BLASTX
NCBI GI	g3152660

BLAST score	327
E value	6.0e-30
Match length	272
% identity	28
NCBI Description	(AF064603) GA17 protein [Homo sapiens]

Seq. No.	194794
Contig ID	15513_1.R1039
5'-most EST	LIB3165-009-P1-K1-C9
Method	BLASTN
NCBI GI	g1403661
BLAST score	60
E value	6.0e-25
Match length	355
% identity	83
NCBI Description	Arabidopsis thaliana BIO2 protein (BIO2) mRNA, complete cds

Seq. No.	194795
Contig ID	15514_1.R1039
5'-most EST	LIB3145-055-Q1-K1-C9
Method	BLASTX
NCBI GI	g1705463
BLAST score	799
E value	1.0e-85
Match length	169
% identity	86
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi|2129547|pir||S71201 biotin sythase - Arabidopsis thaliana >gi|1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi|1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi|1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi|2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi|1589016|prf||2209438A biotin synthase [Arabidopsis thaliana]

Seq. No.	194796
Contig ID	15519_1.R1039
5'-most EST	LIB3135-033-Q1-K1-A10

Seq. No.	194797
Contig ID	15522_1.R1039
5'-most EST	LIB3135-033-Q1-K1-A3
Method	BLASTX
NCBI GI	g4006872
BLAST score	311
E value	2.0e-28
Match length	80
% identity	76
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	194798
Contig ID	15526_1.R1039
5'-most EST	g5047139
Method	BLASTX
NCBI GI	g746510
BLAST score	445

E value	4.0e-44
Match length	136
% identity	59
NCBI Description	(U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]

Seq. No.	194799
Contig ID	15526_2.R1039
5'-most EST	LIB3196-017-P1-M1-G1
Method	BLASTX
NCBI GI	g746510
BLAST score	292
E value	2.0e-26
Match length	90
% identity	56
NCBI Description	(U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]

Seq. No.	194800
Contig ID	15531_1.R1039
5'-most EST	LIB3145-030-Q1-K1-D5

Seq. No.	194801
Contig ID	15531_2.R1039
5'-most EST	LIB3147-041-Q1-K1-E12

Seq. No.	194802
Contig ID	15533_1.R1039
5'-most EST	LIB3135-033-Q1-K1-B8

Seq. No.	194803
Contig ID	15536_1.R1039
5'-most EST	LIB3135-033-Q1-K1-B7

Seq. No.	194804
Contig ID	15538_1.R1039
5'-most EST	LIB3135-037-Q1-K1-C11
Method	BLASTX
NCBI GI	g2499115
BLAST score	447
E value	2.0e-44
Match length	138
% identity	62
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi|1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	194805
Contig ID	15542_1.R1039
5'-most EST	LIB3147-035-Q1-K1-F1

Seq. No.	194806
Contig ID	15551_1.R1039
5'-most EST	LIB3135-033-Q1-K1-D7
Method	BLASTX
NCBI GI	g4038044
BLAST score	338
E value	1.0e-31

Match length	99
% identity	61
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana] >gi|4406788|gb|AAD20098| (AC006532) unknown protein [Arabidopsis thaliana]
Seq. No.	194807
Contig ID	15567_1.R1039
5'-most EST	uC-gsflmaxxa076g04b1
Method	BLASTX
NCBI GI	g986969
BLAST score	209
E value	4.0e-34
Match length	173
% identity	50
NCBI Description	(L28005) TGACG-motif-binding protein [Glycine max]
Seq. No.	194808
Contig ID	15576_1.R1039
5'-most EST	uC-gsronu33B130c11b1
Method	BLASTX
NCBI GI	g1723242
BLAST score	145
E value	7.0e-09
Match length	51
% identity	57
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I >gi|1177363|emb|CAA93239| (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]
Seq. No.	194809
Contig ID	15582_1.R1039
5'-most EST	LIB3146-033-Q1-K1-G11
Method	BLASTX
NCBI GI	g136739
BLAST score	151
E value	2.0e-09
Match length	51
% identity	65
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi|67061|pir||XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi|218001|dbj|BAA00570| (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.	194810
Contig ID	15582_2.R1039
5'-most EST	g5048417
Seq. No.	194811
Contig ID	15587_1.R1039
5'-most EST	uC-gsflnu33B012c02b1
Seq. No.	194812
Contig ID	15588_1.R1039
5'-most EST	uC-gsronu33B079a12b1
Method	BLASTX

NCBI GI	g2916917
BLAST score	491
E value	3.0e-49
Match length	220
% identity	46
NCBI Description	(AL022004) hypothetical protein Rv0858c [Mycobacterium tuberculosis]

Seq. No.	194813
Contig ID	15592_1.R1039
5'-most EST	uC-gsronu33B144f12b1
Method	BLASTX
NCBI GI	g2335098
BLAST score	269
E value	1.0e-23
Match length	82
% identity	62
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	194814
Contig ID	15594_1.R1039
5'-most EST	LIB3146-005-Q1-K1-A7
Method	BLASTX
NCBI GI	g2780365
BLAST score	225
E value	3.0e-18
Match length	90
% identity	52
NCBI Description	(AB007693) Elongin C [Drosophila melanogaster]

Seq. No.	194815
Contig ID	15598_1.R1039
5'-most EST	g5048210
Method	BLASTX
NCBI GI	g4309758
BLAST score	260
E value	3.0e-22
Match length	64
% identity	80
NCBI Description	(AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194816
Contig ID	15599_1.R1039
5'-most EST	LIB3135-034-Q1-K1-G11
Method	BLASTX
NCBI GI	g3327222
BLAST score	219
E value	9.0e-18
Match length	122
% identity	40
NCBI Description	(AB014604) KIAA0704 protein [Homo sapiens]

Seq. No.	194817
Contig ID	15607_1.R1039
5'-most EST	g5049348
Method	BLASTX
NCBI GI	g135053

BLAST score 412
E value 4.0e-40
Match length 196
% identity 46
NCBI Description SULFITE OXIDASE >gi|86440|pir||A34180 sulfite oxidase (EC 1.8.3.1), hepatic - chicken

Seq. No. 194818
Contig ID 15611_1.R1039
5'-most EST LIB3135-034-Q1-K1-B6

Seq. No. 194819
Contig ID 15612_1.R1039
5'-most EST g3326462
Method BLASTX
NCBI GI g3914239
BLAST score 321
E value 1.0e-35
Match length 164
% identity 53
NCBI Description PROTEIN PHOSPHATASE 2C ABI2 (PP2C) >gi|1945140|emb|CAA70163| (Y08966) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi|1945142|emb|CAA70162| (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi|2564213|emb|CAA72538| (Y11840) ABI2 [Arabidopsis thaliana]

Seq. No. 194820
Contig ID 15613_1.R1039
5'-most EST LIB3135-034-Q1-K1-B8

Seq. No. 194821
Contig ID 15622_1.R1039
5'-most EST LIB3165-007-P1-K1-H7
Method BLASTX
NCBI GI g1246823
BLAST score 330
E value 2.0e-35
Match length 122
% identity 67
NCBI Description (X89865) unknown [Phoenix dactylifera]

Seq. No. 194822
Contig ID 15633_2.R1039
5'-most EST uC-gsflmaxxa047f09b1
Method BLASTX
NCBI GI g3860249
BLAST score 403
E value 5.0e-39
Match length 126
% identity 67
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 194823
Contig ID 15636_1.R1039
5'-most EST LIB3135-034-Q1-K1-E11
Method BLASTX

NCBI GI	g2706544
BLAST score	823
E value	2.0e-88
Match length	182
% identity	87
NCBI Description	(Y15899) Sig1 [Sinapis alba]

Seq. No.	194824
Contig ID	15640_1.R1039
5'-most EST	LIB3135-034-Q1-K1-E4

Seq. No.	194825
Contig ID	15652_1.R1039
5'-most EST	LIB3135-034-Q1-K1-F5
Method	BLASTX
NCBI GI	g1361983
BLAST score	487
E value	4.0e-49
Match length	153
% identity	67
NCBI Description	ARP protein - Arabidopsis thaliana >gi|886434|emb|CAA89858| (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	194826
Contig ID	15659_1.R1039
5'-most EST	LIB3135-034-Q1-K1-G2
Method	BLASTN
NCBI GI	g886433
BLAST score	51
E value	1.0e-19
Match length	275
% identity	80
NCBI Description	A.thaliana mRNA for ARP protein

Seq. No.	194827
Contig ID	15663_1.R1039
5'-most EST	LIB3135-034-Q1-K1-G6

Seq. No.	194828
Contig ID	15670_1.R1039
5'-most EST	LIB3145-044-Q1-K1-G11
Method	BLASTX
NCBI GI	g3540199
BLAST score	167
E value	1.0e-11
Match length	66
% identity	58
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	194829
Contig ID	15671_1.R1039
5'-most EST	uC-gsflmaxxa048g08b1
Method	BLASTX
NCBI GI	g2492782
BLAST score	652
E value	2.0e-68

Match length	165
% identity	68
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi|504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	194830
Contig ID	15680_1.R1039
5'-most EST	LIB3148-057-Q1-K1-H10
Method	BLASTX
NCBI GI	g294845
BLAST score	532
E value	5.0e-54
Match length	208
% identity	50
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	194831
Contig ID	15684_1.R1039
5'-most EST	uC-gsronu33B124c09b1
Method	BLASTX
NCBI GI	g1345642
BLAST score	822
E value	5.0e-88
Match length	288
% identity	53
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 75A1) (CYPLXXVA1) >gi|629710|pir||S38985 flavonoid 3',5'-hydroxylase Hf1 - garden petunia >gi|311656|emb|CAA80266| (Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi|1853972|dbj|BAA03438| (D14588) flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi|3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi|738772|prf||2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No.	194832
Contig ID	15685_1.R1039
5'-most EST	uC-gsronu33B149g04b1

Seq. No.	194833
Contig ID	15690_1.R1039
5'-most EST	LIB3146-040-Q1-K1-D12
Method	BLASTX
NCBI GI	g2842486
BLAST score	324
E value	5.0e-30
Match length	105
% identity	64
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	194834
Contig ID	15693_1.R1039
5'-most EST	LIB3196-030-P1-M1-C4

Seq. No. 194835
Contig ID 15694_1.R1039
5'-most EST LIB3145-023-Q1-K1-E6
Method BLASTX
NCBI GI g2982466
BLAST score 253
E value 9.0e-22
Match length 98
% identity 46
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 194836
Contig ID 15696_1.R1039
5'-most EST LIB3196-028-P1-M1-G9
Method BLASTX
NCBI GI g4406775
BLAST score 323
E value 2.0e-29
Match length 332
% identity 31
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 194837
Contig ID 15699_1.R1039
5'-most EST LIB3146-043-Q1-K1-B7
Method BLASTX
NCBI GI g1354849
BLAST score 419
E value 9.0e-57
Match length 171
% identity 62
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 194838
Contig ID 15712_1.R1039
5'-most EST g3326748
Method BLASTX
NCBI GI g4103635
BLAST score 244
E value 4.0e-20
Match length 124
% identity 37
NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No. 194839
Contig ID 15722_1.R1039
5'-most EST LIB3148-002-P1-K1-G8

Seq. No. 194840
Contig ID 15724_1.R1039
5'-most EST LIB3166-013-P1-K1-B12
Method BLASTX
NCBI GI g4107276
BLAST score 261
E value 2.0e-22
Match length 59
% identity 90

NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No. 194841
Contig ID 15732_1.R1039
5'-most EST LIB3135-062-Q1-K1-F5
Method BLASTX
NCBI GI g548751
BLAST score 213
E value 7.0e-17
Match length 140
% identity 38
NCBI Description 60S RIBOSOMAL PROTEIN L19 >gi|1079135|pir||A61627 ribosomal protein L19 - fruit fly (Drosophila melanogaster) >gi|400448|emb|CAA52784| (X74776) ribosomal protein L19 [Drosophila melanogaster]

Seq. No. 194842
Contig ID 15743_1.R1039
5'-most EST LIB3135-036-Q1-K1-A5

Seq. No. 194843
Contig ID 15744_1.R1039
5'-most EST g5047311
Method BLASTX
NCBI GI g3377517
BLAST score 354
E value 2.0e-33
Match length 211
% identity 37
NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 194844
Contig ID 15747_1.R1039
5'-most EST LIB3135-036-Q1-K1-A3

Seq. No. 194845
Contig ID 15751_1.R1039
5'-most EST uC-gsronu33B163c01b2
Method BLASTX
NCBI GI g2642432
BLAST score 211
E value 7.0e-17
Match length 49
% identity 88
NCBI Description (AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]

Seq. No. 194846
Contig ID 15752_1.R1039
5'-most EST uC-gsflmaxxa041d12b1
Method BLASTX
NCBI GI g3776013
BLAST score 261
E value 2.0e-22
Match length 52
% identity 90
NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]

Seq. No.	194847
Contig ID	15761_1.R1039
5'-most EST	LIB3135-036-Q1-K1-B8
Method	BLASTX
NCBI GI	g2688824
BLAST score	272
E value	7.0e-28
Match length	110
% identity	68
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	194848
Contig ID	15771_1.R1039
5'-most EST	uC-gsflnu33B071h02b1
Method	BLASTX
NCBI GI	g2688824
BLAST score	309
E value	8.0e-28
Match length	126
% identity	63
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	194849
Contig ID	15771_2.R1039
5'-most EST	uC-gsronu33b023d07b1
Method	BLASTN
NCBI GI	g2688823
BLAST score	37
E value	4.0e-11
Match length	104
% identity	88
NCBI Description	Prunus armeniaca putative auxin-repressed protein mRNA, complete cds

Seq. No.	194850
Contig ID	15772_1.R1039
5'-most EST	uC-gsronu33B130f04b1
Method	BLASTX
NCBI GI	g3341697
BLAST score	672
E value	1.0e-70
Match length	160
% identity	81
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194851
Contig ID	15775_1.R1039
5'-most EST	uC-gsflnu33B025g12b1
Method	BLASTX
NCBI GI	g2345100
BLAST score	292
E value	2.0e-45
Match length	175
% identity	57

NCBI Description	(AF014465) Pad1 homolog [Schistosoma mansoni]
Seq. No.	194852
Contig ID	15778_1.R1039
5'-most EST	LIB3145-017-Q1-K1-H11
Seq. No.	194853
Contig ID	15779_1.R1039
5'-most EST	LIB3135-036-Q1-K1-D3
Method	BLASTX
NCBI GI	g627469
BLAST score	167
E value	1.0e-11
Match length	109
% identity	7
NCBI Description	hypothetical protein 2 - human (fragment)
Seq. No.	194854
Contig ID	15780_1.R1039
5'-most EST	LIB3135-036-Q1-K1-D4
Method	BLASTX
NCBI GI	g3757522
BLAST score	513
E value	5.0e-52
Match length	204
% identity	67
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.	194855
Contig ID	15783_1.R1039
5'-most EST	LIB3135-036-Q1-K1-D7
Seq. No.	194856
Contig ID	15786_1.R1039
5'-most EST	LIB3135-036-Q1-K1-E5
Method	BLASTX
NCBI GI	g1304227
BLAST score	430
E value	2.0e-42
Match length	139
% identity	53
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi|2764804|emb|CAA55293| (X78547) epoxide hydrolase [Glycine max]
Seq. No.	194857
Contig ID	15788_1.R1039
5'-most EST	LIB3135-036-Q1-K1-E11
Method	BLASTX
NCBI GI	g2665890
BLAST score	688
E value	1.0e-72
Match length	154
% identity	84
NCBI Description	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No. 194858
Contig ID 15794_1.R1039
5'-most EST LIB3135-036-Q1-K1-E7

Seq. No. 194859
Contig ID 15799_1.R1039
5'-most EST LIB3147-033-Q1-K1-E5
Method BLASTX
NCBI GI g4263721
BLAST score 778
E value 3.0e-86
Match length 172
% identity 96
NCBI Description (AC006223) putative DNA repair protein RAD50 [Arabidopsis thaliana]

Seq. No. 194860
Contig ID 15806_1.R1039
5'-most EST LIB3135-036-Q1-K1-G5

Seq. No. 194861
Contig ID 15807_1.R1039
5'-most EST LIB3135-036-Q1-K1-G10
Method BLASTX
NCBI GI g2826884
BLAST score 523
E value 3.0e-53
Match length 189
% identity 59
NCBI Description (AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No. 194862
Contig ID 15815_1.R1039
5'-most EST LIB3135-036-Q1-K1-G7

Seq. No. 194863
Contig ID 15822_2.R1039
5'-most EST uC-gsflmaxxa106g12b1

Seq. No. 194864
Contig ID 15837_1.R1039
5'-most EST LIB3145-058-Q1-K1-H7
Method BLASTX
NCBI GI g461729
BLAST score 414
E value 2.0e-40
Match length 97
% identity 77
NCBI Description 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi|2146744|pir||S65597 probable chaperonin, 10K - Arabidopsis thaliana >gi|166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana]

Seq. No. 194865
Contig ID 15848_1.R1039
5'-most EST LIB3196-032-P1-M1-A9

Method	BLASTX
NCBI GI	g683553
BLAST score	296
E value	2.0e-26
Match length	124
% identity	53
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi|1582679|prf||2119230A oleosin homolog [Citrus sinensis]

Seq. No.	194866
Contig ID	15855_1.R1039
5'-most EST	LIB3149-027-Q1-K1-D6
Method	BLASTX
NCBI GI	g2911044
BLAST score	193
E value	4.0e-20
Match length	121
% identity	49
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	194867
Contig ID	15866_1.R1039
5'-most EST	LIB3135-037-Q1-K1-E3

Seq. No.	194868
Contig ID	15867_1.R1039
5'-most EST	LIB3148-054-Q1-K1-A10
Method	BLASTX
NCBI GI	g2129496
BLAST score	669
E value	2.0e-70
Match length	143
% identity	87
NCBI Description	acetolactate synthase (EC 4.1.3.18) precursor (clone A19) - upland cotton

Seq. No.	194869
Contig ID	15871_1.R1039
5'-most EST	LIB3189-045-P1-K1-E3
Method	BLASTX
NCBI GI	g4457219
BLAST score	306
E value	6.0e-28
Match length	105
% identity	66
NCBI Description	(AF127796) acyl carrier protein [Capsicum chinense]

Seq. No.	194870
Contig ID	15878_1.R1039
5'-most EST	LIB3146-025-Q1-K2-B7

Seq. No.	194871
Contig ID	15880_1.R1039
5'-most EST	LIB3135-037-Q1-K1-F5
Method	BLASTX
NCBI GI	g1931647
BLAST score	283

E value	6.0e-25
Match length	71
% identity	77
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	194872
Contig ID	15886_1.R1039
5'-most EST	LIB3147-007-Q1-K1-A1
Method	BLASTX
NCBI GI	g2632254
BLAST score	249
E value	3.0e-27
Match length	129
% identity	56
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	194873
Contig ID	15886_7.R1039
5'-most EST	LIB3149-027-Q1-K1-D5

Seq. No.	194874
Contig ID	15886_11.R1039
5'-most EST	LIB3196-054-P1-M1-E10
Method	BLASTX
NCBI GI	g3080416
BLAST score	413
E value	2.0e-40
Match length	96
% identity	88
NCBI Description	(AL022604) UDP-galactose transporter - like protein [Arabidopsis thaliana]

Seq. No.	194875
Contig ID	15895_1.R1039
5'-most EST	LIB3272-007-P1-K1-C2
Method	BLASTX
NCBI GI	g3881649
BLAST score	478
E value	5.0e-48
Match length	89
% identity	90
NCBI Description	(Z70757) Similarity to yeast hypothetical protein PIR accession number S52511; cDNA EST EMBL:D73067 comes from this gene; cDNA EST EMBL:D74461 comes from this gene; cDNA EST EMBL:D76044 comes from this gene; cDNA EST yk504c7.3

Seq. No.	194876
Contig ID	15895_2.R1039
5'-most EST	LIB3135-049-Q1-K1-B1
Method	BLASTN
NCBI GI	g871468
BLAST score	101
E value	3.0e-49
Match length	291
% identity	92
NCBI Description	H.annuus mitochondrion genes trnH and trnE

Seq. No.	194877
Contig ID	15895_4.R1039
5'-most EST	LIB3135-037-Q1-K1-H1
Method	BLASTX
NCBI GI	g3881649
BLAST score	431
E value	2.0e-42
Match length	86
% identity	86
NCBI Description	(Z70757) Similarity to yeast hypothetical protein PIR accession number S52511; cDNA EST EMBL:D73067 comes from this gene; cDNA EST EMBL:D74461 comes from this gene; cDNA EST EMBL:D76044 comes from this gene; cDNA EST yk504c7.3

Seq. No.	194878
Contig ID	15900_1.R1039
5'-most EST	LIB3135-037-Q1-K1-H6
Method	BLASTX
NCBI GI	g2677830
BLAST score	544
E value	6.0e-56
Match length	115
% identity	93
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	194879
Contig ID	15903_1.R1039
5'-most EST	LIB3272-023-P1-K1-C12
Method	BLASTX
NCBI GI	g4371282
BLAST score	739
E value	1.0e-78
Match length	163
% identity	87
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	194880
Contig ID	15903_2.R1039
5'-most EST	LIB3189-001-P1-K1-C12
Method	BLASTN
NCBI GI	g2677829
BLAST score	92
E value	3.0e-44
Match length	344
% identity	82
NCBI Description	Prunus armeniaca ribosomal protein L12 mRNA, complete cds

Seq. No.	194881
Contig ID	15904_1.R1039
5'-most EST	uC-gsflmaxxa026d06b1
Method	BLASTX
NCBI GI	g3426045
BLAST score	331
E value	1.0e-30
Match length	147

% identity	51
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]
Seq. No.	194882
Contig ID	15907_1.R1039
5'-most EST	LIB3135-038-Q1-K1-A2
Seq. No.	194883
Contig ID	15911_1.R1039
5'-most EST	LIB3149-017-Q1-K1-E3
Method	BLASTX
NCBI GI	g627424
BLAST score	497
E value	6.0e-50
Match length	197
% identity	49
NCBI Description	dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50kD subunit - human >gi|2135018|pir||S66254 dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50K chain - human
Seq. No.	194884
Contig ID	15912_1.R1039
5'-most EST	LIB3166-038-P1-K1-B6
Seq. No.	194885
Contig ID	15923_1.R1039
5'-most EST	uC-gsflnu33B057f10b1
Seq. No.	194886
Contig ID	15923_2.R1039
5'-most EST	LIB3148-054-Q1-K1-E10
Seq. No.	194887
Contig ID	15923_3.R1039
5'-most EST	LIB3272-001-P1-K1-A3
Seq. No.	194888
Contig ID	15925_1.R1039
5'-most EST	LIB3147-031-Q1-K1-G5
Method	BLASTX
NCBI GI	g3062806
BLAST score	426
E value	7.0e-42
Match length	134
% identity	57
NCBI Description	(D86198) dolichol-phosphate-mannose synthase [Homo sapiens] >gi|4503363|ref|NP_003850.1|pDPM1| UNKNOWN
Seq. No.	194889
Contig ID	15935_1.R1039
5'-most EST	g5046978
Method	BLASTX
NCBI GI	g4510345
BLAST score	394
E value	8.0e-38
Match length	178

% identity	46
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	194890
Contig ID	15935_3.R1039
5'-most EST	LIB3149-028-Q1-K1-B7
Method	BLASTX
NCBI GI	g4510345
BLAST score	275
E value	5.0e-24
Match length	63
% identity	75
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	194891
Contig ID	15949_1.R1039
5'-most EST	LIB3135-038-Q1-K1-E3

Seq. No.	194892
Contig ID	15950_1.R1039
5'-most EST	LIB3135-038-Q1-K1-E4
Method	BLASTX
NCBI GI	g3135261
BLAST score	263
E value	1.0e-22
Match length	100
% identity	58
NCBI Description	(AC003058) putative 18.5 KDa class I heat shock protein [Arabidopsis thaliana]

Seq. No.	194893
Contig ID	15954_1.R1039
5'-most EST	LIB3135-038-Q1-K1-F11

Seq. No.	194894
Contig ID	15957_1.R1039
5'-most EST	LIB3147-009-Q1-K1-A4
Method	BLASTX
NCBI GI	g3212862
BLAST score	467
E value	1.0e-46
Match length	122
% identity	70
NCBI Description	(AC004005) putative riboflavin synthase [Arabidopsis thaliana]

Seq. No.	194895
Contig ID	15959_1.R1039
5'-most EST	LIB3135-038-Q1-K1-F6

Seq. No.	194896
Contig ID	15960_1.R1039
5'-most EST	g3326474
Method	BLASTX
NCBI GI	g3169012
BLAST score	358
E value	1.0e-49

Match length	181
% identity	57
NCBI Description	(AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No.	194897
Contig ID	15966_1.R1039
5'-most EST	g5046067
Method	BLASTX
NCBI GI	g3242659
BLAST score	740
E value	2.0e-78
Match length	151
% identity	91
NCBI Description	(AB015599) spermidine synthase [Coffea arabica]

Seq. No.	194898
Contig ID	15976_1.R1039
5'-most EST	uC-gsflnu33B094b12b1
Method	BLASTX
NCBI GI	g2980793
BLAST score	274
E value	3.0e-24
Match length	115
% identity	43
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	194899
Contig ID	15977_1.R1039
5'-most EST	LIB3145-046-Q1-K1-H4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	194900
Contig ID	15981_1.R1039
5'-most EST	LIB3147-037-Q1-K1-F12

Seq. No.	194901
Contig ID	15985_1.R1039
5'-most EST	LIB3135-055-Q1-K1-E7

Seq. No.	194902
Contig ID	15988_1.R1039
5'-most EST	LIB3147-047-Q1-K1-C10
Method	BLASTX
NCBI GI	g1362009
BLAST score	508
E value	2.0e-51
Match length	120
% identity	54
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	194903
Contig ID	15988_2.R1039
5'-most EST	uC-gsflmaxxa010b03b1
Method	BLASTX
NCBI GI	g1362009
BLAST score	662
E value	2.0e-69
Match length	154
% identity	88
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	194904
Contig ID	15991_1.R1039
5'-most EST	LIB3135-039-Q1-K1-B10
Method	BLASTX
NCBI GI	g1934730
BLAST score	353
E value	2.0e-33
Match length	90
% identity	73
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	194905
Contig ID	15998_1.R1039
5'-most EST	LIB3135-050-Q1-K1-C12

Seq. No.	194906
Contig ID	16001_1.R1039
5'-most EST	uC-gsflnu33B055d02b1
Method	BLASTX
NCBI GI	g400650
BLAST score	200
E value	3.0e-15
Match length	96
% identity	43
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX I-13KD-B) (CI-13KD-B) (B13) >gi|346535|pir||S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 - bovine >gi|238|emb|CAA44903| (X63218) NADH dehydrogenase [Bos taurus]

Seq. No.	194907
Contig ID	16001_2.R1039
5'-most EST	LIB3197-041-Q1-M1-G7

Seq. No.	194908
Contig ID	16001_3.R1039
5'-most EST	LIB3147-003-Q1-K1-B11
Method	BLASTX
NCBI GI	g2827713
BLAST score	376
E value	3.0e-36
Match length	126
% identity	63
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]

Seq. No.	194909
Contig ID	16003_1.R1039
5'-most EST	g5044838
Method	BLASTX
NCBI GI	g2129726
BLAST score	970
E value	1.0e-105
Match length	224
% identity	83
NCBI Description	RNA polymerase II third largest chain RPB35.5A - Arabidopsis thaliana >gi|514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi|4544370|gb|AAD22281.1|AC006920_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No.	194910
Contig ID	16020_1.R1039
5'-most EST	LIB3135-039-Q1-K1-D9
Method	BLASTX
NCBI GI	g1082211
BLAST score	241
E value	5.0e-20
Match length	199
% identity	4
NCBI Description	ankyrin 3, long form - human >gi|608025 (U13616) ankyrin G [Homo sapiens]

Seq. No.	194911
Contig ID	16027_1.R1039
5'-most EST	g3326052
Method	BLASTX
NCBI GI	g3287857
BLAST score	723
E value	2.0e-76
Match length	263
% identity	55
NCBI Description	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD) >gi|1209052 (U32229) HbdA [Bradyrhizobium japonicum]

Seq. No.	194912
Contig ID	16028_1.R1039
5'-most EST	LIB3272-020-P1-K1-D12
Method	BLASTX
NCBI GI	g4262154
BLAST score	730
E value	2.0e-77
Match length	194
% identity	77
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	194913
Contig ID	16030_1.R1039
5'-most EST	LIB3135-039-Q1-K1-F12
Method	BLASTN
NCBI GI	g3821780

BLAST score 36
E value 1.0e-10
Match length 47
% identity 49
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 194914
Contig ID 16042_1.R1039
5'-most EST LIB3165-051-Q1-K1-G6
Method BLASTX
NCBI GI g4539262
BLAST score 171
E value 7.0e-12
Match length 112
% identity 35
NCBI Description (AL049495) conserved phosducin-like hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 194915
Contig ID 16048_1.R1039
5'-most EST LIB3135-039-Q1-K1-H11

Seq. No. 194916
Contig ID 16052_1.R1039
5'-most EST LIB3147-001-Q1-K2-G12
Method BLASTX
NCBI GI g549742
BLAST score 145
E value 6.0e-09
Match length 58
% identity 41
NCBI Description HYPOTHETICAL 47.4 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION >gi|539215|pir||S38032 hypothetical protein YKL195w - yeast (Saccharomyces cerevisiae) >gi|486347|emb|CAA82039| (Z28195) ORF YKL195w [Saccharomyces cerevisiae]

Seq. No. 194917
Contig ID 16054_1.R1039
5'-most EST LIB3146-007-Q1-K1-A5
Method BLASTX
NCBI GI g3687251
BLAST score 576
E value 3.0e-59
Match length 143
% identity 76
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 194918
Contig ID 16054_2.R1039
5'-most EST LIB3147-035-Q1-K1-F3
Method BLASTX
NCBI GI g3687251
BLAST score 579
E value 1.0e-59
Match length 143
% identity 78
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	194919
Contig ID	16055_1.R1039
5'-most EST	LIB3272-009-P1-K1-C8
Method	BLASTX
NCBI GI	g529353
BLAST score	320
E value	2.0e-48
Match length	213
% identity	45
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	194920
Contig ID	16066_1.R1039
5'-most EST	LIB3135-040-Q1-K1-B12
Method	BLASTX
NCBI GI	g480618
BLAST score	545
E value	6.0e-56
Match length	129
% identity	80
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi|1345506|emb|CAA52771| (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	194921
Contig ID	16067_1.R1039
5'-most EST	LIB3135-040-Q1-K1-B3
Method	BLASTN
NCBI GI	g398603
BLAST score	95
E value	7.0e-46
Match length	358
% identity	82
NCBI Description	A.thaliana ATAF1 mRNA

Seq. No.	194922
Contig ID	16069_1.R1039
5'-most EST	LIB3145-033-Q1-K1-A1
Method	BLASTX
NCBI GI	g1420887
BLAST score	167
E value	1.0e-11
Match length	72
% identity	46
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	194923
Contig ID	16069_2.R1039
5'-most EST	LIB3135-040-Q1-K1-B5
Method	BLASTX
NCBI GI	g1420887
BLAST score	141
E value	3.0e-09
Match length	68
% identity	51

NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	194924
Contig ID	16073_1.R1039
5'-most EST	uC-gsflnu33B056d09b1
Method	BLASTX
NCBI GI	g1172816
BLAST score	740
E value	3.0e-80
Match length	180
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi|624938|emb|CAA57395| (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	194925
Contig ID	16073_2.R1039
5'-most EST	g5048774
Method	BLASTX
NCBI GI	g1172817
BLAST score	783
E value	2.0e-83
Match length	181
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi|550547|emb|CAA57396| (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi|4539392|emb|CAB37458.1| (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	194926
Contig ID	16077_1.R1039
5'-most EST	uC-gsflmaxxa054e10b1
Method	BLASTX
NCBI GI	g4336205
BLAST score	492
E value	3.0e-49
Match length	260
% identity	41
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	194927
Contig ID	16079_1.R1039
5'-most EST	LIB3135-040-Q1-K1-C4
Method	BLASTX
NCBI GI	g2829894
BLAST score	309
E value	7.0e-28
Match length	226
% identity	51
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	194928
Contig ID	16084_1.R1039
5'-most EST	g5050260
Method	BLASTX
NCBI GI	g112925
BLAST score	231

E value	5.0e-19
Match length	134
% identity	40
NCBI Description	41-2 PROTEIN ANTIGEN PRECURSOR >gi|320938|pir||A45503 41-2 protein antigen precursor - Plasmodium falciparum >gi|160039 (J04656) 41-2 protein antigen [Plasmodium falciparum]

Seq. No.	194929
Contig ID	16087_1.R1039
5'-most EST	LIB3147-049-Q1-K1-E7

Seq. No.	194930
Contig ID	16089_1.R1039
5'-most EST	uC-gsronu33B021f07b1
Method	BLASTX
NCBI GI	g1169199
BLAST score	596
E value	1.0e-61
Match length	172
% identity	65
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102 >gi|479739|pir||S35271 hypothetical protein - Arabidopsis thaliana >gi|166928 (L11368) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	194931
Contig ID	16098_1.R1039
5'-most EST	LIB3149-044-Q1-K1-A11
Method	BLASTX
NCBI GI	g2648032
BLAST score	1013
E value	1.0e-110
Match length	279
% identity	68
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	194932
Contig ID	16101_1.R1039
5'-most EST	uC-gsflmaxxa088e06b1
Method	BLASTX
NCBI GI	g114682
BLAST score	719
E value	8.0e-76
Match length	219
% identity	67
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi|100471|pir||A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi|168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	194933
Contig ID	16107_1.R1039
5'-most EST	uC-gsflmaxxa040a10b1

Method	BLASTX
NCBI GI	g1209703
BLAST score	1385
E value	1.0e-154
Match length	389
% identity	65
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	194934
Contig ID	16120_1.R1039
5'-most EST	g5047096

Seq. No.	194935
Contig ID	16126_1.R1039
5'-most EST	LIB3135-040-Q1-K1-H1
Method	BLASTX
NCBI GI	g4262181
BLAST score	167
E value	2.0e-11
Match length	77
% identity	56
NCBI Description	(AC005508) 37496 [Arabidopsis thaliana]

Seq. No.	194936
Contig ID	16127_1.R1039
5'-most EST	LIB3165-025-P1-K1-D5
Method	BLASTX
NCBI GI	g2493494
BLAST score	426
E value	7.0e-42
Match length	110
% identity	74
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi|619351|bbs|153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]

Seq. No.	194937
Contig ID	16129_1.R1039
5'-most EST	LIB3165-008-P1-K1-B10
Method	BLASTX
NCBI GI	g1171577
BLAST score	1618
E value	0.0e+00
Match length	390
% identity	78
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	194938
Contig ID	16131_1.R1039
5'-most EST	LIB3148-031-Q1-K1-G7
Method	BLASTX
NCBI GI	g2642638
BLAST score	930
E value	1.0e-100
Match length	206
% identity	86

NCBI Description	(AF032472) ADP-glucose pyrophosphorylase large subunit 1 [Citrullus lanatus]
Seq. No.	194939
Contig ID	16132_1.R1039
5'-most EST	g5045949
Seq. No.	194940
Contig ID	16133_1.R1039
5'-most EST	LIB3135-040-Q1-K1-H3
Method	BLASTX
NCBI GI	g2275204
BLAST score	186
E value	1.0e-13
Match length	83
% identity	45
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]
Seq. No.	194941
Contig ID	16134_1.R1039
5'-most EST	LIB3135-040-Q1-K1-H4
Method	BLASTX
NCBI GI	g3176681
BLAST score	160
E value	7.0e-11
Match length	91
% identity	42
NCBI Description	(AC003671) F17O7.11 [Arabidopsis thaliana]
Seq. No.	194942
Contig ID	16145_1.R1039
5'-most EST	LIB3147-034-Q1-K1-D11
Method	BLASTN
NCBI GI	g3334857
BLAST score	239
E value	1.0e-132
Match length	371
% identity	92
NCBI Description	Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2 genes
Seq. No.	194943
Contig ID	16150_1.R1039
5'-most EST	LIB3135-041-Q1-K1-B10
Seq. No.	194944
Contig ID	16159_1.R1039
5'-most EST	LIB3145-058-Q1-K1-B4
Seq. No.	194945
Contig ID	16162_1.R1039
5'-most EST	LIB3197-045-Q1-M1-A1
Method	BLASTX
NCBI GI	g3342798
BLAST score	635
E value	5.0e-66

Match length 192
% identity 62
NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica papaya]

Seq. No. 194946
Contig ID 16163_1.R1039
5'-most EST uC-gsflmaxxa043c10b1
Method BLASTX
NCBI GI g4335751
BLAST score 602
E value 2.0e-62
Match length 139
% identity 52
NCBI Description (AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No. 194947
Contig ID 16172_1.R1039
5'-most EST LIB3135-041-Q1-K1-D11

Seq. No. 194948
Contig ID 16173_1.R1039
5'-most EST LIB3147-028-Q1-K1-C11
Method BLASTX
NCBI GI g2213558
BLAST score 254
E value 1.0e-21
Match length 121
% identity 44
NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 194949
Contig ID 16182_1.R1039
5'-most EST LIB3135-041-Q1-K1-E2

Seq. No. 194950
Contig ID 16183_1.R1039
5'-most EST LIB3135-041-Q1-K1-E4
Method BLASTX
NCBI GI g3135997
BLAST score 185
E value 1.0e-13
Match length 120
% identity 33
NCBI Description (AL023589) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 194951
Contig ID 16188_1.R1039
5'-most EST LIB3145-050-Q1-K1-C2
Method BLASTX
NCBI GI g2244847
BLAST score 843
E value 3.0e-90
Match length 300
% identity 61
NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]

Seq. No.	194952
Contig ID	16193_1.R1039
5'-most EST	uC-gsflnu33B005g09b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	34
E value	3.0e-09
Match length	34
% identity	59
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	194953
Contig ID	16193_2.R1039
5'-most EST	LIB3166-022-P1-K1-F11
Method	BLASTX
NCBI GI	g1161575
BLAST score	402
E value	5.0e-39
Match length	123
% identity	67
NCBI Description	(X94947) homeobox [Lycopersicon esculentum]

Seq. No.	194954
Contig ID	16195_1.R1039
5'-most EST	LIB3189-052-P1-K1-F4
Method	BLASTX
NCBI GI	g3123745
BLAST score	530
E value	8.0e-54
Match length	212
% identity	46
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	194955
Contig ID	16195_2.R1039
5'-most EST	LIB3272-014-P1-K1-E10
Method	BLASTX
NCBI GI	g3123745
BLAST score	338
E value	2.0e-31
Match length	152
% identity	44
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	194956
Contig ID	16196_1.R1039
5'-most EST	LIB3149-020-Q1-K1-G9

Seq. No.	194957
Contig ID	16199_1.R1039
5'-most EST	LIB3147-051-Q1-K1-F3
Method	BLASTX
NCBI GI	g3548818
BLAST score	702
E value	3.0e-74

Match length	154
% identity	82
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	194958
Contig ID	16200_1.R1039
5'-most EST	LIB3146-004-P1-K1-E7
Method	BLASTX
NCBI GI	g4263528
BLAST score	150
E value	3.0e-09
Match length	132
% identity	33
NCBI Description	(AC004044) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	194959
Contig ID	16203_1.R1039
5'-most EST	uC-gsflnu33B012f02b1
Method	BLASTX
NCBI GI	g3023847
BLAST score	1571
E value	1.0e-175
Match length	324
% identity	90
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi|2385376|emb|CAA69934| (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	194960
Contig ID	16203_2.R1039
5'-most EST	LIB3146-022-Q1-K1-D8
Method	BLASTX
NCBI GI	g3023858
BLAST score	1386
E value	1.0e-154
Match length	301
% identity	52
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi|1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	194961
Contig ID	16213_1.R1039
5'-most EST	LIB3135-041-Q1-K1-H4

Seq. No.	194962
Contig ID	16220_1.R1039
5'-most EST	LIB3135-042-Q1-K1-A3

Seq. No.	194963
Contig ID	16225_1.R1039
5'-most EST	LIB3145-050-Q1-K1-H7
Method	BLASTX
NCBI GI	g2218150
BLAST score	846
E value	5.0e-91

Match length	176
% identity	87
NCBI Description	(AF005278) type IIIa membrane protein cp-wap11 [Vigna unguiculata]

Seq. No.	194964
Contig ID	16228_1.R1039
5'-most EST	uC-gsflmaxxa069a08b1
Method	BLASTX
NCBI GI	g2497953
BLAST score	224
E value	2.0e-18
Match length	131
% identity	38
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi|1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi|4469123|emb|CAB38312| (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	194965
Contig ID	16229_1.R1039
5'-most EST	LIB3135-042-Q1-K1-B2
Method	BLASTX
NCBI GI	g2213783
BLAST score	234
E value	2.0e-19
Match length	103
% identity	50
NCBI Description	(U89256) Pti5 [Lycopersicon esculentum]

Seq. No.	194966
Contig ID	16230_1.R1039
5'-most EST	LIB3147-004-Q1-K1-F6
Method	BLASTX
NCBI GI	g4191788
BLAST score	556
E value	6.0e-57
Match length	129
% identity	78
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	194967
Contig ID	16240_1.R1039
5'-most EST	LIB3189-036-P1-K1-A2
Method	BLASTX
NCBI GI	g1110502
BLAST score	522
E value	1.0e-61
Match length	239
% identity	52
NCBI Description	(U40387) coil protein [Medicago sativa]

Seq. No.	194968
Contig ID	16244_1.R1039
5'-most EST	uC-gsflmaxxa027c06b1

Method	BLASTX
NCBI GI	g462187
BLAST score	1654
E value	0.0e+00
Match length	358
% identity	89
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi|282928|pir||A42906 serine hydroxymethyltransferase - garden pea >gi|169158 (M87649) serine hydroxymethyltransferase [Pisum sativum]

Seq. No.	194969
Contig ID	16245_1.R1039
5'-most EST	LIB3135-042-Q1-K1-C7
Method	BLASTX
NCBI GI	g3128220
BLAST score	646
E value	2.0e-72
Match length	184
% identity	77
NCBI Description	(AC004077) putative urease accessory protein [Arabidopsis thaliana] >gi|3337375 (AC004481) putative urease accessory protein [Arabidopsis thaliana]

Seq. No.	194970
Contig ID	16248_1.R1039
5'-most EST	LIB3135-042-Q1-K1-D10
Method	BLASTN
NCBI GI	g4324677
BLAST score	89
E value	5.0e-42
Match length	431
% identity	82
NCBI Description	Arabidopsis thaliana urease accessory protein UREG (UREG) mRNA, complete cds

Seq. No.	194971
Contig ID	16251_1.R1039
5'-most EST	LIB3135-042-Q1-K1-D3
Method	BLASTX
NCBI GI	g2583130
BLAST score	171
E value	7.0e-12
Match length	123
% identity	33
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	194972
Contig ID	16252_1.R1039
5'-most EST	LIB3148-017-Q1-K1-F7
Method	BLASTX
NCBI GI	g4455207
BLAST score	435
E value	6.0e-43
Match length	91

% identity	91
NCBI Description	(AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	194973
Contig ID	16264_1.R1039
5'-most EST	g5049748
Method	BLASTX
NCBI GI	g2130052
BLAST score	1112
E value	1.0e-127
Match length	285
% identity	75
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi|1296809|emb|CAA64545| (X95257) xylose isomerase [Hordeum vulgare]

Seq. No.	194974
Contig ID	16268_1.R1039
5'-most EST	LIB3135-042-Q1-K1-F1
Method	BLASTX
NCBI GI	g2129915
BLAST score	489
E value	3.0e-49
Match length	128
% identity	71
NCBI Description	ferredoxin precursor - sweet orange >gi|1360725|emb|CAA87068| (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	194975
Contig ID	16268_2.R1039
5'-most EST	LIB3147-050-Q1-K1-E5
Method	BLASTX
NCBI GI	g2129915
BLAST score	472
E value	2.0e-47
Match length	119
% identity	74
NCBI Description	ferredoxin precursor - sweet orange >gi|1360725|emb|CAA87068| (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	194976
Contig ID	16270_1.R1039
5'-most EST	uC-gsflnu33B137a03b1

Seq. No.	194977
Contig ID	16275_1.R1039
5'-most EST	LIB3166-016-P1-K1-A5
Method	BLASTX
NCBI GI	g4220541
BLAST score	609
E value	5.0e-63
Match length	296
% identity	49
NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]

Seq. No.	194978
Contig ID	16276_1.R1039
5'-most EST	LIB3166-002-Q1-K1-F6

Seq. No.	194979
Contig ID	16276_2.R1039
5'-most EST	uC-gsronu33B001b12b1
Method	BLASTX
NCBI GI	g478673
BLAST score	467
E value	3.0e-46
Match length	197
% identity	55
NCBI Description	proline-rich protein precursor - kidney bean >gi|21046|emb|CAA42942| (X60391) proline-rich protein [Phaseolus vulgaris]

Seq. No.	194980
Contig ID	16319_1.R1039
5'-most EST	LIB3197-021-Q1-M1-D10
Method	BLASTX
NCBI GI	g4468802
BLAST score	682
E value	2.0e-71
Match length	274
% identity	50
NCBI Description	(AL035601) cytochrome p450-like protein [Arabidopsis thaliana]

Seq. No.	194981
Contig ID	16326_1.R1039
5'-most EST	LIB3135-043-P1-K1-D5

Seq. No.	194982
Contig ID	16335_1.R1039
5'-most EST	g5048409
Method	BLASTX
NCBI GI	g2501572
BLAST score	122
E value	1.0e-14
Match length	144
% identity	35
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi|1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	194983
Contig ID	16336_1.R1039
5'-most EST	LIB3135-043-P1-K1-E6
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	2.0e-30
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi|481909|pir||S40089 ribosomal protein S25 - tomato >gi|435679|emb|CAA54132| (X76714)

ribosomal protein S25 [Lycopersicon esculentum]
>gi|1584836|prf||2123431A ribosomal protein S25
[Lycopersicon esculentum]

Seq. No.	194984
Contig ID	16336_2.R1039
5'-most EST	LIB3135-062-Q1-K1-F12
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	3.0e-30
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi|481909|pir||S40089 ribosomal protein S25 - tomato >gi|435679|emb|CAA54132| (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi|1584836|prf||2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	194985
Contig ID	16336_3.R1039
5'-most EST	uC-gsronu33B145b04b1
Method	BLASTX
NCBI GI	g4567232
BLAST score	372
E value	2.0e-35
Match length	82
% identity	89
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	194986
Contig ID	16344_1.R1039
5'-most EST	LIB3135-044-Q1-K1-F8
Method	BLASTX
NCBI GI	g1777386
BLAST score	163
E value	5.0e-11
Match length	87
% identity	51
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	194987
Contig ID	16352_1.R1039
5'-most EST	g5048379
Method	BLASTX
NCBI GI	g3892052
BLAST score	689
E value	2.0e-72
Match length	188
% identity	67
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	194988
Contig ID	16356_1.R1039
5'-most EST	LIB3146-051-Q1-K1-A7

Method	BLASTX
NCBI GI	g3947448
BLAST score	559
E value	6.0e-57
Match length	366
% identity	36
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi|3947543|emb|CAA88952| (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	194989
Contig ID	16365_1.R1039
5'-most EST	LIB3196-055-P1-M1-B11

Seq. No.	194990
Contig ID	16371_1.R1039
5'-most EST	LIB3189-012-P1-K1-H5
Method	BLASTX
NCBI GI	g3860259
BLAST score	215
E value	6.0e-17
Match length	112
% identity	45
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	194991
Contig ID	16376_1.R1039
5'-most EST	g5049837

Seq. No.	194992
Contig ID	16384_1.R1039
5'-most EST	uC-gsronu33B143d11b1

Seq. No.	194993
Contig ID	16394_1.R1039
5'-most EST	LIB3146-061-Q1-K1-E12

Seq. No.	194994
Contig ID	16407_1.R1039
5'-most EST	LIB3135-044-Q1-K1-E11
Method	BLASTX
NCBI GI	g4567281
BLAST score	337
E value	1.0e-31
Match length	130
% identity	54
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	194995
Contig ID	16408_1.R1039
5'-most EST	g5044402

Method	BLASTX
NCBI GI	g3785987
BLAST score	334
E value	7.0e-31
Match length	158
% identity	44
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	194996
Contig ID	16413_1.R1039
5'-most EST	LIB3135-044-Q1-K1-E7
Method	BLASTX
NCBI GI	g629722
BLAST score	170
E value	6.0e-12
Match length	125
% identity	32
NCBI Description	finger protein pcp1 - potato >gi|563623|emb|CAA57772| (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq. No.	194997
Contig ID	16414_1.R1039
5'-most EST	LIB3135-044-Q1-K1-E8

Seq. No.	194998
Contig ID	16418_1.R1039
5'-most EST	uC-gsronu33B109b02b1
Method	BLASTX
NCBI GI	g3395432
BLAST score	505
E value	4.0e-57
Match length	143
% identity	80
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	194999
Contig ID	16418_2.R1039
5'-most EST	uC-gsflnu33B133a01b1
Method	BLASTX
NCBI GI	g3395432
BLAST score	606
E value	4.0e-63
Match length	148
% identity	77
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	195000
Contig ID	16419_1.R1039
5'-most EST	LIB3135-044-Q1-K1-F12
Method	BLASTX
NCBI GI	g2947063
BLAST score	285
E value	2.0e-25
Match length	165
% identity	48
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No.	195001
Contig ID	16423_1.R1039
5'-most EST	LIB3135-044-Q1-K1-F5

Seq. No.	195002
Contig ID	16428_1.R1039
5'-most EST	LIB3166-058-P1-K1-D6

Seq. No.	195003
Contig ID	16435_1.R1039
5'-most EST	LIB3135-044-Q1-K1-G8
Method	BLASTX
NCBI GI	g3152583
BLAST score	391
E value	9.0e-38
Match length	175
% identity	51
NCBI Description	(AC002986) Contains similarity to inhibitor of apoptosis protein gb|U45881 from D. melanogaster. [Arabidopsis thaliana]

Seq. No.	195004
Contig ID	16436_1.R1039
5'-most EST	uC-gsflmaxxa009f10b1
Method	BLASTX
NCBI GI	g984756
BLAST score	415
E value	2.0e-40
Match length	106
% identity	75
NCBI Description	(Z54153) chilling-inducible protein [Oryza sativa]

Seq. No.	195005
Contig ID	16459_1.R1039
5'-most EST	LIB3135-045-Q1-K1-B11
Method	BLASTX
NCBI GI	g2462761
BLAST score	208
E value	4.0e-17
Match length	69
% identity	58
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	195006
Contig ID	16461_1.R1039
5'-most EST	uC-gsronu33B147b01b1

Seq. No.	195007
Contig ID	16466_1.R1039
5'-most EST	LIB3166-023-P1-K1-G9
Method	BLASTX
NCBI GI	g3451075
BLAST score	819
E value	6.0e-88

Match length	180
% identity	82
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	195008
Contig ID	16467_1.R1039
5'-most EST	LIB3145-019-Q1-K1-F2

Seq. No.	195009
Contig ID	16469_1.R1039
5'-most EST	LIB3135-045-Q1-K1-C1
Method	BLASTX
NCBI GI	g4038035
BLAST score	283
E value	5.0e-25
Match length	95
% identity	57
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	195010
Contig ID	16482_1.R1039
5'-most EST	LIB3135-045-Q1-K1-D8

Seq. No.	195011
Contig ID	16504_1.R1039
5'-most EST	uC-gsronu33b112c06b1

Seq. No.	195012
Contig ID	16510_1.R1039
5'-most EST	LIB3135-046-Q1-K1-A2

Seq. No.	195013
Contig ID	16515_1.R1039
5'-most EST	LIB3135-046-Q1-K1-A7
Method	BLASTX
NCBI GI	g2801536
BLAST score	646
E value	1.0e-67
Match length	187
% identity	63
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	195014
Contig ID	16517_1.R1039
5'-most EST	LIB3166-028-P1-K1-D9
Method	BLASTX
NCBI GI	g2245066
BLAST score	622
E value	1.0e-64
Match length	253
% identity	51
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	195015
Contig ID	16521_1.R1039
5'-most EST	LIB3135-046-Q1-K1-B12

Seq. No.	195016
Contig ID	16528_1.R1039
5'-most EST	LIB3145-015-Q1-K1-B3
Method	BLASTN
NCBI GI	g531251
BLAST score	34
E value	2.0e-09
Match length	77
% identity	96
NCBI Description	Apple mitochondrial atp9 gene for F0-ATPase subunit 9 (complete cds) and nad5 gene for NADH dehydrogehase subunit 5 (exon a and b)

Seq. No.	195017
Contig ID	16532_1.R1039
5'-most EST	LIB3135-046-Q1-K1-C11
Method	BLASTX
NCBI GI	g2498565
BLAST score	242
E value	4.0e-20
Match length	145
% identity	33
NCBI Description	C-MYC BINDING PROTEIN MM-1 >gi|1731809|dbj|BAA14006| (D89667) c-myc binding protein [Homo sapiens] >gi|4505743|ref|NP_002615.1|pPFDN5| prefoldin

Seq. No.	195018
Contig ID	16536_2.R1039
5'-most EST	LIB3135-046-Q1-K1-C4
Method	BLASTX
NCBI GI	g4056455
BLAST score	308
E value	5.0e-28
Match length	83
% identity	65
NCBI Description	(AC005990) Similar to gb|L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF|00484. EST gb|Z235745 comes from this gene. [Arabidopsis thaliana]

Seq. No.	195019
Contig ID	16562_1.R1039
5'-most EST	LIB3135-054-Q1-K1-A6
Method	BLASTX
NCBI GI	g3746069
BLAST score	153
E value	1.0e-09
Match length	97
% identity	35
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	195020
Contig ID	16564_1.R1039
5'-most EST	LIB3135-046-Q1-K1-F12

Seq. No.	195021
Contig ID	16594_1.R1039
5'-most EST	LIB3135-047-Q1-K1-A12
Method	BLASTX
NCBI GI	g1762933
BLAST score	695
E value	4.0e-73
Match length	193
% identity	70
NCBI Description	(U66263) tumor-related protein [Nicotiana tabacum]

Seq. No.	195022
Contig ID	16599_1.R1039
5'-most EST	LIB3135-047-Q1-K1-A7
Method	BLASTX
NCBI GI	g3687251
BLAST score	354
E value	1.0e-33
Match length	97
% identity	70
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	195023
Contig ID	16602_1.R1039
5'-most EST	g5050631
Method	BLASTX
NCBI GI	g4490302
BLAST score	699
E value	5.0e-75
Match length	224
% identity	71
NCBI Description	(AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No.	195024
Contig ID	16610_1.R1039
5'-most EST	LIB3135-047-Q1-K1-C11
Method	BLASTX
NCBI GI	g3510540
BLAST score	223
E value	1.0e-18
Match length	91
% identity	56
NCBI Description	(AF038815) expansin [Prunus armeniaca]

Seq. No.	195025
Contig ID	16610_2.R1039
5'-most EST	LIB3272-004-P1-K1-G12
Method	BLASTX
NCBI GI	g3510540
BLAST score	850
E value	2.0e-91
Match length	196
% identity	78
NCBI Description	(AF038815) expansin [Prunus armeniaca]

Seq. No.	195026
Contig ID	16622_1.R1039

5'-most EST	LIB3135-047-Q1-K1-D4
Method	BLASTX
NCBI GI	g4322327
BLAST score	715
E value	1.0e-75
Match length	229
% identity	59
NCBI Description	(AF080545) peptide transporter [Nepenthes alata]

Seq. No.	195027
Contig ID	16628_1.R1039
5'-most EST	LIB3135-047-Q1-K1-E10
Method	BLASTX
NCBI GI	g940288
BLAST score	139
E value	9.0e-16
Match length	84
% identity	53
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	195028
Contig ID	16642_1.R1039
5'-most EST	LIB3196-017-P1-M1-C4

Seq. No.	195029
Contig ID	16651_1.R1039
5'-most EST	LIB3135-047-Q1-K1-G5

Seq. No.	195030
Contig ID	16653_1.R1039
5'-most EST	uC-gsf1nu33B093f07b1
Method	BLASTX
NCBI GI	g3450842
BLAST score	225
E value	5.0e-18
Match length	85
% identity	53
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	195031
Contig ID	16655_1.R1039
5'-most EST	g5050181
Method	BLASTX
NCBI GI	g2827559
BLAST score	422
E value	2.0e-41
Match length	167
% identity	50
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi|3292808|emb|CAA19798| (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	195032
Contig ID	16655_2.R1039
5'-most EST	LIB3145-007-Q1-K1-C12

Method	BLASTX
NCBI GI	g2827559
BLAST score	352
E value	5.0e-33
Match length	148
% identity	47
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi|3292808|emb|CAA19798| (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	195033
Contig ID	16671_1.R1039
5'-most EST	LIB3149-015-Q1-K1-F11
Method	BLASTX
NCBI GI	g416730
BLAST score	742
E value	1.0e-78
Match length	200
% identity	67
NCBI Description	BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE) (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE) >gi|285064|pir||S27881 beta-alanine synthase - rat >gi|203106 (M97662) beta-alanine synthase [Rattus norvegicus]

Seq. No.	195034
Contig ID	16676_1.R1039
5'-most EST	LIB3197-048-Q1-M1-H9
Method	BLASTX
NCBI GI	g599956
BLAST score	340
E value	2.0e-31
Match length	160
% identity	47
NCBI Description	(Z31559) chloroplast inner membrane protein [Pisum sativum]

Seq. No.	195035
Contig ID	16677_1.R1039
5'-most EST	LIB3135-048-Q1-K1-B3
Method	BLASTX
NCBI GI	g1432058
BLAST score	510
E value	8.0e-52
Match length	157
% identity	67
NCBI Description	(U58540) WRKY2 [Petroselinum crispum]

Seq. No.	195036
Contig ID	16678_1.R1039
5'-most EST	uC-gsflnu33B009c08b1
Method	BLASTX
NCBI GI	g2244797
BLAST score	281
E value	1.0e-24
Match length	165
% identity	39
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195037
Contig ID	16683_1.R1039
5'-most EST	uC-gsflnu33B129g03b1
Method	BLASTX
NCBI GI	g100535
BLAST score	293
E value	2.0e-26
Match length	70
% identity	80
NCBI Description	hypothetical protein - swollen duckweed >gi|1929057|emb|CAA32236| (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	195038
Contig ID	16688_1.R1039
5'-most EST	LIB3135-048-Q1-K1-C4
Method	BLASTX
NCBI GI	g2980781
BLAST score	263
E value	8.0e-23
Match length	86
% identity	56
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	195039
Contig ID	16689_1.R1039
5'-most EST	uC-gsronu33B143g04b1

Seq. No.	195040
Contig ID	16692_1.R1039
5'-most EST	LIB3145-054-Q1-K1-G1
Method	BLASTX
NCBI GI	g2983642
BLAST score	523
E value	6.0e-53
Match length	285
% identity	40
NCBI Description	(AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]

Seq. No.	195041
Contig ID	16710_1.R1039
5'-most EST	LIB3146-019-Q1-K1-H2

Seq. No.	195042
Contig ID	16714_1.R1039
5'-most EST	LIB3146-054-Q1-K1-A6
Method	BLASTX
NCBI GI	g3046693
BLAST score	707
E value	6.0e-75
Match length	137
% identity	91
NCBI Description	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No.	195043

Contig ID 16715_1.R1039
5'-most EST LIB3135-048-Q1-K1-F1

Seq. No. 195044
Contig ID 16719_1.R1039
5'-most EST LIB3135-048-Q1-K1-F4

Seq. No. 195045
Contig ID 16730_1.R1039
5'-most EST LIB3135-048-Q1-K1-G5
Method BLASTX
NCBI GI g3582340
BLAST score 483
E value 2.0e-48
Match length 232
% identity 47
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 195046
Contig ID 16731_1.R1039
5'-most EST LIB3135-048-Q1-K1-G6
Method BLASTX
NCBI GI g4206196
BLAST score 526
E value 2.0e-53
Match length 131
% identity 77
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 195047
Contig ID 16739_1.R1039
5'-most EST uC-gsronu33B104d01b1
Method BLASTX
NCBI GI g3080365
BLAST score 278
E value 2.0e-24
Match length 112
% identity 51
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 195048
Contig ID 16753_1.R1039
5'-most EST LIB3166-028-P1-K1-D10
Method BLASTX
NCBI GI g1762945
BLAST score 465
E value 4.0e-46
Match length 156
% identity 58
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 195049
Contig ID 16765_1.R1039
5'-most EST LIB3146-044-Q1-K1-B4

Seq. No. 195050

Contig ID	16789_1.R1039
5'-most EST	LIB3165-028-P1-K1-D12
Method	BLASTX
NCBI GI	g3894172
BLAST score	774
E value	2.0e-82
Match length	276
% identity	50
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	195051
Contig ID	16794_1.R1039
5'-most EST	LIB3135-049-Q1-K1-G10

Seq. No.	195052
Contig ID	16807_1.R1039
5'-most EST	LIB3135-050-Q1-K1-A5
Method	BLASTX
NCBI GI	g1076511
BLAST score	165
E value	2.0e-11
Match length	42
% identity	81
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi|758250|emb|CAA59799| (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	195053
Contig ID	16811_1.R1039
5'-most EST	LIB3146-004-P1-K1-F10
Method	BLASTX
NCBI GI	g4557060
BLAST score	466
E value	5.0e-49
Match length	147
% identity	74
NCBI Description	(AC007154) putative chromosome-associated polypeptide, 5' partial [Arabidopsis thaliana]

Seq. No.	195054
Contig ID	16819_1.R1039
5'-most EST	LIB3148-053-Q1-K1-H12
Method	BLASTX
NCBI GI	g2982469
BLAST score	161
E value	1.0e-10
Match length	34
% identity	91
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	195055
Contig ID	16820_1.R1039
5'-most EST	LIB3135-050-Q1-K1-D7

Seq. No.	195056
Contig ID	16824_1.R1039

5'-most EST	LIB3135-050-Q1-K1-B8
Seq. No.	195057
Contig ID	16847_1.R1039
5'-most EST	LIB3135-050-Q1-K1-E1
Method	BLASTX
NCBI GI	g3236242
BLAST score	434
E value	9.0e-43
Match length	103
% identity	86
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]
Seq. No.	195058
Contig ID	16850_1.R1039
5'-most EST	LIB3149-039-Q1-K1-E7
Seq. No.	195059
Contig ID	16857_1.R1039
5'-most EST	LIB3135-050-Q1-K1-E9
Method	BLASTX
NCBI GI	g82263
BLAST score	546
E value	6.0e-62
Match length	145
% identity	75
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato
Seq. No.	195060
Contig ID	16876_1.R1039
5'-most EST	LIB3135-050-Q1-K1-G5
Seq. No.	195061
Contig ID	16882_1.R1039
5'-most EST	LIB3135-050-Q1-K1-H2
Seq. No.	195062
Contig ID	16885_1.R1039
5'-most EST	LIB3135-050-Q1-K1-H6
Method	BLASTX
NCBI GI	g2213590
BLAST score	161
E value	5.0e-22
Match length	127
% identity	49
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]
Seq. No.	195063
Contig ID	16891_1.R1039
5'-most EST	LIB3145-021-Q1-K1-A9
Method	BLASTX
NCBI GI	g4006878
BLAST score	385
E value	5.0e-37
Match length	155

% identity	47
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	195064
Contig ID	16892_1.R1039
5'-most EST	uC-gsflnu33B144a10b1
Method	BLASTX
NCBI GI	g2292907
BLAST score	486
E value	7.0e-49
Match length	196
% identity	25
NCBI Description	(Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No.	195065
Contig ID	16905_1.R1039
5'-most EST	LIB3146-023-Q1-K1-D9
Method	BLASTX
NCBI GI	g416650
BLAST score	451
E value	6.0e-45
Match length	147
% identity	60
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi|100304|pir||S16268 auxin-induced protein (clone pGNT35) - common tobacco >gi|19797|emb|CAA39706| (X56265) auxin-induced protein [Nicotiana tabacum] >gi|19801|emb|CAA39710| (X56269) auxin-induced protein [Nicotiana tabacum]

Seq. No.	195066
Contig ID	16906_1.R1039
5'-most EST	LIB3145-045-Q1-K1-A2

Seq. No.	195067
Contig ID	16906_2.R1039
5'-most EST	LIB3165-025-P1-K1-F8

Seq. No.	195068
Contig ID	16907_1.R1039
5'-most EST	LIB3135-051-Q1-K1-B8

Seq. No.	195069
Contig ID	16908_1.R1039
5'-most EST	uC-gsflnu33B037b11b1

Seq. No.	195070
Contig ID	16914_1.R1039
5'-most EST	LIB3197-049-Q1-M1-H7

Seq. No.	195071
Contig ID	16918_1.R1039
5'-most EST	LIB3166-048-P1-K1-A11
Method	BLASTX
NCBI GI	g3850108
BLAST score	488
E value	4.0e-49

Match length 190
% identity 51
NCBI Description (AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]

Seq. No. 195072
Contig ID 16919_1.R1039
5'-most EST uC-gsronu33B178b11b1
Method BLASTX
NCBI GI g4544434
BLAST score 464
E value 4.0e-46
Match length 144
% identity 67
NCBI Description (AC006955) putative DNA-directed RNA polymerase II [Arabidopsis thaliana]

Seq. No. 195073
Contig ID 16924_1.R1039
5'-most EST LIB3135-051-Q1-K1-D2
Method BLASTX
NCBI GI g4127781
BLAST score 176
E value 2.0e-12
Match length 38
% identity 23
NCBI Description (AJ012588) Notchless protein [Drosophila melanogaster]

Seq. No. 195074
Contig ID 16925_1.R1039
5'-most EST LIB3146-033-Q1-K1-E4
Method BLASTX
NCBI GI g122007
BLAST score 422
E value 3.0e-41
Match length 110
% identity 79
NCBI Description HISTONE H2A >gi|100161|pir||S11498 histone H2A - parsley >gi|20448|emb|CAA37828| (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No. 195075
Contig ID 16947_1.R1039
5'-most EST LIB3272-041-P1-K1-B2
Method BLASTX
NCBI GI g3184098
BLAST score 639
E value 2.0e-66
Match length 366
% identity 42
NCBI Description (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No. 195076
Contig ID 16952_1.R1039
5'-most EST LIB3165-047-Q1-K1-F6
Method BLASTX

NCBI GI	g729880
BLAST score	807
E value	2.0e-86
Match length	189
% identity	78
NCBI Description	CASEIN KINASE II BETA CHAIN (CK II) >gi|1076299|pir||S47967 casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis thaliana >gi|468264 (L22563) casein kinase II beta subunit CKB1 [Arabidopsis thaliana]

Seq. No.	195077
Contig ID	16955_1.R1039
5'-most EST	g5045177
Method	BLASTX
NCBI GI	g3193298
BLAST score	167
E value	3.0e-11
Match length	109
% identity	36
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	195078
Contig ID	16964_1.R1039
5'-most EST	g5048729
Method	BLASTX
NCBI GI	g462679
BLAST score	206
E value	9.0e-16
Match length	172
% identity	34
NCBI Description	MYOSIN IB HEAVY CHAIN >gi|102252|pir||A33284 myosin heavy chain IB - slime mold (Dictyostelium discoideum) >gi|167839 (M26037) myosin I heavy chain [Dictyostelium discoideum]

Seq. No.	195079
Contig ID	16970_1.R1039
5'-most EST	LIB3148-010-Q1-K1-C12

Seq. No.	195080
Contig ID	17002_1.R1039
5'-most EST	LIB3135-052-Q1-K1-C9

Seq. No.	195081
Contig ID	17003_2.R1039
5'-most EST	LIB3135-052-Q1-K1-D1

Seq. No.	195082
Contig ID	17010_1.R1039
5'-most EST	LIB3166-007-P1-K1-F5
Method	BLASTX
NCBI GI	g3250676
BLAST score	325
E value	3.0e-35
Match length	109
% identity	76
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	195083
Contig ID	17011_1.R1039
5'-most EST	LIB3196-059-P1-M1-E4
Method	BLASTX
NCBI GI	g542184
BLAST score	451
E value	1.0e-44
Match length	229
% identity	44
NCBI Description	globulin-1S, GLB1S - maize

Seq. No.	195084
Contig ID	17016_1.R1039
5'-most EST	LIB3189-036-P1-K1-H4
Method	BLASTX
NCBI GI	g1174867
BLAST score	336
E value	2.0e-31
Match length	72
% identity	88
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi|633687|emb|CAA55862| (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi|1094912|prf||2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No.	195085
Contig ID	17018_1.R1039
5'-most EST	LIB3135-052-Q1-K1-E6

Seq. No.	195086
Contig ID	17022_1.R1039
5'-most EST	LIB3135-052-Q1-K1-F10
Method	BLASTX
NCBI GI	g2204224
BLAST score	214
E value	5.0e-17
Match length	82
% identity	50
NCBI Description	(Y13849) alpha-galactosidase [Hordeum vulgare]

Seq. No.	195087
Contig ID	17023_1.R1039
5'-most EST	LIB3149-024-Q1-K1-C4
Method	BLASTX
NCBI GI	g1743354
BLAST score	961
E value	1.0e-104
Match length	223
% identity	81
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	195088
Contig ID	17043_1.R1039
5'-most EST	LIB3197-003-P1-M1-B1

Seq. No.	195089
Contig ID	17046_1.R1039
5'-most EST	LIB3135-052-Q1-K1-H5
Method	BLASTX
NCBI GI	g3878494
BLAST score	224
E value	5.0e-18
Match length	125
% identity	34
NCBI Description	(Z79602) predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST EMBL:T01631 comes from this gene; cDNA EST EMBL:M88949 comes from this gene [Caenorhabditis elegans]

Seq. No.	195090
Contig ID	17049_1.R1039
5'-most EST	g5045935
Method	BLASTX
NCBI GI	g2244847
BLAST score	307
E value	1.0e-27
Match length	223
% identity	35
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	195091
Contig ID	17049_2.R1039
5'-most EST	LIB3145-056-Q1-K1-A8
Method	BLASTN
NCBI GI	g3985934
BLAST score	54
E value	2.0e-21
Match length	218
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	195092
Contig ID	17054_1.R1039
5'-most EST	g3326103
Method	BLASTX
NCBI GI	g2245066
BLAST score	664
E value	4.0e-69
Match length	376
% identity	37
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	195093
Contig ID	17055_1.R1039
5'-most EST	LIB3135-053-Q1-K1-A4

Seq. No.	195094
Contig ID	17060_1.R1039
5'-most EST	LIB3135-053-Q1-K1-B10
Method	BLASTX

NCBI GI g4512661
BLAST score 197
E value 1.0e-15
Match length 55
% identity 62
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana] >gi|4544468|gb|AAD22375.1|AC006580_7 (AC006580) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 195095
Contig ID 17062_1.R1039
5'-most EST g3326652
Method BLASTX
NCBI GI g1176658
BLAST score 230
E value 9.0e-19
Match length 82
% identity 52
NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi|726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No. 195096
Contig ID 17069_1.R1039
5'-most EST uC-gsflmaxxa046h08b1
Method BLASTX
NCBI GI g2736147
BLAST score 729
E value 3.0e-77
Match length 234
% identity 56
NCBI Description (AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi|3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No. 195097
Contig ID 17081_1.R1039
5'-most EST LIB3135-053-Q1-K1-D11

Seq. No. 195098
Contig ID 17082_1.R1039
5'-most EST LIB3135-053-Q1-K1-D2

Seq. No. 195099
Contig ID 17095_1.R1039
5'-most EST LIB3147-038-Q1-K2-G8
Method BLASTX
NCBI GI g2245125
BLAST score 332
E value 1.0e-30
Match length 166
% identity 47
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 195100
Contig ID 17109_1.R1039
5'-most EST LIB3189-015-P1-K1-F10

Method	BLASTX
NCBI GI	g1351303
BLAST score	397
E value	1.0e-38
Match length	124
% identity	68
NCBI Description	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi|619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana]

Seq. No.	195101
Contig ID	17113_1.R1039
5'-most EST	LIB3135-053-Q1-K1-G12
Method	BLASTX
NCBI GI	g3757515
BLAST score	455
E value	2.0e-45
Match length	142
% identity	64
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195102
Contig ID	17116_1.R1039
5'-most EST	LIB3135-053-Q1-K1-G4
Method	BLASTX
NCBI GI	g3746069
BLAST score	154
E value	7.0e-10
Match length	147
% identity	28
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	195103
Contig ID	17117_1.R1039
5'-most EST	LIB3135-053-Q1-K1-G5

Seq. No.	195104
Contig ID	17121_1.R1039
5'-most EST	uC-gsronu33B106c03b2
Method	BLASTX
NCBI GI	g3702326
BLAST score	862
E value	8.0e-93
Match length	194
% identity	81
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195105
Contig ID	17123_2.R1039
5'-most EST	LIB3145-042-Q1-K1-G7
Method	BLASTX
NCBI GI	g4531444
BLAST score	860
E value	1.0e-92
Match length	198
% identity	79

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 195106
Contig ID 17133_1.R1039
5'-most EST LIB3135-055-Q1-K1-H6

Seq. No. 195107
Contig ID 17146_1.R1039
5'-most EST LIB3135-054-Q1-K1-B4

Seq. No. 195108
Contig ID 17152_1.R1039
5'-most EST uC-gsflmaxxa076g09b1
Method BLASTN
NCBI GI g3510339
BLAST score 38
E value 1.0e-11
Match length 157
% identity 84
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 195109
Contig ID 17152_3.R1039
5'-most EST LIB3146-010-Q1-K1-C8

Seq. No. 195110
Contig ID 17153_1.R1039
5'-most EST LIB3146-049-Q1-K1-H12
Method BLASTX
NCBI GI g1161167
BLAST score 314
E value 7.0e-29
Match length 101
% identity 53
NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]

Seq. No. 195111
Contig ID 17160_1.R1039
5'-most EST g5047570
Method BLASTX
NCBI GI g544358
BLAST score 319
E value 3.0e-29
Match length 140
% identity 41
NCBI Description FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (FVT-1) >gi|481027|pir||S37652 FVT1 protein - human >gi|296186|emb|CAA45197| (X63657) FVT1 gene is disrupted in a t(2;18) chromosomal translocation involving Ig kappa gene in a follicular lymphoma [Homo sapiens] >gi|4503817|ref|NP_002026.1|pFVT1| follicular lymphoma variant translocation

Seq. No. 195112
Contig ID 17167_1.R1039
5'-most EST LIB3135-054-Q1-K1-D4

Method	BLASTX
NCBI GI	g3421109
BLAST score	970
E value	1.0e-105
Match length	204
% identity	91
NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No.	195113
Contig ID	17172_1.R1039
5'-most EST	LIB3147-008-Q1-K1-A1
Method	BLASTX
NCBI GI	g4467137
BLAST score	655
E value	1.0e-68
Match length	180
% identity	68
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	195114
Contig ID	17177_1.R1039
5'-most EST	LIB3146-025-Q1-K2-A6

Seq. No.	195115
Contig ID	17183_1.R1039
5'-most EST	LIB3189-046-P1-K1-D10
Method	BLASTX
NCBI GI	g4538929
BLAST score	246
E value	1.0e-20
Match length	63
% identity	43
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	195116
Contig ID	17183_2.R1039
5'-most EST	LIB3272-023-P1-K1-A12
Method	BLASTX
NCBI GI	g4538929
BLAST score	433
E value	1.0e-42
Match length	178
% identity	42
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	195117
Contig ID	17187_1.R1039
5'-most EST	LIB3135-054-Q1-K1-F2

Seq. No.	195118
Contig ID	17205_1.R1039
5'-most EST	LIB3135-054-Q1-K1-H4

Seq. No. 195119

Contig ID	17211_1.R1039
5'-most EST	LIB3135-055-Q1-K1-A11
Seq. No.	195120
Contig ID	17214_1.R1039
5'-most EST	LIB3146-035-P1-K1-H5
Seq. No.	195121
Contig ID	17215_1.R1039
5'-most EST	LIB3135-055-Q1-K1-A5
Method	BLASTX
NCBI GI	g3775999
BLAST score	450
E value	1.0e-44
Match length	149
% identity	64
NCBI Description	(AJ010463) RNA helicase [Arabidopsis thaliana]
Seq. No.	195122
Contig ID	17216_1.R1039
5'-most EST	LIB3148-008-Q1-K1-H5
Method	BLASTX
NCBI GI	g2811025
BLAST score	751
E value	6.0e-80
Match length	188
% identity	70
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi|1944181|dbj|BAA19607| (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.	195123
Contig ID	17217_1.R1039
5'-most EST	LIB3145-039-Q1-K1-E3
Method	BLASTX
NCBI GI	g4101720
BLAST score	162
E value	7.0e-12
Match length	119
% identity	34
NCBI Description	(AF006466) lymphocyte specific formin related protein [Mus musculus]
Seq. No.	195124
Contig ID	17219_1.R1039
5'-most EST	g5049844
Method	BLASTX
NCBI GI	g4103635
BLAST score	364
E value	3.0e-34
Match length	217
% identity	40
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]
Seq. No.	195125
Contig ID	17220_1.R1039
5'-most EST	LIB3135-055-Q1-K1-D8

Seq. No.	195126
Contig ID	17231_1.R1039
5'-most EST	g5046038
Method	BLASTX
NCBI GI	g231551
BLAST score	181
E value	6.0e-13
Match length	120
% identity	3
NCBI Description	ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)

Seq. No.	195127
Contig ID	17233_1.R1039
5'-most EST	LIB3135-055-Q1-K1-C2
Method	BLASTX
NCBI GI	g3757521
BLAST score	814
E value	3.0e-87
Match length	189
% identity	79
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	195128
Contig ID	17234_1.R1039
5'-most EST	uC-gsflmaxxa002h11b1
Method	BLASTX
NCBI GI	g2407800
BLAST score	526
E value	1.0e-53
Match length	130
% identity	83
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	195129
Contig ID	17237_1.R1039
5'-most EST	uC-gsflmaxxa048e09b1
Method	BLASTX
NCBI GI	g4457221
BLAST score	309
E value	5.0e-28
Match length	100
% identity	69
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	195130
Contig ID	17240_1.R1039
5'-most EST	LIB3147-029-Q1-K1-D1
Method	BLASTX
NCBI GI	g4105794
BLAST score	155
E value	3.0e-13
Match length	114
% identity	39
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	195131
Contig ID	17244_1.R1039
5'-most EST	LIB3135-055-Q1-K1-D2
Method	BLASTX
NCBI GI	g2462753
BLAST score	964
E value	1.0e-105
Match length	214
% identity	79
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	195132
Contig ID	17255_1.R1039
5'-most EST	LIB3145-046-Q1-K1-C3
Method	BLASTX
NCBI GI	g4099914
BLAST score	308
E value	4.0e-28
Match length	109
% identity	59
NCBI Description	(U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No.	195133
Contig ID	17263_1.R1039
5'-most EST	LIB3166-042-P1-K1-H8
Method	BLASTX
NCBI GI	g3122139
BLAST score	919
E value	3.0e-99
Match length	397
% identity	48
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) (ATP-STIMULATED GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP) >gi|484372|pir||JN0606 ATP-stimulated glucocorticoid-receptor translocation promoter protein - rat >gi|433211|dbj|BAA03677| (D16102) ATP-stimulated glucocorticoid-receptor translocaton promoter [Rattus rattus]

Seq. No.	195134
Contig ID	17264_1.R1039
5'-most EST	LIB3135-059-Q1-K1-H9
Method	BLASTX
NCBI GI	g2462762
BLAST score	266
E value	3.0e-23
Match length	69
% identity	75
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	195135
Contig ID	17271_1.R1039
5'-most EST	LIB3149-023-Q1-K1-A4

Method	BLASTX
NCBI GI	g2160182
BLAST score	168
E value	8.0e-12
Match length	59
% identity	54
NCBI Description	(AC000132) ESTs gb|ATTS1236,gb|T43334,gb|N97019,gb|AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	195136
Contig ID	17282_1.R1039
5'-most EST	g5046331
Method	BLASTX
NCBI GI	g4406759
BLAST score	249
E value	5.0e-21
Match length	133
% identity	44
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195137
Contig ID	17289_1.R1039
5'-most EST	LIB3165-040-Q1-K1-D10

Seq. No.	195138
Contig ID	17290_1.R1039
5'-most EST	LIB3272-034-P1-K1-B4

Seq. No.	195139
Contig ID	17293_2.R1039
5'-most EST	LIB3135-056-Q1-K1-A10
Method	BLASTX
NCBI GI	g1514643
BLAST score	600
E value	1.0e-62
Match length	175
% identity	35
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	195140
Contig ID	17296_1.R1039
5'-most EST	uC-gsronu33B159c01b1
Method	BLASTX
NCBI GI	g3193332
BLAST score	137
E value	6.0e-13
Match length	135
% identity	41
NCBI Description	(AF069299) similar to Arabidopsis AT-hook protein 1 (GB:AJ222585) [Arabidopsis thaliana]

Seq. No.	195141
Contig ID	17303_1.R1039
5'-most EST	LIB3145-047-Q1-K1-D12

Seq. No.	195142
Contig ID	17306_1.R1039

5'-most EST	LIB3135-056-Q1-K1-B2
Seq. No.	195143
Contig ID	17314_1.R1039
5'-most EST	LIB3166-023-P1-K1-E11
Method	BLASTX
NCBI GI	g1076621
BLAST score	561
E value	1.0e-57
Match length	134
% identity	77
NCBI Description	cytochrome b5 - common tobacco >gi|296386|emb|CAA50575| (X71441) cytochrome b5 [Nicotiana tabacum]
Seq. No.	195144
Contig ID	17315_1.R1039
5'-most EST	LIB3146-017-Q1-K1-E12
Method	BLASTX
NCBI GI	g2583130
BLAST score	157
E value	2.0e-10
Match length	165
% identity	33
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
Seq. No.	195145
Contig ID	17323_1.R1039
5'-most EST	LIB3149-047-Q1-K1-H6
Method	BLASTX
NCBI GI	g3193303
BLAST score	202
E value	9.0e-16
Match length	100
% identity	40
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]
Seq. No.	195146
Contig ID	17325_1.R1039
5'-most EST	LIB3149-019-Q1-K1-B10
Method	BLASTX
NCBI GI	g3212610
BLAST score	130
E value	2.0e-15
Match length	164
% identity	47
NCBI Description	Chain A, Sulfite Oxidase From Chicken Liver >gi|3212611|pdb|1SOX|B Chain B, Sulfite Oxidase From Chicken Liver
Seq. No.	195147
Contig ID	17332_1.R1039
5'-most EST	uC-gsronu33B167g11b1
Method	BLASTX

NCBI GI	g3759184
BLAST score	367
E value	3.0e-47
Match length	225
% identity	43
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	195148
Contig ID	17333_1.R1039
5'-most EST	LIB3146-047-Q1-K1-H12

Seq. No.	195149
Contig ID	17345_1.R1039
5'-most EST	LIB3135-056-Q1-K1-F4

Seq. No.	195150
Contig ID	17357_1.R1039
5'-most EST	LIB3197-010-P1-M1-B4
Method	BLASTN
NCBI GI	g2924257
BLAST score	63
E value	8.0e-27
Match length	275
% identity	89
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	195151
Contig ID	17372_1.R1039
5'-most EST	uC-gsflnu33B127h11b1
Method	BLASTX
NCBI GI	g3402703
BLAST score	205
E value	9.0e-16
Match length	225
% identity	29
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195152
Contig ID	17374_1.R1039
5'-most EST	LIB3196-045-P1-M1-G11

Seq. No.	195153
Contig ID	17377_1.R1039
5'-most EST	LIB3135-057-Q1-K1-A5

Seq. No.	195154
Contig ID	17389_1.R1039
5'-most EST	uC-gsflnu33B066e01b1
Method	BLASTX
NCBI GI	g2129742
BLAST score	225
E value	5.0e-20
Match length	77
% identity	66
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi|790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen

(bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi|2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	195155
Contig ID	17398_1.R1039
5'-most EST	g5048245
Method	BLASTX
NCBI GI	g2244781
BLAST score	453
E value	7.0e-45
Match length	237
% identity	26
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195156
Contig ID	17401_1.R1039
5'-most EST	uC-gsronu33B167e11b1
Method	BLASTX
NCBI GI	g541816
BLAST score	1272
E value	1.0e-140
Match length	305
% identity	78
NCBI Description	protein kinase - common ice plant >gi|457689|emb|CAA82990| (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	195157
Contig ID	17408_1.R1039
5'-most EST	LIB3135-057-Q1-K1-D6
Method	BLASTX
NCBI GI	g3603230
BLAST score	276
E value	3.0e-24
Match length	129
% identity	41
NCBI Description	(AF026850) cytochrome oxidase assembly factor [Homo sapiens]

Seq. No.	195158
Contig ID	17418_1.R1039
5'-most EST	uC-gsflnu33B026e07b1
Method	BLASTX
NCBI GI	g4314356
BLAST score	231
E value	1.0e-19
Match length	152
% identity	36
NCBI Description	(AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No.	195159
Contig ID	17419_1.R1039
5'-most EST	LIB3135-057-Q1-K1-F2
Method	BLASTX
NCBI GI	g2062164
BLAST score	635

E value	3.0e-66
Match length	232
% identity	26
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	195160
Contig ID	17421_1.R1039
5'-most EST	LIB3149-054-Q1-K1-D5
Method	BLASTX
NCBI GI	g2739379
BLAST score	231
E value	9.0e-19
Match length	82
% identity	52
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195161
Contig ID	17422_1.R1039
5'-most EST	LIB3135-057-Q1-K1-F6
Method	BLASTX
NCBI GI	g2129755
BLAST score	821
E value	5.0e-88
Match length	249
% identity	69
NCBI Description	tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi|619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi|1585768|prf||2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	195162
Contig ID	17427_1.R1039
5'-most EST	LIB3135-057-Q1-K1-G2
Method	BLASTX
NCBI GI	g1928991
BLAST score	379
E value	2.0e-36
Match length	115
% identity	69
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]

Seq. No.	195163
Contig ID	17431_1.R1039
5'-most EST	LIB3135-057-Q1-K1-G6
Method	BLASTX
NCBI GI	g417739
BLAST score	280
E value	8.0e-25
Match length	73
% identity	75
NCBI Description	MITOCHONDRIAL RIBOSOMAL PROTEIN S19 >gi|319911|pir||R3PJ19 ribosomal protein S19 - garden petunia mitochondrion

Seq. No.	195164
Contig ID	17433_1.R1039

5'-most EST	uC-gsronu33B179f09b1
Seq. No.	195165
Contig ID	17452_1.R1039
5'-most EST	uC-gsronu33B134c07b1
Method	BLASTX
NCBI GI	g3953471
BLAST score	1083
E value	1.0e-118
Match length	302
% identity	66
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]
Seq. No.	195166
Contig ID	17459_1.R1039
5'-most EST	LIB3135-058-Q1-K1-B9
Seq. No.	195167
Contig ID	17461_1.R1039
5'-most EST	LIB3147-036-Q1-K1-D5
Method	BLASTX
NCBI GI	g2191150
BLAST score	418
E value	6.0e-41
Match length	115
% identity	32
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
Seq. No.	195168
Contig ID	17475_1.R1039
5'-most EST	LIB3135-058-Q1-K1-D3
Method	BLASTX
NCBI GI	g4105683
BLAST score	700
E value	5.0e-74
Match length	161
% identity	76
NCBI Description	(AF049892) unknown [Oryza sativa] >gi|4105692 (AF050155) embryo-specific protein [Oryza sativa subsp. indica]
Seq. No.	195169
Contig ID	17476_1.R1039
5'-most EST	LIB3145-058-Q1-K1-A11
Seq. No.	195170
Contig ID	17483_1.R1039
5'-most EST	LIB3165-007-P1-K1-F2
Seq. No.	195171
Contig ID	17484_1.R1039
5'-most EST	LIB3189-014-P1-K1-A8
Seq. No.	195172
Contig ID	17486_1.R1039
5'-most EST	LIB3166-028-P1-K1-G3

Seq. No.	195173
Contig ID	17489_1.R1039
5'-most EST	uC-gsronu33B004h05b1
Method	BLASTX
NCBI GI	g2765837
BLAST score	223
E value	7.0e-18
Match length	99
% identity	52
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	195174
Contig ID	17495_1.R1039
5'-most EST	LIB3146-041-Q1-K1-F5
Method	BLASTX
NCBI GI	g3775993
BLAST score	158
E value	2.0e-10
Match length	30
% identity	97
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.	195175
Contig ID	17495_2.R1039
5'-most EST	LIB3135-058-Q1-K1-F3

Seq. No.	195176
Contig ID	17498_1.R1039
5'-most EST	LIB3146-046-Q1-K1-E9
Method	BLASTX
NCBI GI	g2352084
BLAST score	375
E value	7.0e-36
Match length	110
% identity	71
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	195177
Contig ID	17519_1.R1039
5'-most EST	LIB3148-034-Q1-K1-E1
Method	BLASTX
NCBI GI	g1085595
BLAST score	164
E value	3.0e-11
Match length	51
% identity	63
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase - Prunus persica >gi|452671|emb|CAA54449| (X77232) 1-aminocyclopropane-1-carboxylate oxidase [Prunus persica] >gi|3510500 (AF026793) 1-aminocyclopropane-1-carboxylate oxidase; ACC oxidase [Prunus armeniaca]

Seq. No.	195178
Contig ID	17522_1.R1039
5'-most EST	uC-gsronu33B169e10b1
Method	BLASTN
NCBI GI	g3135692

BLAST score	43
E value	1.0e-14
Match length	203
% identity	84
NCBI Description	Gossypium hirsutum tissue-type fiber glutathione S-transferase (GST) mRNA, partial cds

Seq. No.	195179
Contig ID	17522_3.R1039
5'-most EST	uC-gsronu33B114d03b1
Method	BLASTX
NCBI GI	g2213595
BLAST score	577
E value	3.0e-59
Match length	220
% identity	52
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	195180
Contig ID	17527_1.R1039
5'-most EST	LIB3166-015-P1-K1-D9
Method	BLASTX
NCBI GI	g4262236
BLAST score	237
E value	1.0e-35
Match length	116
% identity	65
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	195181
Contig ID	17528_1.R1039
5'-most EST	LIB3135-059-Q1-K1-B10
Method	BLASTX
NCBI GI	g4006859
BLAST score	186
E value	3.0e-15
Match length	82
% identity	55
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	195182
Contig ID	17540_1.R1039
5'-most EST	uC-gsronu33B127d09b1
Method	BLASTX
NCBI GI	g1458245
BLAST score	426
E value	1.0e-41
Match length	251
% identity	38
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	195183
Contig ID	17551_1.R1039

5'-most EST	g5048687
Method	BLASTX
NCBI GI	g3759184
BLAST score	478
E value	6.0e-48
Match length	159
% identity	58
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	195184
Contig ID	17560_1.R1039
5'-most EST	LIB3165-026-P1-K1-D9
Method	BLASTX
NCBI GI	g2739380
BLAST score	272
E value	8.0e-24
Match length	104
% identity	55
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195185
Contig ID	17562_1.R1039
5'-most EST	LIB3166-021-P1-K1-F3

Seq. No.	195186
Contig ID	17565_1.R1039
5'-most EST	uC-gsronu33B160b10b1
Method	BLASTX
NCBI GI	g3328587
BLAST score	300
E value	3.0e-27
Match length	146
% identity	45
NCBI Description	(AE001292) CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia trachomatis]

Seq. No.	195187
Contig ID	17571_1.R1039
5'-most EST	LIB3135-060-Q1-K1-B6
Method	BLASTX
NCBI GI	g2832357
BLAST score	359
E value	1.0e-33
Match length	128
% identity	57
NCBI Description	(Y14071) HMG protein [Arabidopsis thaliana] >gi|3068715 (AF049236) unknown [Arabidopsis thaliana]

Seq. No.	195188
Contig ID	17576_1.R1039
5'-most EST	uC-gsflmaxxa057h08b1

Seq. No.	195189
Contig ID	17576_2.R1039
5'-most EST	uC-gsronu33B144e09b1
Method	BLASTX
NCBI GI	g3335341

BLAST score 161
E value 1.0e-10
Match length 116
% identity 41
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 195190
Contig ID 17579_1.R1039
5'-most EST LIB3146-017-Q1-K1-E7
Method BLASTX
NCBI GI g3935168
BLAST score 306
E value 2.0e-27
Match length 78
% identity 69
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 195191
Contig ID 17580_1.R1039
5'-most EST g3325648

Seq. No. 195192
Contig ID 17581_1.R1039
5'-most EST g3326148
Method BLASTX
NCBI GI g2739389
BLAST score 404
E value 8.0e-45
Match length 201
% identity 30
NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No. 195193
Contig ID 17591_1.R1039
5'-most EST LIB3149-047-Q1-K1-H8

Seq. No. 195194
Contig ID 17597_1.R1039
5'-most EST LIB3166-010-P1-K1-B11
Method BLASTX
NCBI GI g1296816
BLAST score 787
E value 5.0e-94
Match length 229
% identity 87
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]

Seq. No. 195195
Contig ID 17597_2.R1039
5'-most EST uC-gsflmaxxa040b06b1
Method BLASTX
NCBI GI g1345785
BLAST score 1134
E value 1.0e-124
Match length 271
% identity 80
NCBI Description CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)

>gi|567935|dbj|BAA05640| (D26593) chalcone synthase [Camellia sinensis]

Seq. No.	195196
Contig ID	17597_3.R1039
5'-most EST	LIB3145-038-Q1-K1-F1
Method	BLASTN
NCBI GI	g1777714
BLAST score	62
E value	4.0e-26
Match length	66
% identity	98
NCBI Description	Photinia fraseri 18S ribosomal RNA gene, partial sequence

Seq. No.	195197
Contig ID	17611_2.R1039
5'-most EST	LIB3135-060-Q1-K1-F5
Method	BLASTX
NCBI GI	g3264763
BLAST score	240
E value	3.0e-20
Match length	83
% identity	61
NCBI Description	(AF071891) 40S ribosomal protein S4 [Prunus armeniaca]

Seq. No.	195198
Contig ID	17612_1.R1039
5'-most EST	LIB3135-060-Q1-K1-F6
Method	BLASTX
NCBI GI	g3776566
BLAST score	344
E value	2.0e-32
Match length	96
% identity	75
NCBI Description	(AC005388) Strong similarity to histone H2A gb|AJ006768 from Cicer arietinum. [Arabidopsis thaliana]

Seq. No.	195199
Contig ID	17613_1.R1039
5'-most EST	LIB3135-060-Q1-K1-F7
Method	BLASTN
NCBI GI	g3204128
BLAST score	50
E value	4.0e-19
Match length	230
% identity	80
NCBI Description	Cicer arietinum mRNA for histone H2A

Seq. No.	195200
Contig ID	17622_1.R1039
5'-most EST	LIB3135-060-Q1-K1-H1
Method	BLASTX
NCBI GI	g2660670
BLAST score	698
E value	1.0e-73
Match length	171
% identity	80

NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	195201
Contig ID	17632_1.R1039
5'-most EST	LIB3146-021-Q1-K1-H7
Method	BLASTN
NCBI GI	g3449315
BLAST score	53
E value	1.0e-20
Match length	334
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	195202
Contig ID	17633_1.R1039
5'-most EST	LIB3146-028-Q1-K1-B4

Seq. No.	195203
Contig ID	17641_1.R1039
5'-most EST	LIB3145-026-Q1-K1-F1
Method	BLASTX
NCBI GI	g4191782
BLAST score	737
E value	2.0e-78
Match length	160
% identity	84
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	195204
Contig ID	17649_1.R1039
5'-most EST	LIB3146-016-Q1-K1-H2
Method	BLASTN
NCBI GI	g2599091
BLAST score	90
E value	7.0e-43
Match length	397
% identity	85
NCBI Description	Arabidopsis thaliana WD-40 repeat protein MSI4 (MSI4) mRNA, complete cds

Seq. No.	195205
Contig ID	17660_1.R1039
5'-most EST	LIB3147-024-Q1-K1-F11

Seq. No.	195206
Contig ID	17663_1.R1039
5'-most EST	LIB3135-061-Q1-K1-D3

Seq. No.	195207
Contig ID	17668_1.R1039
5'-most EST	LIB3272-005-P1-K1-E5
Method	BLASTX
NCBI GI	g479713
BLAST score	571
E value	6.0e-59

Match length	128
% identity	86
NCBI Description	aspartate carbamoyltransferase - tomato

Seq. No.	195208
Contig ID	17677_1.R1039
5'-most EST	LIB3135-061-Q1-K1-E9
Method	BLASTN
NCBI GI	g495660
BLAST score	52
E value	3.0e-20
Match length	352
% identity	79
NCBI Description	Pisum sativum aspartate transcarbamoylase (pyrB2) mRNA, complete cds

Seq. No.	195209
Contig ID	17678_1.R1039
5'-most EST	LIB3135-061-Q1-K1-F1

Seq. No.	195210
Contig ID	17679_1.R1039
5'-most EST	LIB3189-022-P1-K1-C6

Seq. No.	195211
Contig ID	17689_1.R1039
5'-most EST	g3326037
Method	BLASTX
NCBI GI	g4457221
BLAST score	298
E value	2.0e-26
Match length	136
% identity	51
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	195212
Contig ID	17689_2.R1039
5'-most EST	uC-gsflmaxxa088e03b1

Seq. No.	195213
Contig ID	17689_3.R1039
5'-most EST	LIB3272-017-P1-K1-E2
Method	BLASTN
NCBI GI	g1769890
BLAST score	54
E value	2.0e-21
Match length	98
% identity	89
NCBI Description	A.thaliana ATB2 gene

Seq. No.	195214
Contig ID	17694_1.R1039
5'-most EST	g5048076
Method	BLASTN
NCBI GI	g4235150
BLAST score	42

E value	5.0e-14
Match length	506
% identity	81
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	195215
Contig ID	17701_2.R1039
5'-most EST	LIB3135-061-Q1-K1-H10

Seq. No.	195216
Contig ID	17705_1.R1039
5'-most EST	uC-gsronu33B106b01b2
Method	BLASTX
NCBI GI	g2245139
BLAST score	191
E value	3.0e-14
Match length	62
% identity	56
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195217
Contig ID	17707_1.R1039
5'-most EST	LIB3196-005-P1-M1-B3
Method	BLASTX
NCBI GI	g3023858
BLAST score	992
E value	1.0e-108
Match length	204
% identity	48
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi|1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	195218
Contig ID	17707_2.R1039
5'-most EST	LIB3272-041-P1-K1-H3
Method	BLASTX
NCBI GI	g3023858
BLAST score	431
E value	3.0e-42
Match length	93
% identity	86
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi|1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	195219
Contig ID	17714_1.R1039
5'-most EST	LIB3189-015-P1-K1-D5
Method	BLASTX
NCBI GI	g710626
BLAST score	287
E value	3.0e-25
Match length	136
% identity	60
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi|3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi|3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	195220
Contig ID	17725_1.R1039
5'-most EST	uC-gsflnu33B108e07b1
Method	BLASTX
NCBI GI	g4220535
BLAST score	912
E value	1.0e-154
Match length	313
% identity	89
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	195221
Contig ID	17733_1.R1039
5'-most EST	uC-gsflmaxxa097d08b1

Seq. No.	195222
Contig ID	17733_2.R1039
5'-most EST	LIB3197-023-Q1-M1-H1

Seq. No.	195223
Contig ID	17736_1.R1039
5'-most EST	LIB3135-062-Q1-K1-C3
Method	BLASTX
NCBI GI	g4455270
BLAST score	205
E value	6.0e-16
Match length	57
% identity	63
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	195224
Contig ID	17737_1.R1039
5'-most EST	uC-gsflnu33B115d09b1
Method	BLASTX
NCBI GI	g2829751
BLAST score	215
E value	5.0e-17
Match length	114
% identity	39
NCBI Description	MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) >gi|1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi|2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi]

Seq. No.	195225
Contig ID	17739_1.R1039
5'-most EST	LIB3135-062-Q1-K1-C6

Seq. No.	195226
Contig ID	17741_1.R1039
5'-most EST	g5047176
Method	BLASTX

NCBI GI g2341042
BLAST score 276
E value 7.0e-24
Match length 225
% identity 36
NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]

Seq. No. 195227
Contig ID 17744_1.R1039
5'-most EST LIB3189-013-P1-K1-B7
Method BLASTX
NCBI GI g951427
BLAST score 991
E value 0.0e+00
Match length 396
% identity 80
NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No. 195228
Contig ID 17751_1.R1039
5'-most EST LIB3135-062-Q1-K1-D9
Method BLASTX
NCBI GI g3114968
BLAST score 461
E value 4.0e-46
Match length 138
% identity 60
NCBI Description (Y14997) prolidase [Suberites domuncula]

Seq. No. 195229
Contig ID 17761_1.R1039
5'-most EST LIB3165-043-Q1-K1-G5
Method BLASTN
NCBI GI g2623910
BLAST score 417
E value 0.0e+00
Match length 522
% identity 94
NCBI Description Gossypium hirsutum ATPase B subunit (atpB) and ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) genes, chloroplast genes encoding chloroplast proteins, partial cds, and atpB-rbcL intergenic spacer

Seq. No. 195230
Contig ID 17761_2.R1039
5'-most EST LIB3135-062-Q1-K1-E9
Method BLASTN
NCBI GI g2623911
BLAST score 74
E value 3.0e-33
Match length 100
% identity 95
NCBI Description Gossypium barbadense ATPase B subunit (atpB) and ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) genes, chloroplast genes encoding chloroplast proteins, partial cds, and atpB-rbcL intergenic spacer

Seq. No.	195231
Contig ID	17764_1.R1039
5'-most EST	uC-gsronu33B163e10b2

Seq. No.	195232
Contig ID	17770_1.R1039
5'-most EST	LIB3148-018-Q1-K1-C7
Method	BLASTX
NCBI GI	g1710530
BLAST score	710
E value	4.0e-75
Match length	146
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi|2129719|pir||S71256 ribosomal protein L27a - Arabidopsis thaliana >gi|1107487|emb|CAA63025| (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	195233
Contig ID	17770_2.R1039
5'-most EST	LIB3148-018-Q1-K1-C10
Method	BLASTX
NCBI GI	g1710530
BLAST score	592
E value	3.0e-61
Match length	124
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi|2129719|pir||S71256 ribosomal protein L27a - Arabidopsis thaliana >gi|1107487|emb|CAA63025| (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	195234
Contig ID	17771_1.R1039
5'-most EST	LIB3146-003-P1-K1-A7

Seq. No.	195235
Contig ID	17779_1.R1039
5'-most EST	LIB3135-062-Q1-K1-G4
Method	BLASTX
NCBI GI	g2500523
BLAST score	275
E value	7.0e-24
Match length	128
% identity	48
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi|2190248|dbj|BAA20371| (D84472) translation initiation factor [Candida albicans]

Seq. No.	195236
Contig ID	17783_1.R1039
5'-most EST	LIB3135-062-Q1-K1-G9

Seq. No.	195237
Contig ID	17803_1.R1039
5'-most EST	LIB3145-001-P1-K1-D1

Method	BLASTX
NCBI GI	g4557078
BLAST score	164
E value	6.0e-11
Match length	250
% identity	23
NCBI Description	(AC007045) putative Ta11-1 pol polyprotein, 5' partial [Arabidopsis thaliana]

Seq. No.	195238
Contig ID	17804_1.R1039
5'-most EST	uC-gsronu33B132c04b1

Seq. No.	195239
Contig ID	17806_1.R1039
5'-most EST	uC-gsflmaxxa002g01b1
Method	BLASTX
NCBI GI	g2244956
BLAST score	614
E value	3.0e-96
Match length	390
% identity	49
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	195240
Contig ID	17813_1.R1039
5'-most EST	uC-gsflmaxxa014a03b1
Method	BLASTX
NCBI GI	g1350548
BLAST score	265
E value	4.0e-23
Match length	84
% identity	58
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	195241
Contig ID	17816_1.R1039
5'-most EST	LIB3145-002-P1-K1-A10
Method	BLASTX
NCBI GI	g2982434
BLAST score	278
E value	1.0e-24
Match length	119
% identity	46
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	195242
Contig ID	17821_1.R1039
5'-most EST	LIB3145-002-P1-K1-A6

Seq. No.	195243
Contig ID	17826_1.R1039
5'-most EST	uC-gsronu33B089c11b1
Method	BLASTX
NCBI GI	g3093294
BLAST score	1000

E value	1.0e-109
Match length	309
% identity	50
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	195244
Contig ID	17830_1.R1039
5'-most EST	LIB3145-002-P1-K1-B9

Seq. No.	195245
Contig ID	17837_1.R1039
5'-most EST	LIB3145-002-P1-K1-D2

Seq. No.	195246
Contig ID	17838_1.R1039
5'-most EST	LIB3147-004-Q1-K1-C12

Seq. No.	195247
Contig ID	17845_1.R1039
5'-most EST	LIB3145-002-P1-K1-D9
Method	BLASTX
NCBI GI	g3892051
BLAST score	655
E value	1.0e-68
Match length	167
% identity	78
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	195248
Contig ID	17849_1.R1039
5'-most EST	LIB3145-002-P1-K1-E12

Seq. No.	195249
Contig ID	17851_1.R1039
5'-most EST	LIB3145-002-P1-K1-E5

Seq. No.	195250
Contig ID	17864_1.R1039
5'-most EST	g5047142
Method	BLASTX
NCBI GI	g2146732
BLAST score	821
E value	5.0e-88
Match length	212
% identity	45
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi|1373396 (U57838) rof1 [Arabidopsis thaliana]

Seq. No.	195251
Contig ID	17873_1.R1039
5'-most EST	g5046354
Method	BLASTX
NCBI GI	g3334323
BLAST score	862
E value	1.0e-92
Match length	193

% identity	86
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi|1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi|2104532|gb|AAC78700.1| (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi|2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]
Seq. No.	195252
Contig ID	17892_1.R1039
5'-most EST	LIB3145-004-P1-K1-H10
Seq. No.	195253
Contig ID	17901_1.R1039
5'-most EST	uC-gsflmaxxa049d04b1
Seq. No.	195254
Contig ID	17905_1.R1039
5'-most EST	LIB3145-044-Q1-K1-D8
Method	BLASTX
NCBI GI	g548493
BLAST score	356
E value	2.0e-33
Match length	200
% identity	39
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi|629854|pir||S30067 polygalacturonase - maize >gi|288612|emb|CAA47052| (X66422) polygalacturonase [Zea mays]
Seq. No.	195255
Contig ID	17908_1.R1039
5'-most EST	LIB3165-060-Q1-K1-D11
Seq. No.	195256
Contig ID	17915_1.R1039
5'-most EST	LIB3145-005-Q1-K1-C12
Method	BLASTX
NCBI GI	g478809
BLAST score	441
E value	2.0e-63
Match length	143
% identity	77
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi|170047 (M67449) protein kinase [Glycine max] >gi|444789|prf||1908223A protein kinase [Glycine max]
Seq. No.	195257
Contig ID	17916_1.R1039
5'-most EST	LIB3145-005-Q1-K1-C2
Seq. No.	195258
Contig ID	17919_1.R1039
5'-most EST	LIB3145-005-Q1-K1-C6
Seq. No.	195259
Contig ID	17920_1.R1039

5'-most EST	uC-gsflnu33B061e12b1
Method	BLASTX
NCBI GI	g2244818
BLAST score	385
E value	5.0e-37
Match length	176
% identity	51
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195260
Contig ID	17921_1.R1039
5'-most EST	LIB3145-005-Q1-K1-C8

Seq. No.	195261
Contig ID	17931_1.R1039
5'-most EST	uC-gsflnu33B113b07b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	195262
Contig ID	17933_1.R1039
5'-most EST	uC-gsronu33B078a01b1
Method	BLASTX
NCBI GI	g2244806
BLAST score	247
E value	1.0e-35
Match length	140
% identity	54
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195263
Contig ID	17938_1.R1039
5'-most EST	uC-gsflmaxxa067d12b1
Method	BLASTX
NCBI GI	g128592
BLAST score	423
E value	2.0e-41
Match length	116
% identity	66
NCBI Description	POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi|82190|pir||S22495 pollen-specific protein precursor - common tobacco >gi|19902|emb|CAA43454| (X61146) pollen specific protein [Nicotiana tabacum]

Seq. No.	195264
Contig ID	17938_2.R1039
5'-most EST	LIB3145-031-Q1-K1-F3
Method	BLASTX
NCBI GI	g128592
BLAST score	232
E value	1.0e-26
Match length	93

% identity	67
NCBI Description	POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi|82190|pir||S22495 pollen-specific protein precursor - common tobacco >gi|19902|emb|CAA43454| (X61146) pollen specific protein [Nicotiana tabacum]

Seq. No.	195265
Contig ID	17951_1.R1039
5'-most EST	uC-gsflmaxxa058b05b1
Method	BLASTN
NCBI GI	g1781298
BLAST score	43
E value	1.0e-14
Match length	183
% identity	81
NCBI Description	N.tabacum mRNA for transformer-SR ribonucleoprotein

Seq. No.	195266
Contig ID	17952_1.R1039
5'-most EST	LIB3147-040-Q1-K1-C11
Method	BLASTX
NCBI GI	g1781299
BLAST score	455
E value	4.0e-45
Match length	101
% identity	84
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	195267
Contig ID	17958_1.R1039
5'-most EST	LIB3145-006-Q1-K1-A2
Method	BLASTX
NCBI GI	g4490323
BLAST score	433
E value	7.0e-43
Match length	131
% identity	65
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	195268
Contig ID	17962_1.R1039
5'-most EST	LIB3272-055-P1-K1-G1
Method	BLASTX
NCBI GI	g4567267
BLAST score	470
E value	4.0e-47
Match length	104
% identity	84
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	195269
Contig ID	17967_1.R1039
5'-most EST	g5046896
Method	BLASTX
NCBI GI	g1652942

BLAST score 345
E value 4.0e-32
Match length 250
% identity 37
NCBI Description (D90909) extragenic suppressor [Synechocystis sp.]

Seq. No. 195270
Contig ID 17972_1.R1039
5'-most EST g3326466
Method BLASTX
NCBI GI g3023522
BLAST score 303
E value 2.0e-27
Match length 137
% identity 47
NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi|2454309 (AF002705) beta prime COP [Rattus norvegicus]

Seq. No. 195271
Contig ID 17972_3.R1039
5'-most EST LIB3147-003-Q1-K1-A1

Seq. No. 195272
Contig ID 17972_4.R1039
5'-most EST LIB3145-006-Q1-K1-B5

Seq. No. 195273
Contig ID 17986_1.R1039
5'-most EST g3326319

Seq. No. 195274
Contig ID 17995_1.R1039
5'-most EST LIB3145-006-Q1-K1-E10
Method BLASTX
NCBI GI g3201627
BLAST score 762
E value 5.0e-81
Match length 238
% identity 65
NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 195275
Contig ID 17998_1.R1039
5'-most EST LIB3145-006-Q1-K1-E4

Seq. No. 195276
Contig ID 17999_1.R1039
5'-most EST LIB3149-048-Q1-K1-H1
Method BLASTX
NCBI GI g3402693
BLAST score 509
E value 3.0e-51
Match length 154
% identity 67
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 195277
Contig ID 18005_1.R1039
5'-most EST uC-gsflmaxxa093h01b1

Seq. No. 195278
Contig ID 18008_1.R1039
5'-most EST LIB3165-052-Q1-K1-A1
Method BLASTX
NCBI GI g115473
BLAST score 435
E value 5.0e-43
Match length 140
% identity 61
NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi|170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi|445610|prf||1909357A carbonic anhydrase [Nicotiana tabacum]

Seq. No. 195279
Contig ID 18010_1.R1039
5'-most EST LIB3145-006-Q1-K1-F7

Seq. No. 195280
Contig ID 18013_1.R1039
5'-most EST LIB3145-006-Q1-K1-G10

Seq. No. 195281
Contig ID 18019_1.R1039
5'-most EST g5050796
Method BLASTX
NCBI GI g2982303
BLAST score 1195
E value 1.0e-131
Match length 267
% identity 82
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 195282
Contig ID 18021_1.R1039
5'-most EST LIB3165-013-P1-K1-G9
Method BLASTX
NCBI GI g2088662
BLAST score 232
E value 4.0e-37
Match length 190
% identity 51
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 195283
Contig ID 18027_1.R1039
5'-most EST LIB3147-015-Q1-K1-E7

Seq. No. 195284
Contig ID 18029_1.R1039
5'-most EST LIB3148-054-Q1-K1-E1

Seq. No. 195285

Contig ID 18033_1.R1039
5'-most EST LIB3146-035-P1-K1-C5

Seq. No. 195286
Contig ID 18041_1.R1039
5'-most EST LIB3145-019-Q1-K1-F12
Method BLASTX
NCBI GI g4249418
BLAST score 384
E value 6.0e-37
Match length 108
% identity 43
NCBI Description (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H type domains), 5' partial [Arabidopsis thaliana]

Seq. No. 195287
Contig ID 18042_1.R1039
5'-most EST LIB3145-007-Q1-K1-B6
Method BLASTX
NCBI GI g4049401
BLAST score 173
E value 2.0e-12
Match length 57
% identity 65
NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No. 195288
Contig ID 18043_2.R1039
5'-most EST LIB3166-030-P1-K1-B12
Method BLASTX
NCBI GI g4376203
BLAST score 273
E value 2.0e-26
Match length 136
% identity 42
NCBI Description (U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No. 195289
Contig ID 18045_1.R1039
5'-most EST g5044698
Method BLASTX
NCBI GI g124713
BLAST score 1086
E value 1.0e-119
Match length 280
% identity 72
NCBI Description ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI) (VACUOLAR INVERTASE) >gi|218326|dbj|BAA01107| (D10265) invertase [Vigna radiata] >gi|384325|prf||1905412A acid invertase [Vigna radiata]

Seq. No. 195290
Contig ID 18048_1.R1039
5'-most EST LIB3272-033-P1-K1-B3

Seq. No.	195291
Contig ID	18050_1.R1039
5'-most EST	uC-gsflnu33B112a09b1
Method	BLASTX
NCBI GI	g119778
BLAST score	226
E value	2.0e-21
Match length	97
% identity	50
NCBI Description	FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) >gi|106043|pir||A37926 fumarylacetoacetase (EC 3.7.1.2) - human >gi|182393 (M55150) fumarylacetoacetate hydrolase [Homo sapiens] >gi|4557587|ref|NP_000128.1|pFAH| fumarylacetoacetase

Seq. No.	195292
Contig ID	18050_2.R1039
5'-most EST	uC-gsflmaxxa058c12b1
Method	BLASTX
NCBI GI	g119778
BLAST score	875
E value	2.0e-94
Match length	257
% identity	61
NCBI Description	FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) >gi|106043|pir||A37926 fumarylacetoacetase (EC 3.7.1.2) - human >gi|182393 (M55150) fumarylacetoacetate hydrolase [Homo sapiens] >gi|4557587|ref|NP_000128.1|pFAH| fumarylacetoacetase

Seq. No.	195293
Contig ID	18052_1.R1039
5'-most EST	LIB3145-007-Q1-K1-C6
Method	BLASTX
NCBI GI	g4455313
BLAST score	483
E value	2.0e-48
Match length	176
% identity	53
NCBI Description	(AL035528) fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]

Seq. No.	195294
Contig ID	18055_1.R1039
5'-most EST	uC-gsronu33B038g11b1
Method	BLASTX
NCBI GI	g2501231
BLAST score	457
E value	1.0e-45
Match length	151
% identity	64
NCBI Description	HYPOTHETICAL 38.1 KD PROTEIN >gi|99505|pir||S24930 hypothetical protein - pink corydalis >gi|18258|emb|CAA45139| (X63595) protein of unknown function [Corydalis sempervirens] >gi|444333|prf||1906382A pCSC71 protein [Corydalis sempervirens]

Seq. No.	195295
Contig ID	18056_1.R1039
5'-most EST	LIB3145-007-Q1-K1-D1
Method	BLASTX
NCBI GI	g629561
BLAST score	121
E value	3.0e-13
Match length	107
% identity	44
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi|479047|emb|CAA55654| (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	195296
Contig ID	18057_1.R1039
5'-most EST	LIB3146-053-Q1-K1-E10

Seq. No.	195297
Contig ID	18071_1.R1039
5'-most EST	LIB3145-007-Q1-K1-E2
Method	BLASTX
NCBI GI	g1488043
BLAST score	170
E value	4.0e-12
Match length	47
% identity	72
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	195298
Contig ID	18072_1.R1039
5'-most EST	LIB3145-051-Q1-K1-F5
Method	BLASTX
NCBI GI	g113515
BLAST score	446
E value	3.0e-88
Match length	225
% identity	70
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL5 >gi|81613|pir||E39534 floral homeotic protein AGL5 - Arabidopsis thaliana >gi|166596 (M55553) transcription factor [Arabidopsis thaliana]

Seq. No.	195299
Contig ID	18080_1.R1039
5'-most EST	LIB3145-018-Q1-K1-D7
Method	BLASTX
NCBI GI	g2098705
BLAST score	393
E value	4.0e-38
Match length	154
% identity	49
NCBI Description	(U82973) pectinesterase [Citrus sinensis]

Seq. No.	195300
Contig ID	18083_1.R1039
5'-most EST	LIB3189-005-P1-K1-A3
Method	BLASTX

NCBI GI g3132675
BLAST score 1174
E value 1.0e-129
Match length 251
% identity 85
NCBI Description (AF061740) asparagine synthetase [Elaeagnus umbellata]

Seq. No. 195301
Contig ID 18088_1.R1039
5'-most EST uC-gsronu33B126a07b1
Method BLASTX
NCBI GI g3746069
BLAST score 157
E value 5.0e-10
Match length 100
% identity 35
NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 195302
Contig ID 18088_2.R1039
5'-most EST LIB3145-007-Q1-K1-G2

Seq. No. 195303
Contig ID 18088_4.R1039
5'-most EST LIB3146-024-Q1-K1-C1
Method BLASTX
NCBI GI g2213608
BLAST score 196
E value 5.0e-15
Match length 129
% identity 46
NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana]

Seq. No. 195304
Contig ID 18093_1.R1039
5'-most EST LIB3145-007-Q1-K1-G7
Method BLASTX
NCBI GI g2655008
BLAST score 210
E value 1.0e-16
Match length 100
% identity 39
NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No. 195305
Contig ID 18093_2.R1039
5'-most EST LIB3145-011-Q1-K1-B12

Seq. No. 195306
Contig ID 18094_1.R1039
5'-most EST LIB3145-007-Q1-K1-G8

Seq. No. 195307
Contig ID 18098_1.R1039
5'-most EST uC-gsflnu33B002e12b1

Method	BLASTX
NCBI GI	g1588365
BLAST score	182
E value	2.0e-13
Match length	78
% identity	44
NCBI Description	signal peptidase:SUBUNIT=12kD [Homo sapiens]

Seq. No.	195308
Contig ID	18099_1.R1039
5'-most EST	uC-gsronu33B158d07b2

Seq. No.	195309
Contig ID	18107_1.R1039
5'-most EST	LIB3145-042-Q1-K1-E11
Method	BLASTX
NCBI GI	g2281330
BLAST score	123
E value	1.0e-10
Match length	87
% identity	47
NCBI Description	(U85646) putative pectate lyase Nt59 [Nicotiana tabacum]

Seq. No.	195310
Contig ID	18108_1.R1039
5'-most EST	LIB3145-008-Q1-K1-A11
Method	BLASTX
NCBI GI	g4220479
BLAST score	356
E value	9.0e-54
Match length	150
% identity	77
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	195311
Contig ID	18109_1.R1039
5'-most EST	LIB3145-008-Q1-K1-A12
Method	BLASTX
NCBI GI	g2388586
BLAST score	193
E value	3.0e-14
Match length	53
% identity	75
NCBI Description	(AC000098) Similar to Saccharomyces RAD16 (gb|X78993). [Arabidopsis thaliana]

Seq. No.	195312
Contig ID	18124_1.R1039
5'-most EST	LIB3145-008-Q1-K1-B8
Method	BLASTX
NCBI GI	g2262172
BLAST score	326
E value	3.0e-30
Match length	164
% identity	48
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	195313
Contig ID	18126_1.R1039
5'-most EST	LIB3146-005-Q1-K1-A4

Seq. No.	195314
Contig ID	18133_1.R1039
5'-most EST	g5047351
Method	BLASTX
NCBI GI	g1777312
BLAST score	536
E value	1.0e-54
Match length	211
% identity	52
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	195315
Contig ID	18141_1.R1039
5'-most EST	LIB3189-010-P1-K1-H5
Method	BLASTX
NCBI GI	g4115538
BLAST score	469
E value	2.0e-46
Match length	293
% identity	42
NCBI Description	(AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	195316
Contig ID	18144_1.R1039
5'-most EST	LIB3146-006-Q1-K1-E2
Method	BLASTX
NCBI GI	g3850581
BLAST score	545
E value	9.0e-56
Match length	138
% identity	72
NCBI Description	(AC005278) EST gb|N96383 comes from this gene. [Arabidopsis thaliana]

Seq. No.	195317
Contig ID	18148_1.R1039
5'-most EST	LIB3145-008-Q1-K1-E12
Method	BLASTX
NCBI GI	g2695861
BLAST score	932
E value	1.0e-101
Match length	209
% identity	85
NCBI Description	(Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] >gi|2695863|emb|CAA74645| (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]

Seq. No.	195318
Contig ID	18156_1.R1039

5'-most EST	LIB3145-008-Q1-K1-E9
Seq. No.	195319
Contig ID	18157_1.R1039
5'-most EST	LIB3197-046-Q1-M1-H10
Method	BLASTX
NCBI GI	g3450889
BLAST score	613
E value	1.0e-154
Match length	395
% identity	75
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.	195320
Contig ID	18157_2.R1039
5'-most EST	uC-gsflnu33B097d01b1
Method	BLASTX
NCBI GI	g2642158
BLAST score	480
E value	2.0e-48
Match length	114
% identity	76
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195321
Contig ID	18160_1.R1039
5'-most EST	LIB3145-008-Q1-K1-F2
Method	BLASTX
NCBI GI	g1706473
BLAST score	370
E value	5.0e-35
Match length	236
% identity	41
NCBI Description	DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) >gi|542840|pir||JN0912 heat-shock protein hsp40 - human >gi|575891|dbj|BAA08495| (D49547) HSP40 [Homo sapiens] >gi|1816452|dbj|BAA12819| (D85429) heat shock protein 40 [Homo sapiens]
Seq. No.	195322
Contig ID	18164_1.R1039
5'-most EST	LIB3148-052-Q1-K1-F10
Method	BLASTX
NCBI GI	g3860321
BLAST score	609
E value	2.0e-63
Match length	163
% identity	66
NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]
Seq. No.	195323
Contig ID	18164_2.R1039
5'-most EST	LIB3145-008-Q1-K1-F7
Method	BLASTX
NCBI GI	g2961390
BLAST score	535
E value	1.0e-54

Match length 135
% identity 66
NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No. 195324
Contig ID 18165_1.R1039
5'-most EST LIB3145-008-Q1-K1-F8
Method BLASTX
NCBI GI g4455293
BLAST score 638
E value 2.0e-66
Match length 214
% identity 68
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 195325
Contig ID 18169_1.R1039
5'-most EST LIB3197-005-P1-M1-A1

Seq. No. 195326
Contig ID 18170_1.R1039
5'-most EST LIB3145-008-Q1-K1-G12

Seq. No. 195327
Contig ID 18180_1.R1039
5'-most EST LIB3145-008-Q1-K1-H11

Seq. No. 195328
Contig ID 18191_1.R1039
5'-most EST LIB3145-009-Q1-K1-A3
Method BLASTX
NCBI GI g3757520
BLAST score 149
E value 3.0e-09
Match length 57
% identity 53
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 195329
Contig ID 18195_1.R1039
5'-most EST uC-gsflmaxxa001f04b1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 45
% identity 48
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 195330
Contig ID 18195_2.R1039
5'-most EST LIB3145-013-Q1-K1-F5
Method BLASTX
NCBI GI g4567229
BLAST score 348
E value 1.0e-32

Match length	167
% identity	43
NCBI Description	(AC007119) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	195331
Contig ID	18198_1.R1039
5'-most EST	LIB3145-009-Q1-K1-B1
Method	BLASTX
NCBI GI	g729273
BLAST score	657
E value	3.0e-69
Match length	143
% identity	88
NCBI Description	CYPRO4 PROTEIN >gi|322804|pir||S28592 cypro4 protein - cardoon >gi|17959|emb|CAA49354| (X69672) cypro4 [Cynara cardunculus]

Seq. No.	195332
Contig ID	18202_1.R1039
5'-most EST	LIB3145-009-Q1-K1-B3
Method	BLASTX
NCBI GI	g4538939
BLAST score	305
E value	1.0e-27
Match length	204
% identity	37
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	195333
Contig ID	18207_1.R1039
5'-most EST	LIB3145-009-Q1-K1-C10

Seq. No.	195334
Contig ID	18209_1.R1039
5'-most EST	LIB3196-039-P1-M1-D3

Seq. No.	195335
Contig ID	18209_2.R1039
5'-most EST	LIB3189-023-P1-K1-F12
Method	BLASTX
NCBI GI	g2252866
BLAST score	196
E value	1.0e-14
Match length	56
% identity	68
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	195336
Contig ID	18216_1.R1039
5'-most EST	LIB3166-058-P1-K1-D11
Method	BLASTX
NCBI GI	g3763916
BLAST score	318
E value	3.0e-29

Match length 182
% identity 42
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana] >gi|4531439|gb|AAD22124.1|AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No. 195337
Contig ID 18221_1.R1039
5'-most EST LIB3272-006-P1-K1-H3

Seq. No. 195338
Contig ID 18224_1.R1039
5'-most EST LIB3189-007-P1-K1-A12
Method BLASTX
NCBI GI g2136139
BLAST score 474
E value 4.0e-47
Match length 261
% identity 39
NCBI Description sds22 protein homolog - human >gi|1085028|emb|CAA90626| (Z50749) yeast sds22 homolog [Homo sapiens] >gi|1585165|prf||2124310A sds22 gene [Homo sapiens] >gi|4506013|ref|NP_002703.1|pPPP1R7| protein phosphatase 1, regulatory subunit

Seq. No. 195339
Contig ID 18227_1.R1039
5'-most EST LIB3145-009-Q1-K1-E10

Seq. No. 195340
Contig ID 18230_1.R1039
5'-most EST uC-gsronu33B050h08b1

Seq. No. 195341
Contig ID 18231_1.R1039
5'-most EST uC-gsflnu33B082e01b1

Seq. No. 195342
Contig ID 18234_1.R1039
5'-most EST LIB3145-009-Q1-K1-E9

Seq. No. 195343
Contig ID 18245_1.R1039
5'-most EST uC-gsflnu33B127h12b1
Method BLASTX
NCBI GI g1785955
BLAST score 209
E value 1.0e-16
Match length 100
% identity 27
NCBI Description (U38786) calmodulin [Trichomonas vaginalis]

Seq. No. 195344
Contig ID 18246_1.R1039
5'-most EST LIB3146-058-Q1-K1-H4
Method BLASTX
NCBI GI g3461884

BLAST score	351
E value	4.0e-33
Match length	105
% identity	69
NCBI Description	(AB006082) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana] >gi|3461886|dbj|BAA32529| (AB006083) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana]

Seq. No.	195345
Contig ID	18248_1.R1039
5'-most EST	g3326143

Seq. No.	195346
Contig ID	18256_1.R1039
5'-most EST	LIB3149-033-Q1-K1-B12
Method	BLASTX
NCBI GI	g3757522
BLAST score	362
E value	2.0e-34
Match length	98
% identity	67
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	195347
Contig ID	18266_1.R1039
5'-most EST	LIB3166-023-P1-K1-D10

Seq. No.	195348
Contig ID	18266_2.R1039
5'-most EST	LIB3149-006-Q1-K1-A6

Seq. No.	195349
Contig ID	18271_1.R1039
5'-most EST	uC-gsf1nu33B002c05b1
Method	BLASTX
NCBI GI	g2829275
BLAST score	900
E value	4.0e-97
Match length	237
% identity	73
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi|3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi|4539375|emb|CAB40069.1| (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	195350
Contig ID	18277_1.R1039
5'-most EST	LIB3145-010-Q1-K1-B5
Method	BLASTX
NCBI GI	g2244780
BLAST score	258
E value	2.0e-22
Match length	104
% identity	57

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 195351
Contig ID 18290_1.R1039
5'-most EST LIB3145-010-Q1-K1-C8
Method BLASTX
NCBI GI g1711507
BLAST score 468
E value 8.0e-47
Match length 131
% identity 67
NCBI Description SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi|624221 (U19030) signal recognition particle 19 kDa protein subunit SRP19 [Oryza sativa]

Seq. No. 195352
Contig ID 18293_1.R1039
5'-most EST LIB3145-010-Q1-K1-D10

Seq. No. 195353
Contig ID 18296_1.R1039
5'-most EST LIB3145-010-Q1-K1-D4
Method BLASTX
NCBI GI g4115925
BLAST score 588
E value 9.0e-61
Match length 135
% identity 43
NCBI Description (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi|4539439|emb|CAB40027.1| (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 195354
Contig ID 18296_2.R1039
5'-most EST LIB3147-047-Q1-K1-E8
Method BLASTX
NCBI GI g4115925
BLAST score 578
E value 9.0e-60
Match length 128
% identity 49
NCBI Description (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi|4539439|emb|CAB40027.1| (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 195355
Contig ID 18297_1.R1039
5'-most EST g5044253
Method BLASTX
NCBI GI g3249098
BLAST score 204
E value 8.0e-16
Match length 142
% identity 37
NCBI Description (AC003114) ESTs gb|T04610, gb|N38459, gb|T45174, gb|R30481

and gb|N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	195356
Contig ID	18298_1.R1039
5'-most EST	uC-gsronu33B110g03b1

Seq. No.	195357
Contig ID	18313_1.R1039
5'-most EST	LIB3145-010-Q1-K1-F2
Method	BLASTX
NCBI GI	g3850568
BLAST score	227
E value	2.0e-18
Match length	110
% identity	49
NCBI Description	(AC005278) Similar to hypothetical protein SPAC2F7.14c gi|1052797 from Schizosaccharomyces pombe cosmid gb|Z50142. [Arabidopsis thaliana]

Seq. No.	195358
Contig ID	18315_1.R1039
5'-most EST	LIB3145-010-Q1-K1-F5
Method	BLASTX
NCBI GI	g4006882
BLAST score	169
E value	3.0e-12
Match length	93
% identity	38
NCBI Description	(Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	195359
Contig ID	18318_1.R1039
5'-most EST	LIB3146-044-Q1-K1-E3
Method	BLASTX
NCBI GI	g4432860
BLAST score	380
E value	3.0e-36
Match length	134
% identity	16
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	195360
Contig ID	18323_1.R1039
5'-most EST	LIB3145-014-Q1-K1-G6

Seq. No.	195361
Contig ID	18330_1.R1039
5'-most EST	LIB3146-019-Q1-K1-C4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	195362
Contig ID	18339_2.R1039
5'-most EST	LIB3165-048-Q1-K1-H10
Method	BLASTX
NCBI GI	g2914709
BLAST score	426
E value	1.0e-42
Match length	119
% identity	77
NCBI Description	(AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195363
Contig ID	18340_1.R1039
5'-most EST	uC-gsronu33B113a03b1

Seq. No.	195364
Contig ID	18344_1.R1039
5'-most EST	LIB3146-008-Q1-K1-H2

Seq. No.	195365
Contig ID	18354_1.R1039
5'-most EST	LIB3145-011-Q1-K1-B7
Method	BLASTX
NCBI GI	g1731144
BLAST score	155
E value	6.0e-15
Match length	128
% identity	40
NCBI Description	HYPOTHETICAL 28.6 KD PROTEIN T07A5.2 IN CHROMOSOME III >gi|3879519|emb|CAA88132| (Z48055) similar to the yeast hypothetical protein YK10 (Swiss Prot accession number P36125); cDNA EST EMBL:C11826 comes from this gene [Caenorhabditis elegans]

Seq. No.	195366
Contig ID	18356_1.R1039
5'-most EST	uC-gsflmaxxa098a04b1

Seq. No.	195367
Contig ID	18357_1.R1039
5'-most EST	LIB3146-060-Q1-K1-E11
Method	BLASTX
NCBI GI	g100903
BLAST score	182
E value	4.0e-13
Match length	87
% identity	22
NCBI Description	nucleic acid-binding protein - maize >gi|168526 (M74566) nucleic acid-binding protein [Zea mays]

Seq. No.	195368
Contig ID	18358_1.R1039
5'-most EST	LIB3145-037-Q1-K1-G9
Method	BLASTX
NCBI GI	g2290532
BLAST score	506

E value 3.0e-51
Match length 164
% identity 63
NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 195369
Contig ID 18361_1.R1039
5'-most EST LIB3148-035-Q1-K1-B12
Method BLASTX
NCBI GI g461736
BLAST score 790
E value 2.0e-84
Match length 166
% identity 96
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi|478786|pir||S29316 chaperonin 60 - cucurbit >gi|12546|emb|CAA50218| (X70868) chaperonin 60 [Cucurbita sp.]

Seq. No. 195370
Contig ID 18373_1.R1039
5'-most EST uC-gsf1maxxa076e03b1
Method BLASTX
NCBI GI g3386614
BLAST score 374
E value 2.0e-51
Match length 143
% identity 35
NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No. 195371
Contig ID 18388_1.R1039
5'-most EST LIB3145-011-Q1-K1-F10

Seq. No. 195372
Contig ID 18396_1.R1039
5'-most EST LIB3145-011-Q1-K1-G1
Method BLASTX
NCBI GI g4185599
BLAST score 196
E value 5.0e-15
Match length 111
% identity 41
NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No. 195373
Contig ID 18405_1.R1039
5'-most EST LIB3145-011-Q1-K1-G5
Method BLASTX
NCBI GI g2827544
BLAST score 529
E value 4.0e-54
Match length 144
% identity 72
NCBI Description (AL021635) HSP associated protein like [Arabidopsis

thaliana]

Seq. No.	195374
Contig ID	18408_1.R1039
5'-most EST	LIB3145-011-Q1-K1-G9
Method	BLASTX
NCBI GI	g3122638
BLAST score	564
E value	2.0e-58
Match length	115
% identity	40
NCBI Description	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 >gi|1076381|pir||S49820 PRL1 protein - Arabidopsis thaliana >gi|577733|emb|CAA58031| (X82824) PRL1 [Arabidopsis thaliana] >gi|577735|emb|CAA58032| (X82825) PRL1 [Arabidopsis thaliana] >gi|2244947|emb|CAB10369.1| (Z97339) PRL1 protein - Arabidopsis thaliana

Seq. No.	195375
Contig ID	18409_1.R1039
5'-most EST	LIB3145-011-Q1-K1-H2
Method	BLASTX
NCBI GI	g3738329
BLAST score	442
E value	8.0e-48
Match length	145
% identity	75
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	195376
Contig ID	18416_1.R1039
5'-most EST	LIB3146-024-Q1-K1-C8
Method	BLASTX
NCBI GI	g4572674
BLAST score	548
E value	5.0e-56
Match length	164
% identity	65
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	195377
Contig ID	18417_1.R1039
5'-most EST	LIB3145-023-Q1-K1-D5
Method	BLASTX
NCBI GI	g2760326
BLAST score	1056
E value	1.0e-115
Match length	508
% identity	53
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	195378
Contig ID	18417_3.R1039
5'-most EST	LIB3148-057-Q1-K1-F4
Method	BLASTX
NCBI GI	g2760326
BLAST score	164

E value	3.0e-11
Match length	95
% identity	40
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	195379
Contig ID	18419_1.R1039
5'-most EST	LIB3145-011-Q1-K1-H9
Method	BLASTX
NCBI GI	g2702277
BLAST score	296
E value	1.0e-26
Match length	136
% identity	49
NCBI Description	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi|2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]

Seq. No.	195380
Contig ID	18423_1.R1039
5'-most EST	uC-gsronu33B058d01b1
Method	BLASTX
NCBI GI	g2462828
BLAST score	475
E value	1.0e-47
Match length	171
% identity	54
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195381
Contig ID	18424_1.R1039
5'-most EST	LIB3145-012-Q1-K1-A5
Method	BLASTX
NCBI GI	g3885334
BLAST score	1385
E value	1.0e-154
Match length	337
% identity	77
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	195382
Contig ID	18425_1.R1039
5'-most EST	LIB3147-013-Q1-K1-F12

Seq. No.	195383
Contig ID	18427_1.R1039
5'-most EST	uC-gsronu33B019f04b1
Method	BLASTX
NCBI GI	g2961377
BLAST score	389
E value	3.0e-37
Match length	224
% identity	5
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	195384
Contig ID	18429_1.R1039
5'-most EST	uC-gsronu33B050c10b1
Method	BLASTX
NCBI GI	g1814232
BLAST score	155
E value	1.0e-09
Match length	152
% identity	34
NCBI Description	(U64675) BS-63 [Homo sapiens]

Seq. No.	195385
Contig ID	18430_1.R1039
5'-most EST	LIB3145-012-Q1-K1-B12

Seq. No.	195386
Contig ID	18432_1.R1039
5'-most EST	LIB3145-029-Q1-K1-E6

Seq. No.	195387
Contig ID	18442_1.R1039
5'-most EST	uC-gsronu33B158g10b2
Method	BLASTX
NCBI GI	g2827704
BLAST score	380
E value	1.0e-36
Match length	134
% identity	57
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No.	195388
Contig ID	18445_1.R1039
5'-most EST	LIB3166-039-P1-K1-B2
Method	BLASTX
NCBI GI	g1621268
BLAST score	1106
E value	1.0e-121
Match length	291
% identity	73
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	195389
Contig ID	18450_1.R1039
5'-most EST	uC-gsflmaxxa040g12b1
Method	BLASTX
NCBI GI	g125051
BLAST score	632
E value	1.0e-65
Match length	195
% identity	63
NCBI Description	ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi|88038|pir||A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi|306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens] >gi|4504799|ref|NP_002216.1|pIVD| isovaleryl Coenzyme A dehydrogenase

Seq. No.	195390
Contig ID	18450_2.R1039
5'-most EST	LIB3145-012-Q1-K1-D11
Method	BLASTX
NCBI GI	g125051
BLAST score	469
E value	4.0e-47
Match length	144
% identity	65
NCBI Description	ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi|88038|pir||A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi|306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens] >gi|4504799|ref|NP_002216.1|pIVD| isovaleryl Coenzyme A dehydrogenase

Seq. No.	195391
Contig ID	18452_1.R1039
5'-most EST	uC-gsronu33B134a03b1
Method	BLASTX
NCBI GI	g3132478
BLAST score	316
E value	5.0e-29
Match length	149
% identity	46
NCBI Description	(AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	195392
Contig ID	18453_1.R1039
5'-most EST	LIB3145-012-Q1-K1-D3
Method	BLASTX
NCBI GI	g116054
BLAST score	654
E value	2.0e-68
Match length	143
% identity	85
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi|280393|pir||A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi|169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]

Seq. No.	195393
Contig ID	18458_1.R1039
5'-most EST	LIB3145-012-Q1-K1-D8
Method	BLASTX
NCBI GI	g4322563
BLAST score	146
E value	8.0e-09
Match length	111
% identity	31
NCBI Description	(AF089838) phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae]

Seq. No.	195394
Contig ID	18461_1.R1039
5'-most EST	uC-gsflmaxxa054g02b1

Seq. No.	195395
Contig ID	18472_1.R1039
5'-most EST	LIB3145-012-Q1-K1-F10
Method	BLASTX
NCBI GI	g3759184
BLAST score	261
E value	2.0e-22
Match length	209
% identity	31
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	195396
Contig ID	18476_1.R1039
5'-most EST	LIB3146-044-Q1-K1-C3
Method	BLASTX
NCBI GI	g3023961
BLAST score	728
E value	2.0e-77
Match length	162
% identity	86
NCBI Description	HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi|1946222|emb|CAA96512| (Z71980) knotted1-like homeobox protein [Malus domestica]

Seq. No.	195397
Contig ID	18477_1.R1039
5'-most EST	LIB3145-012-Q1-K1-F4

Seq. No.	195398
Contig ID	18488_1.R1039
5'-most EST	LIB3145-012-Q1-K1-G5
Method	BLASTX
NCBI GI	g4538903
BLAST score	393
E value	5.0e-38
Match length	81
% identity	89
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	195399
Contig ID	18489_1.R1039
5'-most EST	LIB3145-012-Q1-K1-G6
Method	BLASTX
NCBI GI	g4097547
BLAST score	217
E value	1.0e-17
Match length	88
% identity	30
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	195400
Contig ID	18491_1.R1039
5'-most EST	LIB3149-022-Q1-K1-G2

Seq. No.	195401
Contig ID	18492_1.R1039
5'-most EST	g3326299
Method	BLASTX

NCBI GI g2245115
BLAST score 235
E value 3.0e-19
Match length 154
% identity 38
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 195402
Contig ID 18496_1.R1039
5'-most EST LIB3145-012-Q1-K1-H12

Seq. No. 195403
Contig ID 18497_1.R1039
5'-most EST LIB3145-012-Q1-K1-H5
Method BLASTX
NCBI GI g4432840
BLAST score 225
E value 7.0e-35
Match length 112
% identity 71
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 195404
Contig ID 18506_1.R1039
5'-most EST LIB3145-049-Q1-K1-C4
Method BLASTX
NCBI GI g3702121
BLAST score 446
E value 2.0e-44
Match length 130
% identity 72
NCBI Description (AJ011681) retinoblastoma-related protein [Chenopodium rubrum]

Seq. No. 195405
Contig ID 18508_1.R1039
5'-most EST LIB3145-013-Q1-K1-A6
Method BLASTX
NCBI GI g3377509
BLAST score 768
E value 7.0e-82
Match length 206
% identity 77
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No. 195406
Contig ID 18513_1.R1039
5'-most EST LIB3149-004-P1-K1-D3

Seq. No. 195407
Contig ID 18526_1.R1039
5'-most EST g5048557
Method BLASTX
NCBI GI g4191784
BLAST score 517
E value 2.0e-52
Match length 176

% identity	57
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	195408
Contig ID	18530_1.R1039
5'-most EST	LIB3197-049-Q1-M1-G12
Method	BLASTX
NCBI GI	g3746069
BLAST score	169
E value	2.0e-11
Match length	96
% identity	34
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	195409
Contig ID	18530_2.R1039
5'-most EST	LIB3148-037-Q1-K1-H9

Seq. No.	195410
Contig ID	18531_1.R1039
5'-most EST	LIB3166-005-P1-K1-B8

Seq. No.	195411
Contig ID	18543_1.R1039
5'-most EST	uC-gsflmaxxa098e09b1
Method	BLASTX
NCBI GI	g2760322
BLAST score	627
E value	2.0e-65
Match length	202
% identity	56
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	195412
Contig ID	18543_2.R1039
5'-most EST	LIB3189-051-P1-K1-B1
Method	BLASTX
NCBI GI	g2760322
BLAST score	245
E value	9.0e-21
Match length	93
% identity	53
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	195413
Contig ID	18544_1.R1039
5'-most EST	LIB3145-034-Q1-K1-E5
Method	BLASTX
NCBI GI	g3024386
BLAST score	1459
E value	1.0e-162
Match length	400
% identity	67
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi|2129500|pir||S52006 polygalacturonase - upland cotton

>gi|606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No.	195414
Contig ID	18548_1.R1039
5'-most EST	LIB3147-032-Q1-K1-C10

Seq. No.	195415
Contig ID	18549_1.R1039
5'-most EST	LIB3146-055-Q1-K1-G9
Method	BLASTX
NCBI GI	g4467157
BLAST score	381
E value	2.0e-36
Match length	171
% identity	48
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	195416
Contig ID	18550_1.R1039
5'-most EST	LIB3166-002-Q1-K1-D7
Method	BLASTX
NCBI GI	g4416347
BLAST score	416
E value	7.0e-41
Match length	87
% identity	92
NCBI Description	(AF109403) MADS C-2 protein; MADS-box protein [Sinapis alba]

Seq. No.	195417
Contig ID	18560_1.R1039
5'-most EST	LIB3145-013-Q1-K1-G12
Method	BLASTX
NCBI GI	g2500579
BLAST score	178
E value	6.0e-13
Match length	74
% identity	16
NCBI Description	G-RICH SEQUENCE FACTOR-1 (GRSF-1) >gi|517196 (U07231) G-rich sequence factor-1 [Homo sapiens] >gi|4504161|ref|NP_002083.1|pGRSF1| G-rich RNA sequence binding factor

Seq. No.	195418
Contig ID	18568_1.R1039
5'-most EST	LIB3149-022-Q1-K1-E4
Method	BLASTX
NCBI GI	g1495366
BLAST score	350
E value	6.0e-33
Match length	144
% identity	49
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	195419
Contig ID	18576_1.R1039

5'-most EST	uC-gsflnu33B111e01b1
Method	BLASTX
NCBI GI	g3924603
BLAST score	605
E value	5.0e-63
Match length	145
% identity	51
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	195420
Contig ID	18577_1.R1039
5'-most EST	LIB3145-013-Q1-K1-H9
Method	BLASTX
NCBI GI	g3912968
BLAST score	267
E value	7.0e-23
Match length	310
% identity	26
NCBI Description	ALPHA-ADAPTIN HOMOLOG >gi|1890329|emb|CAA71991| (Y11104) alpha-adaptin [Drosophila melanogaster]

Seq. No.	195421
Contig ID	18581_1.R1039
5'-most EST	uC-gsflmaxxa091a02b1

Seq. No.	195422
Contig ID	18587_1.R1039
5'-most EST	LIB3145-014-Q1-K1-B1
Method	BLASTX
NCBI GI	g2746826
BLAST score	145
E value	5.0e-09
Match length	91
% identity	34
NCBI Description	(AF040646) No definition line found [Caenorhabditis elegans]

Seq. No.	195423
Contig ID	18590_1.R1039
5'-most EST	LIB3145-014-Q1-K1-B2

Seq. No.	195424
Contig ID	18592_1.R1039
5'-most EST	LIB3145-014-Q1-K1-B4
Method	BLASTX
NCBI GI	g132908
BLAST score	155
E value	5.0e-10
Match length	42
% identity	69
NCBI Description	50S RIBOSOMAL PROTEIN L34 >gi|79021|pir||JQ0732 ribosomal protein L34 - Proteus mirabilis >gi|150877 (M58352) ribosomal protein L34 [Proteus mirabilis]

Seq. No.	195425
Contig ID	18593_1.R1039

5'-most EST	uC-gsflmaxxa088h09b1
Seq. No.	195426
Contig ID	18594_1.R1039
5'-most EST	LIB3145-037-Q1-K1-C6
Seq. No.	195427
Contig ID	18601_1.R1039
5'-most EST	LIB3145-014-Q1-K1-C12
Seq. No.	195428
Contig ID	18602_2.R1039
5'-most EST	LIB3145-014-Q1-K1-C2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	195429
Contig ID	18613_1.R1039
5'-most EST	LIB3149-005-Q1-K2-H6
Method	BLASTX
NCBI GI	g4432835
BLAST score	426
E value	9.0e-42
Match length	145
% identity	52
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	195430
Contig ID	18614_1.R1039
5'-most EST	uC-gsflmaxxa061h06b1
Method	BLASTX
NCBI GI	g4567250
BLAST score	423
E value	3.0e-41
Match length	211
% identity	41
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195431
Contig ID	18615_1.R1039
5'-most EST	LIB3145-014-Q1-K1-D6
Method	BLASTX
NCBI GI	g2194132
BLAST score	611
E value	2.0e-63
Match length	231
% identity	56
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.	195432
Contig ID	18616_1.R1039
5'-most EST	LIB3145-014-Q1-K1-D7

Method	BLASTX
NCBI GI	g2342735
BLAST score	188
E value	6.0e-14
Match length	51
% identity	75
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	195433
Contig ID	18616_2.R1039
5'-most EST	uC-gsflnu33B129d04b1
Method	BLASTX
NCBI GI	g2342735
BLAST score	417
E value	6.0e-41
Match length	106
% identity	79
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	195434
Contig ID	18624_1.R1039
5'-most EST	uC-gsflnu33B089e01b1
Method	BLASTX
NCBI GI	g4263714
BLAST score	547
E value	3.0e-56
Match length	130
% identity	79
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	195435
Contig ID	18630_1.R1039
5'-most EST	uC-gsronu33B080e12b1
Method	BLASTX
NCBI GI	g3355468
BLAST score	508
E value	2.0e-51
Match length	120
% identity	88
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	195436
Contig ID	18632_2.R1039
5'-most EST	LIB3145-014-Q1-K1-F3
Method	BLASTX
NCBI GI	g2739168
BLAST score	283
E value	3.0e-25
Match length	128
% identity	44
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	195437
Contig ID	18637_1.R1039

5'-most EST	g5047977
Method	BLASTX
NCBI GI	g548441
BLAST score	1580
E value	1.0e-177
Match length	301
% identity	95
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT >gi|486805|pir||S35502 phosphoprotein phosphatase (EC 3.1.3.16) 2A - alfalfa >gi|287811|emb|CAA49849| (X70399) phosphoprotein phosphatase type 2A [Medicago sativa]

Seq. No.	195438
Contig ID	18638_1.R1039
5'-most EST	uC-gsflnu33B071g12b1
Method	BLASTX
NCBI GI	g232190
BLAST score	615
E value	5.0e-64
Match length	167
% identity	67
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG 6P229 >gi|100291|pir||S20501 glutathione peroxidase homolog - wood tobacco >gi|19739|emb|CAA42780| (X60219) homologous to animal glutathione peroxidases [Nicotiana sylvestris]

Seq. No.	195439
Contig ID	18641_1.R1039
5'-most EST	LIB3145-014-Q1-K1-G4
Method	BLASTX
NCBI GI	g4490702
BLAST score	335
E value	3.0e-31
Match length	150
% identity	55
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195440
Contig ID	18651_1.R1039
5'-most EST	LIB3145-056-Q1-K1-G8
Method	BLASTX
NCBI GI	g3377843
BLAST score	378
E value	3.0e-36
Match length	126
% identity	63
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	195441
Contig ID	18654_1.R1039
5'-most EST	LIB3145-046-Q1-K1-H12
Method	BLASTX
NCBI GI	g2760326
BLAST score	437
E value	2.0e-56
Match length	220

% identity	51
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	195442
Contig ID	18666_1.R1039
5'-most EST	LIB3196-004-P1-M1-D5

Seq. No.	195443
Contig ID	18674_1.R1039
5'-most EST	LIB3145-015-Q1-K1-B9

Seq. No.	195444
Contig ID	18676_1.R1039
5'-most EST	LIB3146-006-Q1-K1-G4
Method	BLASTX
NCBI GI	g1402888
BLAST score	165
E value	2.0e-11
Match length	66
% identity	47
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	195445
Contig ID	18681_1.R1039
5'-most EST	uC-gsflmaxxa096h09b1

Seq. No.	195446
Contig ID	18681_2.R1039
5'-most EST	LIB3145-015-Q1-K1-C5

Seq. No.	195447
Contig ID	18686_1.R1039
5'-most EST	LIB3145-015-Q1-K1-D10
Method	BLASTX
NCBI GI	g3204106
BLAST score	399
E value	1.0e-38
Match length	127
% identity	64
NCBI Description	(AJ006763) putative beta-amilase [Cicer arietinum]

Seq. No.	195448
Contig ID	18687_1.R1039
5'-most EST	LIB3145-015-Q1-K1-D11

Seq. No.	195449
Contig ID	18690_1.R1039
5'-most EST	LIB3145-053-Q1-K1-F10

Seq. No.	195450
Contig ID	18690_2.R1039
5'-most EST	LIB3145-015-Q1-K1-D5

Seq. No.	195451
Contig ID	18692_1.R1039
5'-most EST	LIB3145-015-Q1-K1-D7

Seq. No. 195452
Contig ID 18703_2.R1039
5'-most EST LIB3145-015-Q1-K1-F1

Seq. No. 195453
Contig ID 18705_1.R1039
5'-most EST LIB3145-015-Q1-K1-F11

Seq. No. 195454
Contig ID 18718_1.R1039
5'-most EST uC-gsflmaxxa061d08b1
Method BLASTN
NCBI GI g21308
BLAST score 33
E value 8.0e-09
Match length 57
% identity 89
NCBI Description S.oleracea mRNA for a 28kD RNA binding protein, involved in plastid mRNA 3' processing

Seq. No. 195455
Contig ID 18719_1.R1039
5'-most EST LIB3189-053-P1-K1-B2
Method BLASTX
NCBI GI g1752734
BLAST score 699
E value 7.0e-74
Match length 181
% identity 68
NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No. 195456
Contig ID 18730_1.R1039
5'-most EST LIB3145-015-Q1-K1-H2
Method BLASTX
NCBI GI g2117725
BLAST score 474
E value 4.0e-79
Match length 163
% identity 85
NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis thaliana (fragment) >gi|726490 (U22428) starch branching enzyme class II [Arabidopsis thaliana]

Seq. No. 195457
Contig ID 18740_1.R1039
5'-most EST uC-gsflnu33B137d08b1
Method BLASTX
NCBI GI g3201680
BLAST score 333
E value 4.0e-31
Match length 141
% identity 52
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No. 195458

Contig ID	18745_1.R1039
5'-most EST	LIB3146-033-Q1-K1-G5

Seq. No.	195459
Contig ID	18746_1.R1039
5'-most EST	LIB3145-016-Q1-K1-B1
Method	BLASTX
NCBI GI	g115607
BLAST score	527
E value	1.0e-53
Match length	192
% identity	52
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC) >gi|68033|pir||QYEC phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Escherichia coli >gi|4558284|pdb|1FIY| Three-Dimensional Structure Of Phosphoenolpyruvate Carboxylase From Escherichia Coli At 2.8 A Resolution. >gi|48666|emb|CAA29332| (X05903) PEP carboxylase (AA 1-883) [Escherichia coli] >gi|396303 (U00006) phosphoenolpyruvate carboxylase [Escherichia coli] >gi|1790393 (AE000469) phosphoenolpyruvate carboxylase [Escherichia coli] >gi|352091|prf||1005219A carboxylase,phosphoenolpyruvate [Escherichia coli]

Seq. No.	195460
Contig ID	18751_1.R1039
5'-most EST	uC-gsflmaxxa040c12b1
Method	BLASTX
NCBI GI	g3193316
BLAST score	1386
E value	1.0e-154
Match length	415
% identity	65
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	195461
Contig ID	18754_1.R1039
5'-most EST	uC-gsflmaxxa061h10b1

Seq. No.	195462
Contig ID	18757_1.R1039
5'-most EST	g5048479
Method	BLASTX
NCBI GI	g3885336
BLAST score	309
E value	1.0e-40
Match length	432
% identity	33
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	195463
Contig ID	18759_1.R1039
5'-most EST	LIB3196-023-P1-M1-F9
Method	BLASTX
NCBI GI	g2462077

BLAST score	157
E value	2.0e-10
Match length	41
% identity	66
NCBI Description	(Y11871) Oxa1 protein [Arabidopsis thaliana]

Seq. No.	195464
Contig ID	18762_1.R1039
5'-most EST	LIB3145-016-Q1-K1-C6

Seq. No.	195465
Contig ID	18767_1.R1039
5'-most EST	LIB3145-040-Q1-K1-B12

Seq. No.	195466
Contig ID	18769_1.R1039
5'-most EST	uC-gsflmaxxa047a09b1

Seq. No.	195467
Contig ID	18786_1.R1039
5'-most EST	LIB3145-016-Q1-K1-F1

Seq. No.	195468
Contig ID	18791_1.R1039
5'-most EST	g5048144
Method	BLASTX
NCBI GI	g4539324
BLAST score	416
E value	2.0e-40
Match length	137
% identity	67
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	195469
Contig ID	18794_1.R1039
5'-most EST	LIB3145-016-Q1-K1-F6

Seq. No.	195470
Contig ID	18806_1.R1039
5'-most EST	LIB3147-007-Q1-K1-H5
Method	BLASTX
NCBI GI	g4105190
BLAST score	493
E value	2.0e-49
Match length	243
% identity	44
NCBI Description	(AF044127) peroxisomal short-chain alcohol dehydrogenase [Homo sapiens]

Seq. No.	195471
Contig ID	18808_1.R1039
5'-most EST	LIB3147-026-Q1-K1-E8
Method	BLASTX
NCBI GI	g602586
BLAST score	240
E value	3.0e-20
Match length	84

% identity	51
NCBI Description	(X83229) 1-amniocyclopropane-1-carboxylate oxidase [Nicotiana tabacum]

Seq. No.	195472
Contig ID	18811_1.R1039
5'-most EST	LIB3148-013-Q1-K1-A8

Seq. No.	195473
Contig ID	18812_1.R1039
5'-most EST	uC-gsronu33B106b06b2

Seq. No.	195474
Contig ID	18825_1.R1039
5'-most EST	uC-gsflnu33B063a09b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	51
E value	1.0e-19
Match length	270
% identity	40
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	195475
Contig ID	18826_1.R1039
5'-most EST	LIB3166-040-P1-K1-E1
Method	BLASTX
NCBI GI	g3540181
BLAST score	312
E value	1.0e-28
Match length	133
% identity	49
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	195476
Contig ID	18835_1.R1039
5'-most EST	LIB3145-017-Q1-K1-B2

Seq. No.	195477
Contig ID	18838_1.R1039
5'-most EST	LIB3145-017-Q1-K1-B6

Seq. No.	195478
Contig ID	18847_1.R1039
5'-most EST	g5050663
Method	BLASTX
NCBI GI	g2854153
BLAST score	487
E value	7.0e-49
Match length	177
% identity	53
NCBI Description	(AF045640) No definition line found [Caenorhabditis elegans]

Seq. No.	195479
Contig ID	18850_1.R1039

5'-most EST	LIB3148-034-Q1-K1-H8
Seq. No.	195480
Contig ID	18854_1.R1039
5'-most EST	LIB3147-004-Q1-K1-E6
Method	BLASTX
NCBI GI	g122106
BLAST score	386
E value	3.0e-37
Match length	78
% identity	100
NCBI Description	HISTONE H4 >gi|70771|pir||HSZM4 histone H4 - maize >gi|81642|pir||S06904 histone H4 - Arabidopsis thaliana >gi|2119028|pir||S60475 histone H4 - garden pea >gi|21795|emb|CAA24924| (X00043) histone H4 [Triticum aestivum] >gi|166740 (M17132) histone H4 [Arabidopsis thaliana] >gi|166742 (M17133) histone H4 [Arabidopsis thaliana] >gi|168499 (M36659) histone H4 (H4C13) [Zea mays] >gi|168501 (M13370) histone H4 [Zea mays] >gi|168503 (M13377) histone H4 [Zea mays] >gi|498898 (U10042) histone H4 homolog [Pisum sativum] >gi|1806285|emb|CAB01914| (Z79638) histone H4 homologue [Sesbania rostrata] >gi|3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi|4580385|gb|AAD24364.1|AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi|225838|prf||1314298A histone H4 [Arabidopsis thaliana]
Seq. No.	195481
Contig ID	18854_2.R1039
5'-most EST	LIB3149-038-Q1-K1-C5
Method	BLASTX
NCBI GI	g122106
BLAST score	375
E value	2.0e-36
Match length	90
% identity	94
NCBI Description	HISTONE H4 >gi|70771|pir||HSZM4 histone H4 - maize >gi|81642|pir||S06904 histone H4 - Arabidopsis thaliana >gi|2119028|pir||S60475 histone H4 - garden pea >gi|21795|emb|CAA24924| (X00043) histone H4 [Triticum aestivum] >gi|166740 (M17132) histone H4 [Arabidopsis thaliana] >gi|166742 (M17133) histone H4 [Arabidopsis thaliana] >gi|168499 (M36659) histone H4 (H4C13) [Zea mays] >gi|168501 (M13370) histone H4 [Zea mays] >gi|168503 (M13377) histone H4 [Zea mays] >gi|498898 (U10042) histone H4 homolog [Pisum sativum] >gi|1806285|emb|CAB01914| (Z79638) histone H4 homologue [Sesbania rostrata] >gi|3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi|4580385|gb|AAD24364.1|AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi|225838|prf||1314298A histone H4 [Arabidopsis thaliana]
Seq. No.	195482
Contig ID	18861_1.R1039
5'-most EST	LIB3145-017-Q1-K1-D8
Method	BLASTX
NCBI GI	g2244765

BLAST score	204
E value	1.0e-15
Match length	226
% identity	16
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195483
Contig ID	18865_1.R1039
5'-most EST	LIB3149-016-Q1-K1-F11
Method	BLASTX
NCBI GI	g3746069
BLAST score	154
E value	1.0e-09
Match length	128
% identity	30
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	195484
Contig ID	18866_1.R1039
5'-most EST	LIB3145-017-Q1-K1-E3
Method	BLASTX
NCBI GI	g2760325
BLAST score	705
E value	2.0e-74
Match length	201
% identity	69
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	195485
Contig ID	18870_1.R1039
5'-most EST	LIB3145-038-Q1-K1-B9
Method	BLASTX
NCBI GI	g2765366
BLAST score	303
E value	2.0e-27
Match length	143
% identity	45
NCBI Description	(Y14038) putative Ole e 1 protein [Betula pendula]

Seq. No.	195486
Contig ID	18872_1.R1039
5'-most EST	LIB3145-017-Q1-K1-F2
Method	BLASTX
NCBI GI	g2661840
BLAST score	400
E value	5.0e-39
Match length	125
% identity	57
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	195487
Contig ID	18877_1.R1039
5'-most EST	uC-gsflmaxxa027a05b1
Method	BLASTN
NCBI GI	g407800
BLAST score	63

E value	7.0e-27
Match length	79
% identity	95
NCBI Description	G.hirsutum mRNA for ribosomal protein 41, large subunit (RL41)

Seq. No.	195488
Contig ID	18878_1.R1039
5'-most EST	LIB3145-017-Q1-K1-F6

Seq. No.	195489
Contig ID	18879_1.R1039
5'-most EST	g5046850

Seq. No.	195490
Contig ID	18885_1.R1039
5'-most EST	LIB3145-040-Q1-K1-G3
Method	BLASTX
NCBI GI	g2459421
BLAST score	589
E value	5.0e-61
Match length	170
% identity	62
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	195491
Contig ID	18902_1.R1039
5'-most EST	LIB3145-018-Q1-K1-B1
Method	BLASTX
NCBI GI	g3850111
BLAST score	249
E value	6.0e-21
Match length	84
% identity	51
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	195492
Contig ID	18903_1.R1039
5'-most EST	LIB3148-034-Q1-K1-G6

Seq. No.	195493
Contig ID	18906_1.R1039
5'-most EST	LIB3146-048-Q1-K1-H11

Seq. No.	195494
Contig ID	18911_1.R1039
5'-most EST	LIB3145-018-Q1-K1-B6

Seq. No.	195495
Contig ID	18913_1.R1039
5'-most EST	LIB3165-017-P1-K1-F7
Method	BLASTX
NCBI GI	g1351408
BLAST score	523
E value	3.0e-53

Match length	122
% identity	80
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease [Citrus sinensis]

Seq. No.	195496
Contig ID	18914_1.R1039
5'-most EST	LIB3145-018-Q1-K1-B9
Method	BLASTX
NCBI GI	g1946359
BLAST score	266
E value	4.0e-28
Match length	116
% identity	58
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	195497
Contig ID	18921_1.R1039
5'-most EST	LIB3145-018-Q1-K1-C5
Method	BLASTX
NCBI GI	g2947069
BLAST score	163
E value	3.0e-11
Match length	58
% identity	47
NCBI Description	(AC002521) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	195498
Contig ID	18923_1.R1039
5'-most EST	LIB3147-032-Q1-K1-C8
Method	BLASTN
NCBI GI	g2760167
BLAST score	36
E value	2.0e-10
Match length	72
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	195499
Contig ID	18926_1.R1039
5'-most EST	LIB3145-018-Q1-K1-D1
Method	BLASTX
NCBI GI	g3292832
BLAST score	247
E value	5.0e-21
Match length	94
% identity	63
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	195500
Contig ID	18927_1.R1039
5'-most EST	uC-gsflmaxxa097a08b1

Seq. No. 195501
Contig ID 18928_1.R1039
5'-most EST LIB3145-022-Q1-K1-D12
Method BLASTX
NCBI GI g1055161
BLAST score 152
E value 8.0e-10
Match length 112
% identity 35
NCBI Description (U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No. 195502
Contig ID 18930_1.R1039
5'-most EST LIB3145-018-Q1-K1-D3

Seq. No. 195503
Contig ID 18939_1.R1039
5'-most EST LIB3145-018-Q1-K1-E3
Method BLASTX
NCBI GI g4115939
BLAST score 356
E value 5.0e-37
Match length 116
% identity 36
NCBI Description (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No. 195504
Contig ID 18942_1.R1039
5'-most EST LIB3145-022-Q1-K1-D5

Seq. No. 195505
Contig ID 18946_1.R1039
5'-most EST LIB3145-022-Q1-K1-F10

Seq. No. 195506
Contig ID 18949_1.R1039
5'-most EST LIB3147-043-Q1-K1-B10

Seq. No. 195507
Contig ID 18954_1.R1039
5'-most EST LIB3196-022-P1-M1-H10

Seq. No. 195508
Contig ID 18956_1.R1039
5'-most EST LIB3145-053-Q1-K1-C9
Method BLASTX
NCBI GI g2511689
BLAST score 574
E value 5.0e-59
Match length 215
% identity 51
NCBI Description (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 195509

Contig ID 18957_1.R1039
5'-most EST LIB3197-046-Q1-M1-G6

Seq. No. 195510
Contig ID 18971_1.R1039
5'-most EST LIB3145-018-Q1-K1-H4

Seq. No. 195511
Contig ID 18978_1.R1039
5'-most EST LIB3145-019-Q1-K1-A12

Seq. No. 195512
Contig ID 18991_1.R1039
5'-most EST g5045757
Method BLASTX
NCBI GI g4206122
BLAST score 661
E value 3.0e-69
Match length 163
% identity 77
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No. 195513
Contig ID 18992_1.R1039
5'-most EST g5047209
Method BLASTX
NCBI GI g1703394
BLAST score 551
E value 3.0e-56
Match length 173
% identity 58
NCBI Description ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5 >gi|1150556|emb|CAA55338| (X78604) ARF-like protein 5 [Rattus norvegicus]

Seq. No. 195514
Contig ID 18993_1.R1039
5'-most EST uC-gsflmaxxa027a02b1

Seq. No. 195515
Contig ID 18996_1.R1039
5'-most EST LIB3147-052-Q1-K1-E6
Method BLASTX
NCBI GI g2244990
BLAST score 489
E value 3.0e-49
Match length 123
% identity 80
NCBI Description (Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No. 195516
Contig ID 18999_1.R1039
5'-most EST LIB3145-019-Q1-K1-C1

Seq. No. 195517

Contig ID	19009_1.R1039
5'-most EST	LIB3145-019-Q1-K1-C8
Method	BLASTN
NCBI GI	g1109756
BLAST score	35
E value	6.0e-10
Match length	71
% identity	87
NCBI Description	H.sapiens mRNA for p35, cyclin-like CAK1-associated protein >gi|4505224|ref|NM_002431.1|MNAT1| Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1) mRNA

Seq. No.	195518
Contig ID	19010_1.R1039
5'-most EST	LIB3166-002-Q1-K1-C4
Method	BLASTX
NCBI GI	g2980784
BLAST score	236
E value	3.0e-32
Match length	134
% identity	55
NCBI Description	(AL022198) puative protein [Arabidopsis thaliana]

Seq. No.	195519
Contig ID	19022_1.R1039
5'-most EST	LIB3165-017-P1-K1-B6
Method	BLASTX
NCBI GI	g2546954
BLAST score	597
E value	5.0e-62
Match length	154
% identity	76
NCBI Description	(Y15108) translation elongation factor-TU [Glycine max]

Seq. No.	195520
Contig ID	19029_1.R1039
5'-most EST	LIB3145-019-Q1-K1-E4
Method	BLASTX
NCBI GI	g3193284
BLAST score	149
E value	3.0e-09
Match length	36
% identity	78
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	195521
Contig ID	19030_1.R1039
5'-most EST	uC-gsflmaxxa038d06b1

Seq. No.	195522
Contig ID	19034_1.R1039
5'-most EST	LIB3145-019-Q1-K1-E9
Method	BLASTX
NCBI GI	g2160166
BLAST score	904
E value	2.0e-97
Match length	401

% identity	47
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	195523
Contig ID	19037_1.R1039
5'-most EST	LIB3147-022-Q1-K1-H11

Seq. No.	195524
Contig ID	19053_1.R1039
5'-most EST	LIB3145-019-Q1-K1-G4

Seq. No.	195525
Contig ID	19057_1.R1039
5'-most EST	g3326617

Seq. No.	195526
Contig ID	19057_3.R1039
5'-most EST	LIB3166-016-P1-K1-D5

Seq. No.	195527
Contig ID	19070_1.R1039
5'-most EST	uC-gsflmaxxa089f11b1

Seq. No.	195528
Contig ID	19082_1.R1039
5'-most EST	uC-gsflmaxxa039b08b1
Method	BLASTX
NCBI GI	g4490741
BLAST score	354
E value	4.0e-33
Match length	240
% identity	46
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195529
Contig ID	19089_1.R1039
5'-most EST	uC-gsronu33B107h10b1

Seq. No.	195530
Contig ID	19089_2.R1039
5'-most EST	LIB3145-020-Q1-K1-C1

Seq. No.	195531
Contig ID	19091_1.R1039
5'-most EST	LIB3145-020-Q1-K1-C11

Seq. No.	195532
Contig ID	19092_1.R1039
5'-most EST	LIB3145-020-Q1-K1-C12

Seq. No.	195533
Contig ID	19098_1.R1039
5'-most EST	LIB3145-020-Q1-K1-D1

Seq. No.	195534
Contig ID	19105_1.R1039
5'-most EST	uC-gsflmaxxa119d05b1

Seq. No.	195535
Contig ID	19106_1.R1039
5'-most EST	LIB3145-029-Q1-K1-D2
Method	BLASTX
NCBI GI	g130172
BLAST score	747
E value	1.0e-79
Match length	165
% identity	84
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH PHOSPHORYLASE L) >gi|168276 (M64362) starch phosphorylase [Ipomoea batatas]

Seq. No.	195536
Contig ID	19108_1.R1039
5'-most EST	LIB3145-020-Q1-K1-D7

Seq. No.	195537
Contig ID	19109_1.R1039
5'-most EST	uC-gsflmaxxa093g12b1

Seq. No.	195538
Contig ID	19122_1.R1039
5'-most EST	LIB3146-012-Q1-K1-G1
Method	BLASTX
NCBI GI	g1370276
BLAST score	862
E value	9.0e-93
Match length	223
% identity	73
NCBI Description	(X96428) MADS-box protein [Nicotiana tabacum]

Seq. No.	195539
Contig ID	19127_1.R1039
5'-most EST	LIB3145-045-Q1-K1-D7
Method	BLASTX
NCBI GI	g1703446
BLAST score	650
E value	6.0e-68
Match length	244
% identity	56
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi|1076292|pir||S53127 asparaginase - Arabidopsis thaliana >gi|735918|emb|CAA84367| (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	195540
Contig ID	19129_1.R1039
5'-most EST	g5045546
Method	BLASTX
NCBI GI	g114165
BLAST score	526
E value	1.0e-90
Match length	234
% identity	72
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE 1 PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE 1) (EPSP SYNTHASE 1) >gi|100296|pir||S18353 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) - common tobacco >gi|170229 (M61904) 5-enolpyruvylshikimate-3-phosphate synthase [Nicotiana tabacum]

Seq. No.	195541
Contig ID	19134_1.R1039
5'-most EST	LIB3272-004-P1-K1-G7
Method	BLASTX
NCBI GI	g285286
BLAST score	413
E value	3.0e-40
Match length	141
% identity	57
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	195542
Contig ID	19135_1.R1039
5'-most EST	uC-gsronu33B164d12b2
Method	BLASTX
NCBI GI	g3738322
BLAST score	299
E value	7.0e-27
Match length	66
% identity	95
NCBI Description	(AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	195543
Contig ID	19135_2.R1039
5'-most EST	uC-gsronu33B144g09b1
Method	BLASTX
NCBI GI	g3738322
BLAST score	380
E value	1.0e-36
Match length	78
% identity	95
NCBI Description	(AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	195544
Contig ID	19136_1.R1039
5'-most EST	LIB3272-029-P1-K1-H8

Seq. No.	195545
Contig ID	19144_1.R1039
5'-most EST	LIB3145-021-Q1-K1-A1
Method	BLASTX
NCBI GI	g4559334
BLAST score	444
E value	4.0e-44
Match length	156
% identity	47
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 195546

Contig ID 19146_1.R1039
5'-most EST LIB3145-021-Q1-K1-A11
Method BLASTX
NCBI GI g3894183
BLAST score 381
E value 2.0e-36
Match length 195
% identity 33
NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 195547
Contig ID 19149_1.R1039
5'-most EST LIB3146-051-Q1-K1-H2

Seq. No. 195548
Contig ID 19156_1.R1039
5'-most EST uC-gsflnu33B142h01b1
Method BLASTX
NCBI GI g4063752
BLAST score 332
E value 6.0e-31
Match length 107
% identity 60
NCBI Description (AC005851) unknown protein [Arabidopsis thaliana]
>gi|4510410|gb|AAD21496.1| (AC006929) unknown protein
[Arabidopsis thaliana]

Seq. No. 195549
Contig ID 19159_1.R1039
5'-most EST g5050723
Method BLASTX
NCBI GI g3033386
BLAST score 544
E value 2.0e-55
Match length 243
% identity 47
NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No. 195550
Contig ID 19163_1.R1039
5'-most EST LIB3196-032-P1-M1-B7

Seq. No. 195551
Contig ID 19165_1.R1039
5'-most EST uC-gsronu33B107e08b1
Method BLASTX
NCBI GI g3600033
BLAST score 507
E value 2.0e-51
Match length 144
% identity 66
NCBI Description (AF080119) contains similarity to the N terminal domain of
the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis
thaliana]

Seq. No. 195552
Contig ID 19168_1.R1039

5'-most EST	LIB3145-026-Q1-K1-A6
Method	BLASTX
NCBI GI	g3980417
BLAST score	174
E value	2.0e-12
Match length	38
% identity	92
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	195553
Contig ID	19169_1.R1039
5'-most EST	LIB3166-057-P1-K1-A2
Method	BLASTX
NCBI GI	g349379
BLAST score	479
E value	6.0e-48
Match length	132
% identity	78
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	195554
Contig ID	19172_2.R1039
5'-most EST	LIB3196-057-P1-M1-G10
Method	BLASTX
NCBI GI	g1169128
BLAST score	700
E value	4.0e-74
Match length	143
% identity	95
NCBI Description	SERINE/THREONINE-PROTEIN KINASE CTR1 >gi|166680 (L08789) protein kinase [Arabidopsis thaliana] >gi|166682 (L08790) protein kinase [Arabidopsis thaliana]

Seq. No.	195555
Contig ID	19176_1.R1039
5'-most EST	LIB3145-021-Q1-K1-D1
Method	BLASTN
NCBI GI	g2370252
BLAST score	128
E value	1.0e-65
Match length	436
% identity	82
NCBI Description	Lycopersicon esculentum mRNA for putative protein kinase

Seq. No.	195556
Contig ID	19179_1.R1039
5'-most EST	LIB3145-021-Q1-K1-F8
Method	BLASTX
NCBI GI	g3925363
BLAST score	616
E value	2.0e-64
Match length	137
% identity	85
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	195557
Contig ID	19188_1.R1039

5'-most EST	g5050161
Method	BLASTX
NCBI GI	g4454452
BLAST score	667
E value	5.0e-70
Match length	186
% identity	68
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	195558
Contig ID	19191_1.R1039
5'-most EST	LIB3197-005-P1-M1-B12
Method	BLASTX
NCBI GI	g1658193
BLAST score	1041
E value	1.0e-113
Match length	239
% identity	79
NCBI Description	(U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum bicolor]

Seq. No.	195559
Contig ID	19196_1.R1039
5'-most EST	LIB3145-021-Q1-K1-E6
Method	BLASTX
NCBI GI	g1052956
BLAST score	316
E value	4.0e-29
Match length	107
% identity	58
NCBI Description	(U39747) high mobility group protein 2 HMG2 [Ipomoea nil]

Seq. No.	195560
Contig ID	19198_1.R1039
5'-most EST	LIB3272-018-P1-K1-A9
Method	BLASTX
NCBI GI	g3860274
BLAST score	286
E value	2.0e-25
Match length	134
% identity	43
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi|4314397|gb|AAD15607| (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	195561
Contig ID	19198_2.R1039
5'-most EST	LIB3272-042-P1-K1-C2
Method	BLASTX
NCBI GI	g3860274
BLAST score	209
E value	1.0e-16
Match length	53
% identity	72
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi|4314397|gb|AAD15607| (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 195562
Contig ID 19202_1.R1039
5'-most EST LIB3165-037-P1-K1-D9

Seq. No. 195563
Contig ID 19203_1.R1039
5'-most EST LIB3146-004-P1-K1-G8

Seq. No. 195564
Contig ID 19206_1.R1039
5'-most EST uC-gsflnu33B004e06b1
Method BLASTX
NCBI GI g927025
BLAST score 424
E value 1.0e-41
Match length 177
% identity 39
NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 195565
Contig ID 19206_2.R1039
5'-most EST LIB3165-041-Q1-K1-F5

Seq. No. 195566
Contig ID 19207_1.R1039
5'-most EST LIB3145-021-Q1-K1-F5
Method BLASTN
NCBI GI g4322939
BLAST score 40
E value 5.0e-13
Match length 56
% identity 93
NCBI Description Nicotiana tabacum DNA-binding protein 2 (WRKY2) mRNA, complete cds

Seq. No. 195567
Contig ID 19211_1.R1039
5'-most EST LIB3145-021-Q1-K1-G5
Method BLASTX
NCBI GI g3785983
BLAST score 167
E value 6.0e-18
Match length 99
% identity 57
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 195568
Contig ID 19216_1.R1039
5'-most EST g5048888
Method BLASTX
NCBI GI g2252863
BLAST score 199
E value 3.0e-15
Match length 79
% identity 53
NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis

thaliana]

Seq. No.	195569
Contig ID	19217_1.R1039
5'-most EST	uC-gsronu33B016h08b1
Method	BLASTX
NCBI GI	g3885339
BLAST score	379
E value	3.0e-36
Match length	202
% identity	44
NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No.	195570
Contig ID	19224_1.R1039
5'-most EST	g5048055
Method	BLASTX
NCBI GI	g2252836
BLAST score	696
E value	3.0e-73
Match length	228
% identity	64
NCBI Description	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No.	195571
Contig ID	19227_1.R1039
5'-most EST	LIB3145-021-Q1-K1-H3
Method	BLASTN
NCBI GI	g1263094
BLAST score	33
E value	9.0e-09
Match length	61
% identity	89
NCBI Description	A.thaliana mRNA for MYB-related protein (1195 bp)

Seq. No.	195572
Contig ID	19229_1.R1039
5'-most EST	LIB3146-032-Q1-K1-D6

Seq. No.	195573
Contig ID	19232_1.R1039
5'-most EST	g5045911
Method	BLASTX
NCBI GI	g4091806
BLAST score	600
E value	7.0e-62
Match length	290
% identity	52
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	195574
Contig ID	19247_1.R1039
5'-most EST	LIB3145-022-Q1-K1-B11
Method	BLASTX
NCBI GI	g1488255
BLAST score	736

E value	4.0e-78
Match length	183
% identity	74
NCBI Description	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi|2961381|emb|CAA18128| (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi|3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No.	195575
Contig ID	19248_1.R1039
5'-most EST	LIB3197-007-P1-M1-A11

Seq. No.	195576
Contig ID	19268_1.R1039
5'-most EST	LIB3145-022-Q1-K1-D1

Seq. No.	195577
Contig ID	19272_1.R1039
5'-most EST	uC-gsflmaxxa048e11b1
Method	BLASTX
NCBI GI	g4467146
BLAST score	1931
E value	0.0e+00
Match length	571
% identity	61
NCBI Description	(AL035540) galactosidase like protein [Arabidopsis thaliana]

Seq. No.	195578
Contig ID	19275_1.R1039
5'-most EST	LIB3166-058-P1-K1-G3
Method	BLASTX
NCBI GI	g3850816
BLAST score	564
E value	4.0e-58
Match length	108
% identity	92
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	195579
Contig ID	19279_1.R1039
5'-most EST	LIB3189-037-P1-K1-A2
Method	BLASTN
NCBI GI	g2656030
BLAST score	33
E value	9.0e-09
Match length	304
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	195580
Contig ID	19281_1.R1039
5'-most EST	LIB3149-023-Q1-K1-G6
Method	BLASTX
NCBI GI	g625990

BLAST score 469
E value 7.0e-47
Match length 177
% identity 49
NCBI Description porin, plastid - garden pea

Seq. No. 195581
Contig ID 19283_1.R1039
5'-most EST LIB3145-022-Q1-K1-E4
Method BLASTX
NCBI GI g3281846
BLAST score 174
E value 1.0e-12
Match length 92
% identity 43
NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 195582
Contig ID 19285_1.R1039
5'-most EST LIB3145-022-Q1-K1-E6
Method BLASTX
NCBI GI g2191175
BLAST score 195
E value 1.0e-14
Match length 48
% identity 77
NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No. 195583
Contig ID 19286_1.R1039
5'-most EST LIB3145-045-Q1-K1-F4

Seq. No. 195584
Contig ID 19287_1.R1039
5'-most EST LIB3166-044-P1-K1-A4
Method BLASTX
NCBI GI g3023751
BLAST score 502
E value 6.0e-51
Match length 113
% identity 28
NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi|1076772|pir||S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi|854626|emb|CAA60505| (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No. 195585
Contig ID 19292_1.R1039
5'-most EST LIB3148-024-Q1-K1-B12
Method BLASTX
NCBI GI g3548815
BLAST score 333
E value 1.0e-30
Match length 142
% identity 54

NCBI Description	(AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No.	195586
Contig ID	19304_1.R1039
5'-most EST	g5044637
Method	BLASTX
NCBI GI	g2137796
BLAST score	247
E value	1.0e-20
Match length	91
% identity	54
NCBI Description	stromal cell-derived factor 2 - mouse >gi|1741870|dbj|BAA09313| (D50646) SDF2 [Mus musculus]

Seq. No.	195587
Contig ID	19304_2.R1039
5'-most EST	g5049279
Method	BLASTX
NCBI GI	g3482971
BLAST score	517
E value	3.0e-52
Match length	107
% identity	82
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	195588
Contig ID	19308_1.R1039
5'-most EST	uC-gsflnu33B009f11b1
Method	BLASTX
NCBI GI	g2832643
BLAST score	411
E value	5.0e-40
Match length	178
% identity	54
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195589
Contig ID	19310_1.R1039
5'-most EST	LIB3146-014-Q1-K1-G2
Method	BLASTX
NCBI GI	g1345642
BLAST score	1139
E value	1.0e-125
Match length	273
% identity	78
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 75A1) (CYPLXXVA1) >gi|629710|pir||S38985 flavonoid 3',5'-hydroxylase Hf1 - garden petunia >gi|311656|emb|CAA80266| (Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi|1853972|dbj|BAA03438| (D14588) flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi|3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi|738772|prf||2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No.	195590
Contig ID	19320_1.R1039
5'-most EST	uC-gsflmaxxa012c01b1
Method	BLASTX
NCBI GI	g2623310
BLAST score	439
E value	9.0e-55
Match length	223
% identity	56
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi|3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	195591
Contig ID	19322_1.R1039
5'-most EST	g3326455

Seq. No.	195592
Contig ID	19325_1.R1039
5'-most EST	LIB3145-023-Q1-K1-A8
Method	BLASTX
NCBI GI	g3928142
BLAST score	1266
E value	1.0e-140
Match length	291
% identity	25
NCBI Description	(AJ131045) protein phosphatase [Cicer arietinum]

Seq. No.	195593
Contig ID	19325_3.R1039
5'-most EST	LIB3149-053-Q1-K1-E2

Seq. No.	195594
Contig ID	19332_1.R1039
5'-most EST	uC-gsronu33B110b07b1
Method	BLASTX
NCBI GI	g113178
BLAST score	510
E value	2.0e-51
Match length	325
% identity	36
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) >gi|91923|pir||S07624 acylaminoacyl-peptidase (EC 3.4.19.1) - rat >gi|202932 (J04733) acyl-peptide hydrolase [Rattus norvegicus]

Seq. No.	195595
Contig ID	19337_1.R1039
5'-most EST	uC-gsronu33B062c11b1
Method	BLASTX
NCBI GI	g3287683
BLAST score	410
E value	5.0e-40
Match length	171
% identity	20
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb|D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	195596
Contig ID	19346_1.R1039
5'-most EST	LIB3272-055-P1-K1-B1
Method	BLASTX
NCBI GI	g1531758
BLAST score	1729
E value	0.0e+00
Match length	370
% identity	86
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi|3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	195597
Contig ID	19346_2.R1039
5'-most EST	LIB3147-013-Q1-K1-B6
Method	BLASTX
NCBI GI	g1531758
BLAST score	754
E value	7.0e-80
Match length	147
% identity	91
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi|3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	195598
Contig ID	19359_1.R1039
5'-most EST	uC-gsflnu33B026c10b1

Seq. No.	195599
Contig ID	19361_1.R1039
5'-most EST	LIB3145-023-Q1-K1-E1
Method	BLASTN
NCBI GI	g4376087
BLAST score	47
E value	3.0e-17
Match length	119
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	195600
Contig ID	19377_1.R1039
5'-most EST	LIB3272-027-P1-K1-D8
Method	BLASTX
NCBI GI	g3023197
BLAST score	1041
E value	1.0e-114
Match length	247
% identity	82
NCBI Description	14-3-3-LIKE PROTEIN D (SGF14D) >gi|1575731 (U70536) SGF14D [Glycine max]

Seq. No.	195601
Contig ID	19383_1.R1039
5'-most EST	LIB3148-022-Q1-K1-H12

Seq. No.	195602
Contig ID	19385_1.R1039
5'-most EST	g5046375
Method	BLASTX
NCBI GI	g464863
BLAST score	1110
E value	1.0e-122
Match length	242
% identity	89
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN HOMOLOG 10) >gi|422297|pir||JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi|290057 (L16579) HIV1 TAT-binding protein [Dictyostelium discoideum]

Seq. No.	195603
Contig ID	19400_1.R1039
5'-most EST	uC-gsflnu33B063d08b1
Method	BLASTX
NCBI GI	g3894099
BLAST score	235
E value	2.0e-19
Match length	89
% identity	57
NCBI Description	(AJ012750) MCM3 protein [Pisum sativum]

Seq. No.	195604
Contig ID	19417_1.R1039
5'-most EST	g5050365
Method	BLASTX
NCBI GI	g4454009
BLAST score	212
E value	1.0e-16
Match length	189
% identity	32
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	195605
Contig ID	19428_1.R1039
5'-most EST	g5050761
Method	BLASTX
NCBI GI	g3122873
BLAST score	212
E value	1.0e-16
Match length	90
% identity	44
NCBI Description	TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi|1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi|1401053 (U38818) SUPT4H [Homo sapiens] >gi|1401055 (U38817) SUPT4H [Homo sapiens] >gi|1401066 (U43154) Supt4h [Mus musculus] >gi|3779194 (U96809) chromatin structural protein homolog [Mus musculus] >gi|4507311|ref|NP_003159.1|pSUPT4H1| suppressor of Ty (S.cerevisiae) 4 homolog

Seq. No.	195606

Contig ID 19434_1.R1039
5'-most EST g5048693

Seq. No. 195607
Contig ID 19435_1.R1039
5'-most EST uC-gsflnu33B058f11b1
Method BLASTX
NCBI GI g3152606
BLAST score 418
E value 4.0e-41
Match length 81
% identity 86
NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No. 195608
Contig ID 19449_1.R1039
5'-most EST LIB3145-024-Q1-K1-F8
Method BLASTX
NCBI GI g4415916
BLAST score 145
E value 7.0e-09
Match length 103
% identity 30
NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No. 195609
Contig ID 19450_1.R1039
5'-most EST uC-gsronu33B147b09b1
Method BLASTX
NCBI GI g2351374
BLAST score 381
E value 1.0e-36
Match length 82
% identity 89
NCBI Description (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No. 195610
Contig ID 19469_1.R1039
5'-most EST LIB3166-058-P1-K1-D5
Method BLASTX
NCBI GI g3924596
BLAST score 1337
E value 1.0e-148
Match length 306
% identity 84
NCBI Description (AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No. 195611
Contig ID 19474_1.R1039
5'-most EST uC-gsronu33B078h02b1

Seq. No. 195612
Contig ID 19478_1.R1039

5'-most EST	LIB3145-056-Q1-K1-B4
Method	BLASTX
NCBI GI	g2244956
BLAST score	239
E value	8.0e-20
Match length	146
% identity	33
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	195613
Contig ID	19499_1.R1039
5'-most EST	LIB3146-010-Q1-K1-D3
Method	BLASTX
NCBI GI	g1916292
BLAST score	198
E value	4.0e-15
Match length	93
% identity	39
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]

Seq. No.	195614
Contig ID	19502_1.R1039
5'-most EST	uC-gsflnu33B128a02b1
Method	BLASTX
NCBI GI	g2760839
BLAST score	683
E value	7.0e-96
Match length	221
% identity	82
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	195615
Contig ID	19503_1.R1039
5'-most EST	LIB3145-025-Q1-K1-D12
Method	BLASTX
NCBI GI	g1172633
BLAST score	377
E value	4.0e-36
Match length	83
% identity	87
NCBI Description	PROLIFERA PROTEIN >gi|675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

Seq. No.	195616
Contig ID	19504_1.R1039
5'-most EST	LIB3145-025-Q1-K1-D2
Method	BLASTX
NCBI GI	g4105772
BLAST score	502
E value	6.0e-51
Match length	110
% identity	46
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	195617
Contig ID	19506_1.R1039
5'-most EST	LIB3146-047-Q1-K1-F3
Method	BLASTN
NCBI GI	g4105771
BLAST score	54
E value	2.0e-21
Match length	230
% identity	81
NCBI Description	Petunia x hybrida PGP9B (PGP9B) mRNA, complete cds

Seq. No.	195618
Contig ID	19509_1.R1039
5'-most EST	LIB3196-033-P1-M1-C4
Method	BLASTX
NCBI GI	g3769300
BLAST score	572
E value	7.0e-59
Match length	176
% identity	61
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	195619
Contig ID	19509_2.R1039
5'-most EST	uC-gsflnu33B036g10b1
Method	BLASTX
NCBI GI	g2865175
BLAST score	327
E value	2.0e-30
Match length	86
% identity	69
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No.	195620
Contig ID	19511_1.R1039
5'-most EST	uC-gsflmaxxa038e06b1
Method	BLASTX
NCBI GI	g4510364
BLAST score	270
E value	2.0e-23
Match length	194
% identity	39
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195621
Contig ID	19514_1.R1039
5'-most EST	g5048904
Method	BLASTX
NCBI GI	g3342802
BLAST score	941
E value	1.0e-121
Match length	268
% identity	82
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	195622

Contig ID	19516_1.R1039
5'-most EST	uC-gsronu33B155g08b2
Method	BLASTX
NCBI GI	g99737
BLAST score	637
E value	2.0e-66
Match length	142
% identity	85
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi|16189|emb|CAA46815| (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	195623
Contig ID	19517_1.R1039
5'-most EST	uC-gsflnu33B093g05b1
Method	BLASTX
NCBI GI	g2809385
BLAST score	943
E value	1.0e-108
Match length	246
% identity	81
NCBI Description	(AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No.	195624
Contig ID	19517_2.R1039
5'-most EST	LIB3166-022-P1-K1-A7
Method	BLASTN
NCBI GI	g2580498
BLAST score	66
E value	2.0e-28
Match length	346
% identity	80
NCBI Description	Eschscholtzia californica NADPH:ferrihemoprotein oxidoreductase mRNA, complete cds

Seq. No.	195625
Contig ID	19518_1.R1039
5'-most EST	LIB3145-037-Q1-K1-C2

Seq. No.	195626
Contig ID	19519_1.R1039
5'-most EST	LIB3145-025-Q1-K1-E6

Seq. No.	195627
Contig ID	19522_1.R1039
5'-most EST	LIB3145-025-Q1-K1-E9
Method	BLASTX
NCBI GI	g3243274
BLAST score	514
E value	5.0e-52
Match length	182
% identity	60
NCBI Description	(AF072134) TCP3 [Arabidopsis thaliana]

Seq. No.	195628
Contig ID	19523_1.R1039

5'-most EST LIB3145-025-Q1-K1-F1

Seq. No. 195629
Contig ID 19528_1.R1039
5'-most EST LIB3145-025-Q1-K1-F6

Seq. No. 195630
Contig ID 19549_1.R1039
5'-most EST LIB3145-025-Q1-K1-H4
Method BLASTX
NCBI GI g4539008
BLAST score 279
E value 1.0e-24
Match length 129
% identity 53
NCBI Description (AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No. 195631
Contig ID 19554_1.R1039
5'-most EST LIB3165-055-P1-K1-H5
Method BLASTX
NCBI GI g927575
BLAST score 405
E value 2.0e-39
Match length 90
% identity 77
NCBI Description (U12926) alpha galactosidase [Glycine max]

Seq. No. 195632
Contig ID 19555_1.R1039
5'-most EST LIB3166-027-P1-K1-G1

Seq. No. 195633
Contig ID 19556_1.R1039
5'-most EST LIB3145-026-Q1-K1-A10

Seq. No. 195634
Contig ID 19557_1.R1039
5'-most EST LIB3145-026-Q1-K1-A11
Method BLASTX
NCBI GI g4033469
BLAST score 366
E value 1.0e-34
Match length 218
% identity 44
NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41
>gi|1707370|emb|CAA67799| (X99436) splicing factor
[Arabidopsis thaliana]

Seq. No. 195635
Contig ID 19559_1.R1039
5'-most EST LIB3166-047-P1-K1-G11

Seq. No. 195636
Contig ID 19577_1.R1039
5'-most EST LIB3197-015-P1-M1-B12
Method BLASTX

NCBI GI	g2660677
BLAST score	298
E value	5.0e-53
Match length	160
% identity	66
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	195637
Contig ID	19579_1.R1039
5'-most EST	LIB3145-026-Q1-K1-C4

Seq. No.	195638
Contig ID	19580_1.R1039
5'-most EST	LIB3145-026-Q1-K1-C6

Seq. No.	195639
Contig ID	19597_1.R1039
5'-most EST	uC-gsflmaxxa069b05b1
Method	BLASTX
NCBI GI	g1888485
BLAST score	1412
E value	1.0e-157
Match length	325
% identity	80
NCBI Description	(Y11749) dihydroflavonol 4-reductase [Vitis vinifera]

Seq. No.	195640
Contig ID	19610_1.R1039
5'-most EST	LIB3145-051-Q1-K1-F7
Method	BLASTX
NCBI GI	g3894387
BLAST score	209
E value	3.0e-16
Match length	172
% identity	4
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	195641
Contig ID	19636_1.R1039
5'-most EST	LIB3145-027-Q1-K1-G1
Method	BLASTX
NCBI GI	g2414156
BLAST score	688
E value	9.0e-73
Match length	141
% identity	92
NCBI Description	(Y09787) delta-endotoxin [Bacillus thuringiensis]

Seq. No.	195642
Contig ID	19649_1.R1039
5'-most EST	LIB3145-028-Q1-K1-A6

Seq. No.	195643
Contig ID	19652_1.R1039
5'-most EST	LIB3145-028-Q1-K1-B1
Method	BLASTX
NCBI GI	g3822225

BLAST score 322
E value 1.0e-36
Match length 133
% identity 61
NCBI Description (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No. 195644
Contig ID 19655_1.R1039
5'-most EST LIB3145-028-Q1-K1-B12

Seq. No. 195645
Contig ID 19657_1.R1039
5'-most EST LIB3148-038-Q1-K1-B3

Seq. No. 195646
Contig ID 19658_1.R1039
5'-most EST LIB3145-028-Q1-K1-B4

Seq. No. 195647
Contig ID 19658_2.R1039
5'-most EST LIB3145-050-Q1-K1-A2

Seq. No. 195648
Contig ID 19660_1.R1039
5'-most EST LIB3145-028-Q1-K1-B7

Seq. No. 195649
Contig ID 19663_1.R1039
5'-most EST LIB3145-028-Q1-K1-C10
Method BLASTX
NCBI GI g3608495
BLAST score 402
E value 1.0e-48
Match length 145
% identity 73
NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi|4510351|gb|AAD21440.1| (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No. 195650
Contig ID 19666_1.R1039
5'-most EST LIB3146-028-Q1-K1-F5
Method BLASTX
NCBI GI g1707017
BLAST score 205
E value 4.0e-16
Match length 71
% identity 58
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 195651
Contig ID 19667_1.R1039
5'-most EST uC-gsflmaxxa076c09b1
Method BLASTX
NCBI GI g1778376
BLAST score 800

E value 1.0e-127
Match length 295
% identity 76
NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 195652
Contig ID 19668_1.R1039
5'-most EST LIB3166-030-P1-K1-B9
Method BLASTX
NCBI GI g4469023
BLAST score 632
E value 1.0e-65
Match length 186
% identity 74
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 195653
Contig ID 19673_1.R1039
5'-most EST LIB3146-020-Q1-K1-D10
Method BLASTX
NCBI GI g4001803
BLAST score 105
E value 1.0e-11
Match length 59
% identity 61
NCBI Description (AF041474) BAF53a [Homo sapiens] >gi|4218064|dbj|BAA74577|
(AB015907) actin-related protein [Homo sapiens]

Seq. No. 195654
Contig ID 19675_1.R1039
5'-most EST g5046055
Method BLASTX
NCBI GI g1350548
BLAST score 306
E value 1.0e-27
Match length 112
% identity 53
NCBI Description (L47609) heat shock-like protein [Picea glauca]

Seq. No. 195655
Contig ID 19676_1.R1039
5'-most EST LIB3189-024-P1-K1-A12
Method BLASTX
NCBI GI g4580389
BLAST score 668
E value 3.0e-70
Match length 155
% identity 79
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 195656
Contig ID 19688_1.R1039
5'-most EST LIB3272-004-P1-K1-G3
Method BLASTX
NCBI GI g2982297
BLAST score 1107
E value 1.0e-121

Match length 232
% identity 92
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]

Seq. No. 195657
Contig ID 19692_1.R1039
5'-most EST LIB3145-028-Q1-K1-E9

Seq. No. 195658
Contig ID 19700_1.R1039
5'-most EST LIB3145-028-Q1-K1-F6
Method BLASTX
NCBI GI g3128168
BLAST score 830
E value 3.0e-89
Match length 189
% identity 76
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 195659
Contig ID 19708_1.R1039
5'-most EST LIB3145-028-Q1-K1-G2
Method BLASTX
NCBI GI g3860258
BLAST score 161
E value 4.0e-11
Match length 52
% identity 60
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 195660
Contig ID 19709_1.R1039
5'-most EST LIB3145-028-Q1-K1-G3
Method BLASTX
NCBI GI g2244841
BLAST score 292
E value 4.0e-26
Match length 87
% identity 67
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 195661
Contig ID 19714_1.R1039
5'-most EST LIB3149-020-Q1-K1-B12
Method BLASTX
NCBI GI g3873807
BLAST score 254
E value 1.0e-21
Match length 134
% identity 45
NCBI Description (Z49907) B0491.1 [Caenorhabditis elegans]

Seq. No. 195662
Contig ID 19715_1.R1039
5'-most EST LIB3145-028-Q1-K1-H1
Method BLASTN

NCBI GI g4454587
BLAST score 33
E value 5.0e-09
Match length 98
% identity 90
NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 195663
Contig ID 19725_1.R1039
5'-most EST g3326794

Seq. No. 195664
Contig ID 19733_1.R1039
5'-most EST LIB3145-029-Q1-K1-A4

Seq. No. 195665
Contig ID 19737_1.R1039
5'-most EST g3325891
Method BLASTN
NCBI GI g2618604
BLAST score 36
E value 2.0e-10
Match length 178
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 195666
Contig ID 19754_1.R1039
5'-most EST LIB3165-012-P1-K1-E6
Method BLASTX
NCBI GI g1130682
BLAST score 317
E value 3.0e-29
Match length 62
% identity 98
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No. 195667
Contig ID 19762_1.R1039
5'-most EST LIB3197-040-Q1-M1-E10
Method BLASTX
NCBI GI g4415908
BLAST score 334
E value 1.0e-46
Match length 157
% identity 73
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 195668
Contig ID 19776_1.R1039
5'-most EST uC-gsflmaxxa096h10b1
Method BLASTX
NCBI GI g1947137
BLAST score 529
E value 2.0e-53

Match length	312
% identity	38
NCBI Description	(AF000264) similar to the ATP-binding transport protein family (ABC transporters). [Caenorhabditis elegans]

Seq. No.	195669
Contig ID	19779_1.R1039
5'-most EST	LIB3145-029-Q1-K1-E8
Method	BLASTX
NCBI GI	g4049341
BLAST score	180
E value	3.0e-28
Match length	153
% identity	46
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	195670
Contig ID	19780_1.R1039
5'-most EST	LIB3272-039-P1-K1-B2

Seq. No.	195671
Contig ID	19784_1.R1039
5'-most EST	LIB3145-029-Q1-K1-F3
Method	BLASTX
NCBI GI	g2558962
BLAST score	382
E value	5.0e-45
Match length	108
% identity	97
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	195672
Contig ID	19785_1.R1039
5'-most EST	uC-gsflnu33B027e10b1
Method	BLASTN
NCBI GI	g4309679
BLAST score	123
E value	2.0e-62
Match length	278
% identity	44
NCBI Description	Arabidopsis thaliana phosphoribosylanthranilate isomerase (PAI1) and (PAI4) genes, complete cds

Seq. No.	195673
Contig ID	19805_1.R1039
5'-most EST	LIB3145-029-Q1-K1-H6
Method	BLASTX
NCBI GI	g136644
BLAST score	154
E value	5.0e-10
Match length	32
% identity	91
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|100765|pir||A34506 23K ubiquitin carrier protein E2 - wheat >gi|170782 (M28059) ubiquitin carrier protein [Triticum vulgare]

Seq. No.	195674
Contig ID	19817_1.R1039
5'-most EST	LIB3145-030-Q1-K1-B10
Seq. No.	195675
Contig ID	19818_1.R1039
5'-most EST	LIB3148-047-Q1-K1-D9
Seq. No.	195676
Contig ID	19827_1.R1039
5'-most EST	LIB3165-042-Q1-K1-G4
Method	BLASTX
NCBI GI	g542020
BLAST score	914
E value	9.0e-99
Match length	234
% identity	74
NCBI Description	sucrose transport protein - castor bean >gi|468562|emb|CAA83436| (Z31561) sucrose carrier [Ricinus communis]
Seq. No.	195677
Contig ID	19829_1.R1039
5'-most EST	LIB3148-034-Q1-K1-E12
Method	BLASTX
NCBI GI	g2252871
BLAST score	170
E value	7.0e-12
Match length	145
% identity	38
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]
Seq. No.	195678
Contig ID	19840_1.R1039
5'-most EST	LIB3145-030-Q1-K1-D4
Seq. No.	195679
Contig ID	19843_1.R1039
5'-most EST	LIB3145-030-Q1-K1-D7
Seq. No.	195680
Contig ID	19855_1.R1039
5'-most EST	LIB3145-030-Q1-K1-E8
Seq. No.	195681
Contig ID	19863_1.R1039
5'-most EST	uC-gsflnu33B019b09b1
Seq. No.	195682
Contig ID	19869_1.R1039
5'-most EST	uC-gsflmaxxa001a08b1
Seq. No.	195683
Contig ID	19873_1.R1039
5'-most EST	LIB3145-030-Q1-K1-H1
Seq. No.	195684

Contig ID	19874_1.R1039
5'-most EST	LIB3145-030-Q1-K1-H10
Seq. No.	195685
Contig ID	19886_1.R1039
5'-most EST	LIB3145-031-Q1-K1-A6
Method	BLASTX
NCBI GI	g3355467
BLAST score	178
E value	7.0e-24
Match length	150
% identity	38
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195686
Contig ID	19891_1.R1039
5'-most EST	LIB3145-031-Q1-K1-B12
Method	BLASTX
NCBI GI	g3355626
BLAST score	806
E value	2.0e-86
Match length	191
% identity	79
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]
Seq. No.	195687
Contig ID	19894_1.R1039
5'-most EST	LIB3166-017-P1-K1-H3
Method	BLASTX
NCBI GI	g3702327
BLAST score	679
E value	3.0e-71
Match length	227
% identity	62
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	195688
Contig ID	19895_1.R1039
5'-most EST	LIB3166-003-P1-K1-A6
Method	BLASTX
NCBI GI	g3461835
BLAST score	171
E value	4.0e-12
Match length	48
% identity	67
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi|3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]
Seq. No.	195689
Contig ID	19899_1.R1039
5'-most EST	LIB3165-050-Q1-K1-G6
Seq. No.	195690
Contig ID	19906_1.R1039
5'-most EST	LIB3145-031-Q1-K1-C6

Seq. No.	195691
Contig ID	19907_1.R1039
5'-most EST	LIB3145-031-Q1-K1-C7
Method	BLASTX
NCBI GI	g3193292
BLAST score	483
E value	1.0e-48
Match length	139
% identity	65
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	195692
Contig ID	19911_1.R1039
5'-most EST	uC-gsronu33B036a09b1
Method	BLASTX
NCBI GI	g3821280
BLAST score	828
E value	8.0e-89
Match length	192
% identity	81
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	195693
Contig ID	19917_1.R1039
5'-most EST	LIB3166-047-P1-K1-H12
Method	BLASTN
NCBI GI	g3821279
BLAST score	144
E value	6.0e-75
Match length	392
% identity	84
NCBI Description	Phaseolus vulgaris mRNA for asparagine synthetase type II

Seq. No.	195694
Contig ID	19923_1.R1039
5'-most EST	LIB3197-051-Q1-M1-G11
Method	BLASTX
NCBI GI	g3341694
BLAST score	593
E value	1.0e-61
Match length	147
% identity	78
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	195695
Contig ID	19926_1.R1039
5'-most EST	LIB3148-037-Q1-K1-H10

Seq. No.	195696
Contig ID	19930_1.R1039
5'-most EST	LIB3145-031-Q1-K1-E7
Method	BLASTX
NCBI GI	g2979553

BLAST score	239
E value	4.0e-20
Match length	117
% identity	45
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195697
Contig ID	19936_1.R1039
5'-most EST	uC-gsf1nu33B015h02b1

Seq. No.	195698
Contig ID	19942_1.R1039
5'-most EST	LIB3145-031-Q1-K1-F8
Method	BLASTX
NCBI GI	g3327957
BLAST score	169
E value	7.0e-12
Match length	51
% identity	59
NCBI Description	(AF060490) TLS-associated protein TASR-2 [Mus musculus] >gi|3327976 (AF067730) TLS-associated protein TASR-2 [Homo sapiens]

Seq. No.	195699
Contig ID	19943_1.R1039
5'-most EST	LIB3145-031-Q1-K1-F9
Method	BLASTX
NCBI GI	g1916292
BLAST score	116
E value	4.0e-09
Match length	87
% identity	43
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]

Seq. No.	195700
Contig ID	19944_1.R1039
5'-most EST	LIB3145-031-Q1-K1-G1
Method	BLASTX
NCBI GI	g3182981
BLAST score	849
E value	3.0e-91
Match length	193
% identity	84
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi|1695692|dbj|BAA13096| (D86494) diminuto [Pisum sativum]

Seq. No.	195701
Contig ID	19945_1.R1039
5'-most EST	LIB3189-018-P1-K1-H7

Seq. No.	195702
Contig ID	19947_1.R1039
5'-most EST	LIB3272-009-P1-K1-B4
Method	BLASTX
NCBI GI	g1730910
BLAST score	186
E value	2.0e-13

Match length	215
% identity	31
NCBI Description	HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION >gi|1256633 (L77246) putative [Bacillus subtilis] >gi|2634609|emb|CAB14107| (Z99115) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	195703
Contig ID	19951_1.R1039
5'-most EST	LIB3145-031-Q1-K1-G5
Method	BLASTX
NCBI GI	g2253583
BLAST score	220
E value	7.0e-18
Match length	84
% identity	61
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195704
Contig ID	19953_1.R1039
5'-most EST	LIB3197-015-P1-M1-A11
Method	BLASTX
NCBI GI	g1351271
BLAST score	1298
E value	1.0e-143
Match length	317
% identity	80
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi|1084309|pir||S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi|806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	195705
Contig ID	19953_2.R1039
5'-most EST	LIB3146-010-Q1-K1-C9
Method	BLASTX
NCBI GI	g1351271
BLAST score	257
E value	2.0e-22
Match length	53
% identity	96
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi|1084309|pir||S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi|806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	195706
Contig ID	19962_1.R1039
5'-most EST	uC-gsflnu33B081f06b1
Method	BLASTX
NCBI GI	g541824
BLAST score	407
E value	2.0e-39
Match length	135
% identity	61

NCBI Description	protein kinase - spinach >gi|457709|emb|CAA82991| (Z30330) protein kinase [Spinacia oleracea]
Seq. No.	195707
Contig ID	19966_1.R1039
5'-most EST	LIB3149-028-Q1-K1-E8
Seq. No.	195708
Contig ID	19970_1.R1039
5'-most EST	LIB3147-034-Q1-K1-D1
Seq. No.	195709
Contig ID	19973_1.R1039
5'-most EST	LIB3146-008-Q1-K1-F2
Method	BLASTX
NCBI GI	g2695925
BLAST score	365
E value	1.0e-34
Match length	96
% identity	75
NCBI Description	(AJ222776) hypothetical protein [Hordeum vulgare]
Seq. No.	195710
Contig ID	19979_1.R1039
5'-most EST	LIB3146-021-Q1-K1-C6
Method	BLASTX
NCBI GI	g3056595
BLAST score	586
E value	1.0e-74
Match length	235
% identity	63
NCBI Description	(AC004255) T1F9.16 [Arabidopsis thaliana]
Seq. No.	195711
Contig ID	19981_1.R1039
5'-most EST	LIB3146-053-Q1-K1-F10
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	7.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]
Seq. No.	195712
Contig ID	19987_1.R1039
5'-most EST	g5048334
Method	BLASTX
NCBI GI	g2801442
BLAST score	740
E value	2.0e-78
Match length	161
% identity	82
NCBI Description	(AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis thaliana]
Seq. No.	195713

Contig ID 19988_1.R1039
5'-most EST g5047781
Method BLASTX
NCBI GI g3746059
BLAST score 452
E value 7.0e-45
Match length 201
% identity 72
NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi|4432812|gb|AAD20662| (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 195714
Contig ID 19989_1.R1039
5'-most EST uC-gsflmaxxa040f04b1
Method BLASTX
NCBI GI g3461833
BLAST score 261
E value 2.0e-22
Match length 54
% identity 87
NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 195715
Contig ID 19995_1.R1039
5'-most EST LIB3145-032-Q1-K1-F2
Method BLASTX
NCBI GI g2827641
BLAST score 416
E value 8.0e-41
Match length 151
% identity 55
NCBI Description (AL021636) Cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No. 195716
Contig ID 19996_1.R1039
5'-most EST LIB3189-016-P1-K1-E2
Method BLASTX
NCBI GI g1841870
BLAST score 501
E value 3.0e-50
Match length 219
% identity 50
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No. 195717
Contig ID 19999_1.R1039
5'-most EST g5050420

Seq. No. 195718
Contig ID 20007_1.R1039
5'-most EST uC-gsflnu33B001c08b1
Method BLASTX
NCBI GI g170507
BLAST score 234
E value 2.0e-19

Match length	96
% identity	52
NCBI Description	(M59251) ORF [Lycopersicon esculentum] >gi|1172167 (U44386) heat shock protein [Solanum lycopersicum]

Seq. No.	195719
Contig ID	20008_1.R1039
5'-most EST	LIB3145-032-Q1-K1-G8

Seq. No.	195720
Contig ID	20009_1.R1039
5'-most EST	LIB3145-053-Q1-K1-E5
Method	BLASTX
NCBI GI	g4263695
BLAST score	188
E value	4.0e-14
Match length	111
% identity	16
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	195721
Contig ID	20010_1.R1039
5'-most EST	uC-gsflmaxxa042c02b1
Method	BLASTX
NCBI GI	g4325371
BLAST score	363
E value	2.0e-34
Match length	97
% identity	70
NCBI Description	(AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No.	195722
Contig ID	20015_1.R1039
5'-most EST	uC-gsflmaxxa067b09b1
Method	BLASTX
NCBI GI	g3668089
BLAST score	240
E value	3.0e-20
Match length	97
% identity	47
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	195723
Contig ID	20017_1.R1039
5'-most EST	LIB3145-032-Q1-K1-H9

Seq. No.	195724
Contig ID	20021_1.R1039
5'-most EST	LIB3145-033-Q1-K1-A2
Method	BLASTX
NCBI GI	g3319353
BLAST score	404
E value	3.0e-39
Match length	147
% identity	48

NCBI Description	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
Seq. No.	195725
Contig ID	20036_1.R1039
5'-most EST	LIB3145-033-Q1-K1-C2
Seq. No.	195726
Contig ID	20041_1.R1039
5'-most EST	LIB3149-004-P1-K1-C6
Seq. No.	195727
Contig ID	20043_1.R1039
5'-most EST	LIB3146-041-Q1-K1-D2
Method	BLASTX
NCBI GI	g3152613
BLAST score	198
E value	4.0e-15
Match length	105
% identity	43
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195728
Contig ID	20046_1.R1039
5'-most EST	LIB3145-033-Q1-K1-D4
Method	BLASTX
NCBI GI	g4454012
BLAST score	1472
E value	1.0e-164
Match length	394
% identity	66
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]
Seq. No.	195729
Contig ID	20060_1.R1039
5'-most EST	g5049345
Method	BLASTX
NCBI GI	g3426038
BLAST score	894
E value	1.0e-96
Match length	246
% identity	34
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.	195730
Contig ID	20084_1.R1039
5'-most EST	LIB3145-034-Q1-K1-A6
Method	BLASTX
NCBI GI	g2244841
BLAST score	155
E value	4.0e-10
Match length	195
% identity	31
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195731

Contig ID 20085_1.R1039
5'-most EST LIB3145-056-Q1-K1-A1

Seq. No. 195732
Contig ID 20093_1.R1039
5'-most EST LIB3145-040-Q1-K1-G5
Method BLASTX
NCBI GI g2978452
BLAST score 412
E value 2.0e-40
Match length 113
% identity 71
NCBI Description (AE001274) MCAK; L549.3 [Leishmania major]

Seq. No. 195733
Contig ID 20104_1.R1039
5'-most EST g5048441
Method BLASTX
NCBI GI g2911058
BLAST score 691
E value 1.0e-72
Match length 190
% identity 69
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 195734
Contig ID 20107_1.R1039
5'-most EST g5048660
Method BLASTX
NCBI GI g1708423
BLAST score 307
E value 1.0e-27
Match length 130
% identity 43
NCBI Description ISOFLAVONE REDUCTASE HOMOLOG A622 >gi|507823|dbj|BAA05866|
(D28505) A622 [Nicotiana tabacum]

Seq. No. 195735
Contig ID 20112_1.R1039
5'-most EST LIB3165-060-Q1-K1-E10
Method BLASTN
NCBI GI g2244991
BLAST score 38
E value 7.0e-12
Match length 102
% identity 84
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
fragment No

Seq. No. 195736
Contig ID 20114_1.R1039
5'-most EST LIB3145-034-Q1-K1-D5
Method BLASTX
NCBI GI g3860249
BLAST score 479
E value 9.0e-48
Match length 177

% identity	60
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	195737
Contig ID	20116_1.R1039
5'-most EST	uC-gsflnu33B113a05b1

Seq. No.	195738
Contig ID	20127_1.R1039
5'-most EST	LIB3272-013-P1-K1-C7
Method	BLASTX
NCBI GI	g3281869
BLAST score	321
E value	1.0e-29
Match length	102
% identity	65
NCBI Description	(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi|3435094 (AF033586) 9G8-like SR protein [Arabidopsis thaliana]

Seq. No.	195739
Contig ID	20130_1.R1039
5'-most EST	uC-gsflnu33B107c02b1
Method	BLASTX
NCBI GI	g945039
BLAST score	1261
E value	1.0e-139
Match length	304
% identity	78
NCBI Description	(U25027) phosphatidylinositol-specific phospholipase C [Glycine max]

Seq. No.	195740
Contig ID	20142_1.R1039
5'-most EST	uC-gsronu33B147d12b1
Method	BLASTX
NCBI GI	g115524
BLAST score	403
E value	6.0e-39
Match length	147
% identity	52
NCBI Description	CALMODULIN >gi|71687|pir||MCPO calmodulin - potato >gi|169477 (J04559) calmodulin [Solanum tuberosum]

Seq. No.	195741
Contig ID	20149_1.R1039
5'-most EST	LIB3145-034-Q1-K1-H2

Seq. No.	195742
Contig ID	20151_1.R1039
5'-most EST	LIB3196-025-P1-M1-H7

Seq. No.	195743
Contig ID	20152_1.R1039
5'-most EST	LIB3272-055-P1-K1-B5
Method	BLASTX
NCBI GI	g3241945

BLAST score	266
E value	3.0e-23
Match length	128
% identity	44
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	195744
Contig ID	20155_1.R1039
5'-most EST	LIB3145-035-Q1-K1-A1
Method	BLASTX
NCBI GI	g3184285
BLAST score	225
E value	2.0e-18
Match length	63
% identity	65
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195745
Contig ID	20158_1.R1039
5'-most EST	g5048020
Method	BLASTX
NCBI GI	g2244939
BLAST score	259
E value	5.0e-22
Match length	185
% identity	35
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195746
Contig ID	20159_1.R1039
5'-most EST	LIB3146-006-Q1-K1-D10

Seq. No.	195747
Contig ID	20170_1.R1039
5'-most EST	LIB3166-037-P1-K1-B4
Method	BLASTX
NCBI GI	g1279563
BLAST score	412
E value	1.0e-39
Match length	233
% identity	36
NCBI Description	(X88845) nuM1 [Medicago sativa]

Seq. No.	195748
Contig ID	20185_1.R1039
5'-most EST	LIB3148-050-Q1-K1-E4

Seq. No.	195749
Contig ID	20198_1.R1039
5'-most EST	LIB3147-031-Q1-K1-H8
Method	BLASTX
NCBI GI	g2781231
BLAST score	280
E value	1.0e-24
Match length	190
% identity	37
NCBI Description	Chain A, Agglutinin In Complex With T-Disaccharide

>gi|2781232|pdb|1JLX|B Chain B, Agglutinin In Complex With T-Disaccharide >gi|2781233|pdb|1JLY|A Chain A, Crystal Structure Of Amaranthus Caudatus Agglutinin >gi|2781234|pdb|1JLY|B Chain B, Crystal Structure Of Amaranthus Caudatus Agglutinin

Seq. No.	195750
Contig ID	20200_1.R1039
5'-most EST	LIB3165-013-P1-K1-B11
Method	BLASTX
NCBI GI	g2738756
BLAST score	1221
E value	1.0e-135
Match length	280
% identity	81
NCBI Description	(AF016282) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	195751
Contig ID	20207_1.R1039
5'-most EST	uC-gsflmaxxa045c05b1

Seq. No.	195752
Contig ID	20221_1.R1039
5'-most EST	LIB3272-044-P1-K1-H10

Seq. No.	195753
Contig ID	20230_1.R1039
5'-most EST	uC-gsronu33B008h03b1

Seq. No.	195754
Contig ID	20234_1.R1039
5'-most EST	uC-gsflnu33B012e07b1
Method	BLASTX
NCBI GI	g3319343
BLAST score	402
E value	2.0e-39
Match length	102
% identity	69
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.91) [Arabidopsis thaliana]

Seq. No.	195755
Contig ID	20235_1.R1039
5'-most EST	LIB3272-028-P1-K1-G6
Method	BLASTX
NCBI GI	g2827559
BLAST score	368
E value	7.0e-35
Match length	151
% identity	52
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi|3292808|emb|CAA19798| (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	195756
Contig ID	20239_1.R1039

5'-most EST	LIB3148-051-Q1-K1-B7
Seq. No.	195757
Contig ID	20242_1.R1039
5'-most EST	LIB3145-037-Q1-K1-C10
Method	BLASTX
NCBI GI	g4539351
BLAST score	278
E value	2.0e-24
Match length	141
% identity	50
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	195758
Contig ID	20256_1.R1039
5'-most EST	LIB3145-037-Q1-K1-D3
Method	BLASTX
NCBI GI	g3915866
BLAST score	688
E value	1.0e-72
Match length	161
% identity	78
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi|2995455|emb|CAA62901| (X91787) tRNA-glutamine synthetase [Lupinus luteus]
Seq. No.	195759
Contig ID	20270_1.R1039
5'-most EST	LIB3145-054-Q1-K1-H12
Method	BLASTX
NCBI GI	g3643602
BLAST score	909
E value	3.0e-98
Match length	244
% identity	72
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]
Seq. No.	195760
Contig ID	20274_1.R1039
5'-most EST	LIB3145-037-Q1-K1-F5
Seq. No.	195761
Contig ID	20278_1.R1039
5'-most EST	LIB3146-025-Q1-K2-E10
Method	BLASTX
NCBI GI	g537639
BLAST score	181
E value	4.0e-13
Match length	97
% identity	41
NCBI Description	(U14168) lipid transfer protein [Nicotiana tabacum]
Seq. No.	195762
Contig ID	20281_1.R1039
5'-most EST	LIB3189-007-P1-K1-C7
Method	BLASTX

NCBI GI	g2880049
BLAST score	185
E value	1.0e-24
Match length	105
% identity	62
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195763
Contig ID	20284_1.R1039
5'-most EST	LIB3166-023-P1-K1-H1
Method	BLASTX
NCBI GI	g4580523
BLAST score	493
E value	1.0e-49
Match length	191
% identity	46
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	195764
Contig ID	20287_1.R1039
5'-most EST	LIB3145-037-Q1-K1-G2
Method	BLASTX
NCBI GI	g2465923
BLAST score	402
E value	3.0e-39
Match length	124
% identity	60
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	195765
Contig ID	20295_1.R1039
5'-most EST	g5047439
Method	BLASTX
NCBI GI	g3915826
BLAST score	546
E value	2.0e-61
Match length	175
% identity	66
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	195766
Contig ID	20307_1.R1039
5'-most EST	LIB3145-038-Q1-K1-A4
Method	BLASTX
NCBI GI	g1362003
BLAST score	1092
E value	1.0e-120
Match length	249
% identity	86
NCBI Description	protein phosphatase 2A B regulatory chain 55K - Arabidopsis thaliana >gi|710330 (U18129) 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana]

Seq. No.	195767
Contig ID	20325_1.R1039
5'-most EST	LIB3145-038-Q1-K1-C10

Method	BLASTX
NCBI GI	g3914007
BLAST score	840
E value	2.0e-90
Match length	218
% identity	78
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi|1848291 (U88087) LON protease homolog [Arabidopsis thaliana]

Seq. No.	195768
Contig ID	20326_1.R1039
5'-most EST	LIB3272-016-P1-K1-E11

Seq. No.	195769
Contig ID	20339_1.R1039
5'-most EST	uC-gsflnu33B037g04b1
Method	BLASTX
NCBI GI	g543565
BLAST score	215
E value	4.0e-17
Match length	68
% identity	56
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi|493721|dbj|BAA06462| (D30802) TED4 [Zinnia elegans] >gi|641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	195770
Contig ID	20340_1.R1039
5'-most EST	LIB3148-033-Q1-K1-D6
Method	BLASTX
NCBI GI	g3182981
BLAST score	1761
E value	0.0e+00
Match length	366
% identity	87
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi|1695692|dbj|BAA13096| (D86494) diminuto [Pisum sativum]

Seq. No.	195771
Contig ID	20341_1.R1039
5'-most EST	LIB3145-038-Q1-K1-D7
Method	BLASTX
NCBI GI	g3548802
BLAST score	256
E value	5.0e-22
Match length	98
% identity	50
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi|4335769|gb|AAD17446| (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	195772
Contig ID	20353_1.R1039
5'-most EST	LIB3146-060-Q1-K1-D2

Seq. No.	195773

Contig ID	20358_1.R1039
5'-most EST	LIB3145-038-Q1-K1-F12
Method	BLASTX
NCBI GI	g511497
BLAST score	419
E value	5.0e-65
Match length	148
% identity	78
NCBI Description	(L20978) oleoyl-acyl carrier protein thioesterase [Coriandrum sativum]

Seq. No.	195774
Contig ID	20361_1.R1039
5'-most EST	LIB3196-048-P1-M1-A6
Method	BLASTX
NCBI GI	g2129842
BLAST score	169
E value	9.0e-12
Match length	53
% identity	57
NCBI Description	SE60 protein - soybean >gi|509769|emb|CAA79164| (Z18359) seed-specific low molecular weight sulfur-rich protein [Glycine max]

Seq. No.	195775
Contig ID	20363_1.R1039
5'-most EST	g5048469
Method	BLASTX
NCBI GI	g4107099
BLAST score	390
E value	3.0e-41
Match length	112
% identity	78
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi|4156245|dbj|BAA37112| (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	195776
Contig ID	20363_2.R1039
5'-most EST	LIB3147-049-Q1-K1-E10
Method	BLASTX
NCBI GI	g4107099
BLAST score	391
E value	8.0e-38
Match length	117
% identity	64
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi|4156245|dbj|BAA37112| (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	195777
Contig ID	20366_1.R1039
5'-most EST	uC-gsflmaxxa055b09b1
Method	BLASTX
NCBI GI	g399940
BLAST score	1045
E value	1.0e-132

Match length	261
% identity	93
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi|100004|pir||S25005 heat shock protein, 70K - kidney bean >gi|22636|emb|CAA47345| (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	195778
Contig ID	20371_1.R1039
5'-most EST	g5045616
Method	BLASTX
NCBI GI	g3046695
BLAST score	125
E value	2.0e-12
Match length	101
% identity	42
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	195779
Contig ID	20372_1.R1039
5'-most EST	LIB3145-038-Q1-K1-G4

Seq. No.	195780
Contig ID	20378_1.R1039
5'-most EST	LIB3145-038-Q1-K1-H1
Method	BLASTX
NCBI GI	g1149595
BLAST score	726
E value	7.0e-77
Match length	189
% identity	74
NCBI Description	(Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	195781
Contig ID	20387_1.R1039
5'-most EST	LIB3166-003-P1-K1-F7
Method	BLASTX
NCBI GI	g4097547
BLAST score	233
E value	2.0e-19
Match length	49
% identity	46
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	195782
Contig ID	20396_1.R1039
5'-most EST	LIB3272-010-P1-K1-B7
Method	BLASTX
NCBI GI	g4469003
BLAST score	345
E value	3.0e-32
Match length	179
% identity	43
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	195783

Contig ID 20397_1.R1039
5'-most EST LIB3145-039-Q1-K1-A8

Seq. No. 195784
Contig ID 20398_1.R1039
5'-most EST LIB3145-039-Q1-K1-B10
Method BLASTX
NCBI GI g1168470
BLAST score 159
E value 8.0e-11
Match length 79
% identity 49
NCBI Description PROTEIN KINASE APK1A >gi|282877|pir||S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi|217829|dbj|BAA02092| (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 195785
Contig ID 20409_1.R1039
5'-most EST LIB3166-001-Q1-K1-C6
Method BLASTX
NCBI GI g3021355
BLAST score 409
E value 5.0e-40
Match length 89
% identity 88
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 195786
Contig ID 20409_2.R1039
5'-most EST LIB3147-056-Q1-K1-A7
Method BLASTX
NCBI GI g3021355
BLAST score 594
E value 1.0e-61
Match length 122
% identity 89
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 195787
Contig ID 20410_1.R1039
5'-most EST LIB3272-009-P1-K1-B10

Seq. No. 195788
Contig ID 20413_2.R1039
5'-most EST LIB3145-039-Q1-K1-C6

Seq. No. 195789
Contig ID 20423_1.R1039
5'-most EST LIB3272-002-P1-K1-A1
Method BLASTX
NCBI GI g3738325
BLAST score 390
E value 9.0e-38

Match length	112
% identity	71
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	195790
Contig ID	20427_2.R1039
5'-most EST	LIB3165-028-P1-K1-H1
Method	BLASTX
NCBI GI	g4103959
BLAST score	178
E value	8.0e-13
Match length	126
% identity	22
NCBI Description	(AF030033) calmodulin [Phaseolus vulgaris]

Seq. No.	195791
Contig ID	20436_1.R1039
5'-most EST	LIB3145-039-Q1-K1-E8
Method	BLASTX
NCBI GI	g3881978
BLAST score	170
E value	6.0e-12
Match length	42
% identity	79
NCBI Description	(Y11348) annexin-like protein [Medicago sativa]

Seq. No.	195792
Contig ID	20440_1.R1039
5'-most EST	uC-gsflmaxxa057h01b1

Seq. No.	195793
Contig ID	20451_1.R1039
5'-most EST	g5049532
Method	BLASTX
NCBI GI	g4544386
BLAST score	606
E value	9.0e-63
Match length	171
% identity	74
NCBI Description	(AC007047) putative cell division control protein [Arabidopsis thaliana]

Seq. No.	195794
Contig ID	20452_1.R1039
5'-most EST	uC-gsronu33B021a03b1
Method	BLASTN
NCBI GI	g1335861
BLAST score	74
E value	2.0e-33
Match length	283
% identity	84
NCBI Description	Glycine max clathrin heavy chain mRNA, complete cds

Seq. No.	195795
Contig ID	20462_1.R1039
5'-most EST	LIB3145-040-Q1-K1-A10

Seq. No.	195796
Contig ID	20464_1.R1039
5'-most EST	uC-gsflnu33B146a04b1
Method	BLASTX
NCBI GI	g3763933
BLAST score	361
E value	3.0e-34
Match length	95
% identity	74
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	195797
Contig ID	20469_1.R1039
5'-most EST	LIB3145-040-Q1-K1-A6
Method	BLASTX
NCBI GI	g2289003
BLAST score	418
E value	7.0e-41
Match length	192
% identity	58
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	195798
Contig ID	20482_1.R1039
5'-most EST	uC-gsflmaxxa054h06b1

Seq. No.	195799
Contig ID	20485_1.R1039
5'-most EST	uC-gsflnu33B001d10b1
Method	BLASTN
NCBI GI	g3128142
BLAST score	34
E value	3.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	195800
Contig ID	20490_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A6
Method	BLASTX
NCBI GI	g3128218
BLAST score	588
E value	9.0e-61
Match length	143
% identity	76
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	195801
Contig ID	20496_1.R1039
5'-most EST	LIB3196-028-P1-M1-C11

Seq. No.	195802
Contig ID	20497_1.R1039

5'-most EST	LIB3272-034-P1-K1-G8
Method	BLASTX
NCBI GI	g2245064
BLAST score	225
E value	2.0e-18
Match length	76
% identity	61
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195803
Contig ID	20502_1.R1039
5'-most EST	LIB3146-056-Q1-K1-G8

Seq. No.	195804
Contig ID	20502_2.R1039
5'-most EST	uC-gsflnu33B091a01b1

Seq. No.	195805
Contig ID	20507_1.R1039
5'-most EST	LIB3145-040-Q1-K1-E3
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	195806
Contig ID	20510_1.R1039
5'-most EST	g3326324

Seq. No.	195807
Contig ID	20517_1.R1039
5'-most EST	uC-gsflmaxxa048c02b1
Method	BLASTX
NCBI GI	g2497219
BLAST score	213
E value	6.0e-17
Match length	119
% identity	37
NCBI Description	HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION >gi|626266|pir||S47453 probable membrane protein YMR292w - yeast (Saccharomyces cerevisiae) >gi|530349|emb|CAA56801| (X80836) len:138, CAI:0.12, potential spliced gene, hydropho bic composition [Saccharomyces cerevisiae]

Seq. No.	195808
Contig ID	20521_1.R1039
5'-most EST	uC-gsronu33B147a04b1
Method	BLASTX
NCBI GI	g3128203
BLAST score	639
E value	9.0e-67
Match length	173
% identity	72
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	195809
Contig ID	20522_1.R1039
5'-most EST	LIB3145-040-Q1-K1-F8
Method	BLASTX
NCBI GI	g3063698
BLAST score	289
E value	2.0e-25
Match length	186
% identity	51
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	195810
Contig ID	20531_1.R1039
5'-most EST	LIB3145-040-Q1-K1-G7

Seq. No.	195811
Contig ID	20535_1.R1039
5'-most EST	LIB3145-040-Q1-K1-H3
Method	BLASTX
NCBI GI	g2262100
BLAST score	207
E value	6.0e-20
Match length	84
% identity	63
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	195812
Contig ID	20539_1.R1039
5'-most EST	LIB3145-040-Q1-K1-H7

Seq. No.	195813
Contig ID	20541_1.R1039
5'-most EST	uC-gsronu33B169c12b1
Method	BLASTX
NCBI GI	g4056488
BLAST score	536
E value	7.0e-55
Match length	112
% identity	84
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	195814
Contig ID	20552_1.R1039
5'-most EST	LIB3148-034-Q1-K1-F11

Seq. No.	195815
Contig ID	20563_1.R1039
5'-most EST	uC-gsflnu33B006b03b1
Method	BLASTX
NCBI GI	g4235644
BLAST score	187
E value	2.0e-23
Match length	184
% identity	36
NCBI Description	(AF119040) polyprotein [Lycopersicon esculentum]

Seq. No. 195816
Contig ID 20564_1.R1039
5'-most EST LIB3145-041-Q1-K1-C2
Method BLASTX
NCBI GI g3170482
BLAST score 211
E value 1.0e-16
Match length 87
% identity 48
NCBI Description (AF052864) PISTILLATA homolog LtPI-1 [Liriodendron tulipifera]

Seq. No. 195817
Contig ID 20565_1.R1039
5'-most EST LIB3145-041-Q1-K1-C3

Seq. No. 195818
Contig ID 20570_1.R1039
5'-most EST uC-gsronu33B080b12b1

Seq. No. 195819
Contig ID 20575_1.R1039
5'-most EST uC-gsflnu33B085d08b1
Method BLASTX
NCBI GI g4539335
BLAST score 687
E value 1.0e-72
Match length 152
% identity 85
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 195820
Contig ID 20591_1.R1039
5'-most EST LIB3145-041-Q1-K1-F1
Method BLASTX
NCBI GI g3157933
BLAST score 650
E value 4.0e-76
Match length 200
% identity 73
NCBI Description (AC002131) Contains similarity to box helicases gb|U29097 from C. elegans and to the ENBP1 gene product gb|X95995 from Vicia sativa. [Arabidopsis thaliana]

Seq. No. 195821
Contig ID 20592_1.R1039
5'-most EST uC-gsflnu33B022g02b1

Seq. No. 195822
Contig ID 20600_1.R1039
5'-most EST LIB3145-041-Q1-K1-F9

Seq. No. 195823
Contig ID 20605_1.R1039
5'-most EST LIB3145-046-Q1-K1-A5
Method BLASTX
NCBI GI g2924777

BLAST score 400
E value 8.0e-39
Match length 192
% identity 48
NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 195824
Contig ID 20607_1.R1039
5'-most EST LIB3166-002-Q1-K1-D12
Method BLASTX
NCBI GI g1871192
BLAST score 171
E value 1.0e-11
Match length 299
% identity 29
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 195825
Contig ID 20616_1.R1039
5'-most EST LIB3145-041-Q1-K1-H2
Method BLASTX
NCBI GI g4455199
BLAST score 548
E value 4.0e-56
Match length 144
% identity 77
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 195826
Contig ID 20619_1.R1039
5'-most EST LIB3147-029-Q1-K1-A8
Method BLASTX
NCBI GI g2213425
BLAST score 510
E value 8.0e-97
Match length 208
% identity 46
NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 195827
Contig ID 20630_1.R1039
5'-most EST LIB3147-039-Q1-K1-C4
Method BLASTX
NCBI GI g4455159
BLAST score 164
E value 3.0e-11
Match length 45
% identity 64
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 195828
Contig ID 20635_1.R1039
5'-most EST uC-gsflnu33B037h06b1
Method BLASTX
NCBI GI g4325371

BLAST score 406
E value 2.0e-39
Match length 102
% identity 75
NCBI Description (AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No. 195829
Contig ID 20645_1.R1039
5'-most EST g5047975

Seq. No. 195830
Contig ID 20646_1.R1039
5'-most EST uC-gsflnu33B015g12b1

Seq. No. 195831
Contig ID 20649_1.R1039
5'-most EST LIB3148-011-Q1-K1-E1
Method BLASTX
NCBI GI g2924512
BLAST score 302
E value 2.0e-27
Match length 119
% identity 49
NCBI Description (AL022023) beta-galactosidase - like protein [Arabidopsis thaliana]

Seq. No. 195832
Contig ID 20654_1.R1039
5'-most EST LIB3145-042-Q1-K1-D11

Seq. No. 195833
Contig ID 20664_1.R1039
5'-most EST LIB3145-042-Q1-K1-E1
Method BLASTX
NCBI GI g3876465
BLAST score 321
E value 1.0e-29
Match length 79
% identity 77
NCBI Description (Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene;

Seq. No. 195834
Contig ID 20665_1.R1039
5'-most EST LIB3272-045-P1-K1-G1
Method BLASTX
NCBI GI g136251
BLAST score 1176
E value 1.0e-129
Match length 288
% identity 81
NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi|99767|pir||A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi|166892 (M23872)

tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	195835
Contig ID	20668_1.R1039
5'-most EST	g5049064
Method	BLASTX
NCBI GI	g728867
BLAST score	559
E value	4.0e-57
Match length	282
% identity	45
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi|99694|pir||S21961 proline-rich protein APG - Arabidopsis thaliana >gi|22599|emb|CAA42925| (X60377) APG [Arabidopsis thaliana]

Seq. No.	195836
Contig ID	20669_1.R1039
5'-most EST	uC-gsronu33B134g11b1

Seq. No.	195837
Contig ID	20677_1.R1039
5'-most EST	LIB3146-012-Q1-K1-G9
Method	BLASTX
NCBI GI	g1061040
BLAST score	330
E value	1.0e-44
Match length	110
% identity	77
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi|1587694|prf||2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	195838
Contig ID	20679_1.R1039
5'-most EST	LIB3165-036-P1-K1-G11
Method	BLASTX
NCBI GI	g3193286
BLAST score	174
E value	2.0e-12
Match length	55
% identity	58
NCBI Description	(AF069298) T14P8.22 gene product [Arabidopsis thaliana]

Seq. No.	195839
Contig ID	20681_1.R1039
5'-most EST	LIB3145-042-Q1-K1-F5
Method	BLASTX
NCBI GI	g4538967
BLAST score	1116
E value	1.0e-122
Match length	275
% identity	79
NCBI Description	(AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No. 195840

Contig ID	20694_1.R1039
5'-most EST	LIB3145-042-Q1-K1-G9
Method	BLASTX
NCBI GI	g1170182
BLAST score	828
E value	7.0e-89
Match length	221
% identity	73
NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi|479793|pir||S35439 transcription factor HBP-1b homolog - Arabidopsis thaliana >gi|217827|dbj|BAA00933| (D10042) AHBP-1b [Arabidopsis thaliana]

Seq. No.	195841
Contig ID	20695_1.R1039
5'-most EST	LIB3166-050-P1-K1-F4

Seq. No.	195842
Contig ID	20700_1.R1039
5'-most EST	LIB3148-059-Q1-K1-B6

Seq. No.	195843
Contig ID	20701_1.R1039
5'-most EST	g5046362
Method	BLASTX
NCBI GI	g4165025
BLAST score	252
E value	2.0e-21
Match length	114
% identity	45
NCBI Description	(AF043611) zinc-finger protein MCG4 [Homo sapiens]

Seq. No.	195844
Contig ID	20719_1.R1039
5'-most EST	g5046257

Seq. No.	195845
Contig ID	20721_1.R1039
5'-most EST	LIB3147-038-Q1-K2-B9

Seq. No.	195846
Contig ID	20725_1.R1039
5'-most EST	LIB3147-001-Q1-K2-E1
Method	BLASTX
NCBI GI	g3024017
BLAST score	502
E value	9.0e-51
Match length	99
% identity	95
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi|2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	195847
Contig ID	20738_2.R1039
5'-most EST	uC-gsflmaxxa089e02b1
Method	BLASTX

NCBI GI	g1345965
BLAST score	375
E value	4.0e-36
Match length	104
% identity	71
NCBI Description	FLORAL HOMEOTIC PROTEIN FBP2 (FLORAL BINDING PROTEIN 2) >gi|1181186 (M91666) transcription factor [Petunia hybrida]

Seq. No.	195848
Contig ID	20741_1.R1039
5'-most EST	uC-gsronu33B147h06b1
Method	BLASTX
NCBI GI	g2829923
BLAST score	645
E value	2.0e-67
Match length	202
% identity	47
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	195849
Contig ID	20756_1.R1039
5'-most EST	g5046140
Method	BLASTX
NCBI GI	g1657617
BLAST score	607
E value	5.0e-63
Match length	156
% identity	74
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi|3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	195850
Contig ID	20759_1.R1039
5'-most EST	LIB3145-043-Q1-K1-F11
Method	BLASTX
NCBI GI	g2982247
BLAST score	302
E value	3.0e-27
Match length	105
% identity	52
NCBI Description	(AF051206) probable thioredoxin H [Picea mariana]

Seq. No.	195851
Contig ID	20761_1.R1039
5'-most EST	LIB3145-043-Q1-K1-F2
Method	BLASTX
NCBI GI	g4432825
BLAST score	829
E value	5.0e-89
Match length	206
% identity	76
NCBI Description	(AC006593) putative SOP2p protein [Arabidopsis thaliana]

Seq. No.	195852
Contig ID	20787_1.R1039

5'-most EST	uC-gsflmaxxa057f02b1
Method	BLASTX
NCBI GI	g629602
BLAST score	537
E value	6.0e-55
Match length	160
% identity	59
NCBI Description	probable imbibition protein - wild cabbage >gi|488787|emb|CAA55893| (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	195853
Contig ID	20790_1.R1039
5'-most EST	uC-gsflmaxxa070a03b1
Method	BLASTX
NCBI GI	g2098705
BLAST score	256
E value	7.0e-22
Match length	129
% identity	47
NCBI Description	(U82973) pectinesterase [Citrus sinensis]

Seq. No.	195854
Contig ID	20792_1.R1039
5'-most EST	g5048583
Method	BLASTX
NCBI GI	g3063701
BLAST score	592
E value	3.0e-61
Match length	145
% identity	79
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	195855
Contig ID	20796_1.R1039
5'-most EST	LIB3145-044-Q1-K1-B11
Method	BLASTX
NCBI GI	g4510395
BLAST score	424
E value	6.0e-42
Match length	100
% identity	82
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	195856
Contig ID	20797_1.R1039
5'-most EST	uC-gsflnu33B110h09b1

Seq. No.	195857
Contig ID	20799_1.R1039
5'-most EST	LIB3145-044-Q1-K1-B3
Method	BLASTX
NCBI GI	g4115377
BLAST score	656
E value	1.0e-68
Match length	248

% identity	50
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	195858
Contig ID	20802_1.R1039
5'-most EST	LIB3145-044-Q1-K1-B6
Method	BLASTX
NCBI GI	g2367392
BLAST score	295
E value	2.0e-26
Match length	154
% identity	43
NCBI Description	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]

Seq. No.	195859
Contig ID	20805_1.R1039
5'-most EST	LIB3145-044-Q1-K1-B9
Method	BLASTX
NCBI GI	g2554835
BLAST score	617
E value	2.0e-64
Match length	124
% identity	93
NCBI Description	Chain I, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi|2554836|pdb|1YVE|J Chain J, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi|2554837|pdb|1YVE|K Chain K, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi|2554838|pdb|1YVE|L Chain L, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate)

Seq. No.	195860
Contig ID	20807_1.R1039
5'-most EST	LIB3148-012-Q1-K1-H1
Method	BLASTX
NCBI GI	g3461849
BLAST score	573
E value	3.0e-59
Match length	152
% identity	67
NCBI Description	(AC005315) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	195861
Contig ID	20809_1.R1039
5'-most EST	uC-gsronu33B016e12b1
Method	BLASTX
NCBI GI	g3688177
BLAST score	642
E value	4.0e-67
Match length	179
% identity	69

NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]
Seq. No.	195862
Contig ID	20822_1.R1039
5'-most EST	g5048187
Method	BLASTX
NCBI GI	g3873678
BLAST score	200
E value	4.0e-15
Match length	200
% identity	32
NCBI Description	(Z71178) Similarity with yeast hypothetical protein (Swiss prot accession number P40526) [Caenorhabditis elegans]
Seq. No.	195863
Contig ID	20827_1.R1039
5'-most EST	LIB3145-044-Q1-K1-E11
Method	BLASTX
NCBI GI	g2367392
BLAST score	417
E value	1.0e-40
Match length	157
% identity	48
NCBI Description	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
Seq. No.	195864
Contig ID	20845_1.R1039
5'-most EST	g5049731
Method	BLASTX
NCBI GI	g4490331
BLAST score	569
E value	2.0e-58
Match length	140
% identity	80
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.	195865
Contig ID	20848_1.R1039
5'-most EST	uC-gsronu33B046g05b1
Method	BLASTX
NCBI GI	g1370186
BLAST score	969
E value	1.0e-105
Match length	199
% identity	92
NCBI Description	(Z73942) RAB7C [Lotus japonicus]
Seq. No.	195866
Contig ID	20848_2.R1039
5'-most EST	g5045367
Method	BLASTX
NCBI GI	g1370186
BLAST score	980
E value	1.0e-106
Match length	207
% identity	89

NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	195867
Contig ID	20859_1.R1039
5'-most EST	g5045894
Method	BLASTX
NCBI GI	g1848214
BLAST score	765
E value	2.0e-81
Match length	169
% identity	85
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No.	195868
Contig ID	20867_1.R1039
5'-most EST	LIB3145-044-Q1-K1-H8
Method	BLASTX
NCBI GI	g3805845
BLAST score	991
E value	1.0e-108
Match length	360
% identity	65
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	195869
Contig ID	20869_1.R1039
5'-most EST	uC-gsronu33B040b11b1
Method	BLASTX
NCBI GI	g3643607
BLAST score	648
E value	7.0e-68
Match length	153
% identity	44
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	195870
Contig ID	20881_1.R1039
5'-most EST	LIB3145-052-Q1-K1-D2
Method	BLASTX
NCBI GI	g4160300
BLAST score	602
E value	2.0e-62
Match length	226
% identity	54
NCBI Description	(AJ011893) cyclin D3.1 protein [Nicotiana tabacum]

Seq. No.	195871
Contig ID	20886_1.R1039
5'-most EST	LIB3145-045-Q1-K1-B3
Method	BLASTN
NCBI GI	g4160299
BLAST score	42
E value	4.0e-14
Match length	154
% identity	85
NCBI Description	Nicotiana tabacum mRNA for cyclin D3.1 protein (CycD3.1)

Seq. No.	195872
Contig ID	20890_1.R1039
5'-most EST	LIB3145-045-Q1-K1-B8
Method	BLASTX
NCBI GI	g2660643
BLAST score	141
E value	1.0e-08
Match length	138
% identity	28
NCBI Description	(AJ001072) galactose-1-phosphate uridylyltransferase [Thermotoga maritima]

Seq. No.	195873
Contig ID	20895_1.R1039
5'-most EST	LIB3148-047-Q1-K1-C12

Seq. No.	195874
Contig ID	20897_1.R1039
5'-most EST	LIB3149-034-Q1-K1-G5
Method	BLASTX
NCBI GI	g4263713
BLAST score	193
E value	2.0e-14
Match length	120
% identity	43
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195875
Contig ID	20917_1.R1039
5'-most EST	uC-gsflnu33B111d06b1
Method	BLASTX
NCBI GI	g2244898
BLAST score	929
E value	1.0e-100
Match length	230
% identity	78
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	195876
Contig ID	20919_1.R1039
5'-most EST	LIB3166-058-P1-K1-E8

Seq. No.	195877
Contig ID	20919_2.R1039
5'-most EST	uC-gsflmaxxa028g02b1
Method	BLASTX
NCBI GI	g1531758
BLAST score	268
E value	3.0e-23
Match length	55
% identity	85
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi|3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	195878

Contig ID	20921_1.R1039
5'-most EST	LIB3189-047-P1-K1-E10
Method	BLASTX
NCBI GI	g3004550
BLAST score	234
E value	3.0e-19
Match length	103
% identity	50
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195879
Contig ID	20933_1.R1039
5'-most EST	uC-gsflnu33B113d05b1
Method	BLASTX
NCBI GI	g3660469
BLAST score	1142
E value	1.0e-125
Match length	246
% identity	91
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi|4512693|gb|AAD21746.1| (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	195880
Contig ID	20937_1.R1039
5'-most EST	uC-gsflmaxxa057h03b1
Method	BLASTN
NCBI GI	g3660468
BLAST score	191
E value	1.0e-103
Match length	767
% identity	81
NCBI Description	Arabidopsis thaliana mRNA for Succinyl-CoA-ligase beta subunit

Seq. No.	195881
Contig ID	20942_1.R1039
5'-most EST	LIB3145-045-Q1-K1-H2
Method	BLASTX
NCBI GI	g3080427
BLAST score	1015
E value	1.0e-111
Match length	228
% identity	85
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	195882
Contig ID	20947_1.R1039
5'-most EST	LIB3166-008-P1-K1-A12
Method	BLASTX
NCBI GI	g4572681
BLAST score	467
E value	2.0e-46
Match length	173
% identity	51
NCBI Description	(AC006954) putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana]

Seq. No.	195883
Contig ID	20948_1.R1039
5'-most EST	LIB3145-045-Q1-K1-H9

Seq. No.	195884
Contig ID	20951_1.R1039
5'-most EST	LIB3145-046-Q1-K1-A11
Method	BLASTX
NCBI GI	g3281855
BLAST score	201
E value	2.0e-15
Match length	129
% identity	37
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195885
Contig ID	20957_1.R1039
5'-most EST	LIB3196-032-P1-M1-H10
Method	BLASTX
NCBI GI	g4220443
BLAST score	219
E value	2.0e-17
Match length	177
% identity	34
NCBI Description	(AC006216) Similar to gb|X74772 SF16 protein from Helianthus annuus and contains calmodulin-binding motif PF|00612. [Arabidopsis thaliana]

Seq. No.	195886
Contig ID	20959_1.R1039
5'-most EST	LIB3146-034-Q1-K1-H12
Method	BLASTX
NCBI GI	g3334245
BLAST score	325
E value	3.0e-30
Match length	74
% identity	84
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi|2909424|emb|CAA12028| (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	195887
Contig ID	20966_1.R1039
5'-most EST	LIB3272-021-P1-K1-F5
Method	BLASTX
NCBI GI	g3334245
BLAST score	344
E value	2.0e-32
Match length	95
% identity	78
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi|2909424|emb|CAA12028| (AJ224520) Glyoxalase I [Cicer

arietinum]

Seq. No.	195888
Contig ID	20966_2.R1039
5'-most EST	LIB3166-027-P1-K1-G9
Method	BLASTX
NCBI GI	g3334245
BLAST score	798
E value	3.0e-85
Match length	181
% identity	81
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi|2909424|emb|CAA12028| (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	195889
Contig ID	20966_3.R1039
5'-most EST	uC-gsronu33B138f03b1
Method	BLASTN
NCBI GI	g2909423
BLAST score	51
E value	1.0e-19
Match length	163
% identity	83
NCBI Description	Cicer arietinum mRNA for glyoxalase I

Seq. No.	195890
Contig ID	20967_1.R1039
5'-most EST	LIB3196-006-P1-M1-F11
Method	BLASTX
NCBI GI	g2244744
BLAST score	356
E value	1.0e-33
Match length	123
% identity	59
NCBI Description	(Y13676) bZIP DNA-binding protein [Antirrhinum majus]

Seq. No.	195891
Contig ID	20970_1.R1039
5'-most EST	LIB3145-046-Q1-K1-C1
Method	BLASTX
NCBI GI	g507166
BLAST score	408
E value	6.0e-40
Match length	143
% identity	57
NCBI Description	(U04819) PITSLRE beta 1 [Homo sapiens]

Seq. No.	195892
Contig ID	20972_2.R1039
5'-most EST	uC-gsflnu33B075f12b1
Method	BLASTN
NCBI GI	g2351072
BLAST score	41
E value	1.0e-13

Match length	113
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No.	195893
Contig ID	20979_1.R1039
5'-most EST	uC-gsronu33B163f09b2

Seq. No.	195894
Contig ID	20981_2.R1039
5'-most EST	LIB3145-046-Q1-K1-D1
Method	BLASTX
NCBI GI	g2707336
BLAST score	748
E value	1.0e-80
Match length	203
% identity	72
NCBI Description	(AF037442) histone acetyltransferase [Arabidopsis thaliana]

Seq. No.	195895
Contig ID	20984_1.R1039
5'-most EST	LIB3147-013-Q1-K1-E3

Seq. No.	195896
Contig ID	20985_1.R1039
5'-most EST	LIB3147-034-Q1-K1-D6
Method	BLASTX
NCBI GI	g3834325
BLAST score	491
E value	1.0e-51
Match length	144
% identity	69
NCBI Description	(AC005679) Strong similarity to gb|AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb|R83955, gb|T45062, gb|T22220, gb|AA586207, gb|AI099851 and gb|AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	195897
Contig ID	20991_1.R1039
5'-most EST	LIB3272-013-P1-K1-G11

Seq. No.	195898
Contig ID	20992_1.R1039
5'-most EST	uC-gsronu33B077f10b1
Method	BLASTX
NCBI GI	g2826882
BLAST score	431
E value	1.0e-42
Match length	90
% identity	92
NCBI Description	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana]

Seq. No.	195899
Contig ID	20995_1.R1039
5'-most EST	LIB3145-046-Q1-K1-E4

Method	BLASTX
NCBI GI	g4206196
BLAST score	235
E value	1.0e-19
Match length	80
% identity	54
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195900
Contig ID	21001_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A11
Method	BLASTX
NCBI GI	g3738306
BLAST score	244
E value	1.0e-20
Match length	140
% identity	46
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	195901
Contig ID	21002_1.R1039
5'-most EST	uC-gsflmaxxa011b03b1
Method	BLASTX
NCBI GI	g2244956
BLAST score	504
E value	5.0e-51
Match length	178
% identity	55
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	195902
Contig ID	21011_1.R1039
5'-most EST	uC-gsflnu33B145g04b1
Method	BLASTX
NCBI GI	g2129622
BLAST score	565
E value	4.0e-58
Match length	132
% identity	80
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi|1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	195903
Contig ID	21016_1.R1039
5'-most EST	LIB3146-014-Q1-K1-A5
Method	BLASTX
NCBI GI	g3643608
BLAST score	713
E value	4.0e-75
Match length	232
% identity	65
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195904
Contig ID	21018_1.R1039
5'-most EST	uC-gsronu33B099h02b1

Method	BLASTX
NCBI GI	g2911071
BLAST score	287
E value	1.0e-25
Match length	130
% identity	51
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195905
Contig ID	21019_1.R1039
5'-most EST	uC-gsflmaxxa001e10b1
Method	BLASTX
NCBI GI	g3184285
BLAST score	212
E value	1.0e-16
Match length	56
% identity	62
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195906
Contig ID	21029_1.R1039
5'-most EST	LIB3145-046-Q1-K1-H8
Method	BLASTX
NCBI GI	g2832664
BLAST score	253
E value	7.0e-22
Match length	104
% identity	49
NCBI Description	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No.	195907
Contig ID	21035_1.R1039
5'-most EST	LIB3145-047-Q1-K1-A4

Seq. No.	195908
Contig ID	21036_1.R1039
5'-most EST	LIB3147-017-Q1-K1-D6
Method	BLASTX
NCBI GI	g585450
BLAST score	478
E value	1.0e-66
Match length	159
% identity	81
NCBI Description	MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 65 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi|1076271|pir||A49983 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial - prince's feather >gi|437104 (U01162) C4 photosynthetic NAD-dependent malic enzyme subunit alpha precursor [Amaranthus hypochondriacus]

Seq. No.	195909
Contig ID	21037_1.R1039
5'-most EST	LIB3149-030-Q1-K1-E12
Method	BLASTX
NCBI GI	g2833311

BLAST score	261
E value	2.0e-22
Match length	75
% identity	64
NCBI Description	HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi|630728|pir||S43605 R07E5.13 protein (clone R07E5) - Caenorhabditis elegans >gi|3878946|emb|CAA83622| (Z32683) R07E5.13 [Caenorhabditis elegans]

Seq. No.	195910
Contig ID	21039_1.R1039
5'-most EST	LIB3145-047-Q1-K1-B1
Method	BLASTX
NCBI GI	g2852684
BLAST score	153
E value	1.0e-09
Match length	135
% identity	28
NCBI Description	(AF017751) resistance protein candidate [Lactuca sativa]

Seq. No.	195911
Contig ID	21046_1.R1039
5'-most EST	LIB3146-024-Q1-K1-C6
Method	BLASTX
NCBI GI	g122007
BLAST score	384
E value	9.0e-37
Match length	99
% identity	78
NCBI Description	HISTONE H2A >gi|100161|pir||S11498 histone H2A - parsley >gi|20448|emb|CAA37828| (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	195912
Contig ID	21046_2.R1039
5'-most EST	LIB3146-061-Q1-K1-A1
Method	BLASTX
NCBI GI	g122003
BLAST score	152
E value	2.0e-22
Match length	68
% identity	87
NCBI Description	HISTONE H2A >gi|82089|pir||JQ1182 histone H2A.1 - tomato

Seq. No.	195913
Contig ID	21047_1.R1039
5'-most EST	g5048458
Method	BLASTX
NCBI GI	g2632254
BLAST score	1185
E value	1.0e-130
Match length	287
% identity	77
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	195914
Contig ID	21067_1.R1039

5'-most EST	LIB3165-020-P1-K1-C10
Method	BLASTX
NCBI GI	g2914706
BLAST score	715
E value	2.0e-75
Match length	238
% identity	56
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	195915
Contig ID	21071_1.R1039
5'-most EST	LIB3145-047-Q1-K1-D9

Seq. No.	195916
Contig ID	21078_1.R1039
5'-most EST	g5048977
Method	BLASTX
NCBI GI	g2160182
BLAST score	550
E value	1.0e-60
Match length	173
% identity	68
NCBI Description	(AC000132) ESTs gb|ATTS1236,gb|T43334,gb|N97019,gb|AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	195917
Contig ID	21085_1.R1039
5'-most EST	LIB3189-015-P1-K1-D10
Method	BLASTX
NCBI GI	g2245021
BLAST score	544
E value	6.0e-61
Match length	188
% identity	64
NCBI Description	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No.	195918
Contig ID	21087_1.R1039
5'-most EST	LIB3148-012-Q1-K1-D11

Seq. No.	195919
Contig ID	21093_1.R1039
5'-most EST	uC-gsflnu33B074e06b1
Method	BLASTX
NCBI GI	g2708743
BLAST score	173
E value	3.0e-12
Match length	147
% identity	28
NCBI Description	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No.	195920
Contig ID	21095_1.R1039
5'-most EST	LIB3147-015-Q1-K1-G8
Method	BLASTX

NCBI GI	g3953471
BLAST score	1355
E value	1.0e-150
Match length	313
% identity	81
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	195921
Contig ID	21098_1.R1039
5'-most EST	uC-gsflnu33B001a06b1

Seq. No.	195922
Contig ID	21101_1.R1039
5'-most EST	LIB3145-047-Q1-K1-H11
Method	BLASTN
NCBI GI	g2924257
BLAST score	33
E value	6.0e-09
Match length	73
% identity	95
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	195923
Contig ID	21111_1.R1039
5'-most EST	LIB3145-048-Q1-K1-A7

Seq. No.	195924
Contig ID	21113_1.R1039
5'-most EST	LIB3145-048-Q1-K1-A2
Method	BLASTX
NCBI GI	g3242077
BLAST score	516
E value	2.0e-52
Match length	122
% identity	79
NCBI Description	(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	195925
Contig ID	21116_1.R1039
5'-most EST	LIB3145-048-Q1-K1-A6

Seq. No.	195926
Contig ID	21120_1.R1039
5'-most EST	LIB3146-056-Q1-K1-C11
Method	BLASTX
NCBI GI	g4126471
BLAST score	268
E value	2.0e-23
Match length	105
% identity	51
NCBI Description	(AB014722) rSALT-1(806) [Rattus norvegicus]

Seq. No.	195927
Contig ID	21123_1.R1039
5'-most EST	LIB3148-008-Q1-K1-E5
Method	BLASTX
NCBI GI	g533692

BLAST score	210
E value	1.0e-16
Match length	72
% identity	62
NCBI Description	(U12150) protease inhibitor [Glycine max]

Seq. No.	195928
Contig ID	21124_1.R1039
5'-most EST	LIB3197-012-P1-M1-C12

Seq. No.	195929
Contig ID	21129_1.R1039
5'-most EST	LIB3146-022-Q1-K1-B1
Method	BLASTX
NCBI GI	g3421384
BLAST score	331
E value	8.0e-40
Match length	129
% identity	65
NCBI Description	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	195930
Contig ID	21132_1.R1039
5'-most EST	LIB3165-020-P1-K1-A2
Method	BLASTN
NCBI GI	g2696018
BLAST score	40
E value	4.0e-13
Match length	80
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	195931
Contig ID	21135_1.R1039
5'-most EST	LIB3165-021-P1-K1-H2
Method	BLASTX
NCBI GI	g3757524
BLAST score	463
E value	6.0e-46
Match length	289
% identity	38
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	195932
Contig ID	21144_1.R1039
5'-most EST	LIB3145-048-Q1-K1-D5
Method	BLASTX
NCBI GI	g1223922
BLAST score	502
E value	9.0e-51
Match length	117
% identity	74
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No.	195933
Contig ID	21145_1.R1039
5'-most EST	uC-gsronu33B153g03b2
Method	BLASTX
NCBI GI	g2827715
BLAST score	785
E value	4.0e-84
Match length	152
% identity	95
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	195934
Contig ID	21151_1.R1039
5'-most EST	LIB3148-030-Q1-K1-E8
Method	BLASTX
NCBI GI	g2760830
BLAST score	1223
E value	1.0e-135
Match length	256
% identity	88
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	195935
Contig ID	21156_1.R1039
5'-most EST	uC-gsronu33B107d03b1
Method	BLASTX
NCBI GI	g4376203
BLAST score	574
E value	8.0e-59
Match length	303
% identity	41
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No.	195936
Contig ID	21158_1.R1039
5'-most EST	LIB3189-041-P1-K1-F7
Method	BLASTX
NCBI GI	g3123161
BLAST score	130
E value	6.0e-10
Match length	93
% identity	25
NCBI Description	HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F35G12.4 IN CHROMOSOME III >gi|3876723|emb|CAA86335| (Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

Seq. No.	195937
Contig ID	21158_2.R1039
5'-most EST	g3326551
Method	BLASTX

NCBI GI	g1091678
BLAST score	232
E value	5.0e-19
Match length	83
% identity	54
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	195938
Contig ID	21179_1.R1039
5'-most EST	LIB3145-048-Q1-K1-H2
Method	BLASTX
NCBI GI	g2244865
BLAST score	569
E value	3.0e-58
Match length	365
% identity	43
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	195939
Contig ID	21193_1.R1039
5'-most EST	LIB3146-055-Q1-K1-E8
Method	BLASTX
NCBI GI	g4490937
BLAST score	255
E value	9.0e-22
Match length	155
% identity	33
NCBI Description	(AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens]

Seq. No.	195940
Contig ID	21196_1.R1039
5'-most EST	LIB3146-025-Q1-K1-D12
Method	BLASTN
NCBI GI	g439521
BLAST score	54
E value	4.0e-21
Match length	160
% identity	88
NCBI Description	M.musculus mRNA for ribosomal protein S3

Seq. No.	195941
Contig ID	21216_1.R1039
5'-most EST	LIB3145-049-Q1-K1-D10
Method	BLASTX
NCBI GI	g4454033
BLAST score	485
E value	6.0e-49
Match length	116
% identity	76
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	195942
Contig ID	21232_1.R1039
5'-most EST	LIB3145-049-Q1-K1-E9
Method	BLASTX

NCBI GI g2460200
BLAST score 321
E value 1.0e-29
Match length 102
% identity 62
NCBI Description (AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No. 195943
Contig ID 21238_1.R1039
5'-most EST LIB3165-016-P1-K1-H4

Seq. No. 195944
Contig ID 21248_1.R1039
5'-most EST LIB3145-049-Q1-K1-H2
Method BLASTX
NCBI GI g2459815
BLAST score 181
E value 2.0e-13
Match length 81
% identity 43
NCBI Description (AF001002) polygalacturonase 4 [Lycopersicon esculentum]

Seq. No. 195945
Contig ID 21261_1.R1039
5'-most EST g5045086

Seq. No. 195946
Contig ID 21264_1.R1039
5'-most EST g5044651
Method BLASTX
NCBI GI g2225877
BLAST score 750
E value 9.0e-80
Match length 228
% identity 66
NCBI Description (AB002406) TIP49 [Rattus norvegicus] >gi|4106528 (AF100694) Pontin52 [Mus musculus] >gi|4521276|dbj|BAA76313.1| (AB001581) DNA helicase p50 [Rattus norvegicus]

Seq. No. 195947
Contig ID 21272_1.R1039
5'-most EST LIB3145-050-Q1-K1-B8

Seq. No. 195948
Contig ID 21274_1.R1039
5'-most EST LIB3145-050-Q1-K1-C1
Method BLASTX
NCBI GI g533692
BLAST score 179
E value 5.0e-13
Match length 59
% identity 58
NCBI Description (U12150) protease inhibitor [Glycine max]

Seq. No. 195949
Contig ID 21290_1.R1039

5'-most EST	LIB3145-050-Q1-K1-D8
Method	BLASTX
NCBI GI	g1778093
BLAST score	573
E value	3.0e-59
Match length	133
% identity	83
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	195950
Contig ID	21292_1.R1039
5'-most EST	LIB3145-050-Q1-K1-E1

Seq. No.	195951
Contig ID	21292_3.R1039
5'-most EST	g5045566
Method	BLASTX
NCBI GI	g1169870
BLAST score	297
E value	1.0e-26
Match length	155
% identity	39
NCBI Description	GCD14 PROTEIN >gi|1077833|pir||S56906 GCD14 protein - yeast (Saccharomyces cerevisiae) >gi|1004315|emb|CAA90863| (Z54149) GCD14 [Saccharomyces cerevisiae] >gi|1008322|emb|CAA89420| (Z49400) ORF YJL125c [Saccharomyces cerevisiae]

Seq. No.	195952
Contig ID	21313_1.R1039
5'-most EST	uC-gsronu33B100g09b1
Method	BLASTX
NCBI GI	g2505940
BLAST score	714
E value	5.0e-83
Match length	207
% identity	79
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No.	195953
Contig ID	21321_1.R1039
5'-most EST	LIB3166-030-P1-K1-D2

Seq. No.	195954
Contig ID	21323_1.R1039
5'-most EST	LIB3165-034-P1-K1-C2
Method	BLASTX
NCBI GI	g416922
BLAST score	578
E value	2.0e-59
Match length	159
% identity	72
NCBI Description	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi|282947|pir||JQ1599 dUTP pyrophosphatase (EC 3.6.1.23) - tomato

>gi|251897|bbs|109276 (S40549) deoxyuridine triphosphatase, dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No.	195955
Contig ID	21324_1.R1039
5'-most EST	g5050218
Method	BLASTN
NCBI GI	g251896
BLAST score	43
E value	1.0e-14
Match length	299
% identity	79
NCBI Description	deoxyuridine triphosphatase [tomatoes, Tiny Tim cultivar LA154, mRNA, 764 nt]

Seq. No.	195956
Contig ID	21329_1.R1039
5'-most EST	LIB3166-005-P1-K1-F3

Seq. No.	195957
Contig ID	21343_1.R1039
5'-most EST	uC-gsflnu33B146h01b1
Method	BLASTX
NCBI GI	g3522938
BLAST score	550
E value	3.0e-56
Match length	209
% identity	57
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	195958
Contig ID	21354_1.R1039
5'-most EST	LIB3149-039-Q1-K1-D6

Seq. No.	195959
Contig ID	21367_1.R1039
5'-most EST	LIB3145-051-Q1-K1-E5
Method	BLASTX
NCBI GI	g3757521
BLAST score	532
E value	9.0e-70
Match length	313
% identity	45
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	195960
Contig ID	21368_1.R1039
5'-most EST	g5046900

Seq. No.	195961
Contig ID	21387_1.R1039
5'-most EST	g3325645
Method	BLASTN
NCBI GI	g2281081
BLAST score	40
E value	6.0e-13

Match length	52
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	195962
Contig ID	21397_1.R1039
5'-most EST	g3326200
Method	BLASTX
NCBI GI	g4508069
BLAST score	296
E value	2.0e-26
Match length	85
% identity	56
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]

Seq. No.	195963
Contig ID	21402_1.R1039
5'-most EST	LIB3145-052-Q1-K1-C2
Method	BLASTX
NCBI GI	g2281330
BLAST score	492
E value	9.0e-50
Match length	142
% identity	65
NCBI Description	(U85646) putative pectate lyase Nt59 [Nicotiana tabacum]

Seq. No.	195964
Contig ID	21410_1.R1039
5'-most EST	LIB3197-039-Q1-M1-C4

Seq. No.	195965
Contig ID	21411_1.R1039
5'-most EST	LIB3145-052-Q1-K1-B11
Method	BLASTX
NCBI GI	g3688600
BLAST score	492
E value	1.0e-49
Match length	125
% identity	71
NCBI Description	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	195966
Contig ID	21412_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A9
Method	BLASTX
NCBI GI	g346685
BLAST score	470
E value	5.0e-47
Match length	121
% identity	69
NCBI Description	developmentally-regulated GTP-binding protein - mouse

Seq. No.	195967
Contig ID	21413_1.R1039
5'-most EST	LIB3145-052-Q1-K1-B2

Seq. No.	195968
Contig ID	21415_1.R1039
5'-most EST	g3325853
Method	BLASTX
NCBI GI	g2827715
BLAST score	1046
E value	1.0e-114
Match length	231
% identity	87
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	195969
Contig ID	21418_1.R1039
5'-most EST	uC-gsronu33B108h06b1
Method	BLASTN
NCBI GI	g2827698
BLAST score	64
E value	3.0e-27
Match length	328
% identity	80
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)

Seq. No.	195970
Contig ID	21421_1.R1039
5'-most EST	LIB3145-052-Q1-K1-C1
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	7.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi|81849|pir||S04520 histone H3 (clone pH3c-1) - alfalfa >gi|82609|pir||A26014 histone H3 - wheat >gi|19607|emb|CAA31964| (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi|19609|emb|CAA31965| (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi|21797|emb|CAA25451| (X00937) H3 histone [Triticum aestivum] >gi|488565 (U09459) histone H3.1 [Medicago sativa] >gi|2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	195971
Contig ID	21426_1.R1039
5'-most EST	LIB3145-052-Q1-K1-C3
Method	BLASTN
NCBI GI	g387566
BLAST score	105
E value	1.0e-51
Match length	377
% identity	82
NCBI Description	A.thaliana histone H3 gene, complete cds

Seq. No.	195972
Contig ID	21427_1.R1039
5'-most EST	LIB3145-052-Q1-K1-C4
Method	BLASTX

NCBI GI	g2979552
BLAST score	1088
E value	1.0e-119
Match length	302
% identity	70
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	195973
Contig ID	21428_1.R1039
5'-most EST	LIB3145-052-Q1-K1-C6
Method	BLASTX
NCBI GI	g1709535
BLAST score	617
E value	4.0e-64
Match length	167
% identity	70
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi|887388|emb|CAA60447| (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi|1669658|emb|CAA70527| (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	195974
Contig ID	21429_1.R1039
5'-most EST	LIB3272-047-P1-K1-G5

Seq. No.	195975
Contig ID	21430_1.R1039
5'-most EST	LIB3166-024-P1-K1-G8
Method	BLASTX
NCBI GI	g3650030
BLAST score	248
E value	5.0e-21
Match length	79
% identity	57
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	195976
Contig ID	21432_1.R1039
5'-most EST	g5046339
Method	BLASTX
NCBI GI	g1350548
BLAST score	303
E value	3.0e-27
Match length	95
% identity	58
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	195977
Contig ID	21437_1.R1039
5'-most EST	uC-gsflmaxxa089d09b1
Method	BLASTX
NCBI GI	g3309243
BLAST score	1111

E value	1.0e-122
Match length	262
% identity	85
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	195978
Contig ID	21438_1.R1039
5'-most EST	g5048140
Method	BLASTX
NCBI GI	g1888557
BLAST score	723
E value	1.0e-76
Match length	160
% identity	78
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No.	195979
Contig ID	21438_3.R1039
5'-most EST	LIB3149-030-Q1-K1-A12
Method	BLASTX
NCBI GI	g1888557
BLAST score	545
E value	5.0e-56
Match length	124
% identity	78
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No.	195980
Contig ID	21442_1.R1039
5'-most EST	uC-gsronu33B154f02b2

Seq. No.	195981
Contig ID	21453_1.R1039
5'-most EST	LIB3166-015-P1-K1-E1
Method	BLASTX
NCBI GI	g3286691
BLAST score	370
E value	4.0e-35
Match length	103
% identity	70
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	195982
Contig ID	21453_2.R1039
5'-most EST	LIB3146-010-Q1-K1-D7
Method	BLASTX
NCBI GI	g3286691
BLAST score	294
E value	2.0e-26
Match length	124
% identity	72
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	195983

Contig ID	21453_3.R1039
5'-most EST	LIB3166-029-P1-K1-G7
Method	BLASTX
NCBI GI	g4006911
BLAST score	302
E value	2.0e-28
Match length	71
% identity	93
NCBI Description	(Z99708) trichohyalin like protein [Arabidopsis thaliana]

Seq. No.	195984
Contig ID	21455_1.R1039
5'-most EST	LIB3145-052-Q1-K1-F9

Seq. No.	195985
Contig ID	21457_1.R1039
5'-most EST	uC-gsronu33B138b04b1

Seq. No.	195986
Contig ID	21470_1.R1039
5'-most EST	LIB3272-054-P1-K1-B11

Seq. No.	195987
Contig ID	21475_1.R1039
5'-most EST	LIB3146-051-Q1-K1-G11

Seq. No.	195988
Contig ID	21484_1.R1039
5'-most EST	LIB3145-053-Q1-K1-A6
Method	BLASTX
NCBI GI	g4325371
BLAST score	271
E value	1.0e-23
Match length	151
% identity	45
NCBI Description	(AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No.	195989
Contig ID	21491_1.R1039
5'-most EST	LIB3145-053-Q1-K1-B2
Method	BLASTX
NCBI GI	g4567210
BLAST score	520
E value	9.0e-53
Match length	109
% identity	88
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	195990
Contig ID	21493_2.R1039
5'-most EST	uC-gsflmaxxa097b07b1
Method	BLASTX
NCBI GI	g1168529
BLAST score	175
E value	2.0e-21
Match length	69

% identity	83
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi|541890|pir||S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi|166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi|1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	195991
Contig ID	21499_1.R1039
5'-most EST	LIB3145-053-Q1-K1-C11
Method	BLASTX
NCBI GI	g3287881
BLAST score	276
E value	3.0e-24
Match length	154
% identity	41
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi|2655053 (AF020351) NADH:ubiquinone oxidoreductase 18 kDa IP subunit [Homo sapiens] >gi|4505369|ref|NP_002486.1|pNDUFS4| NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)

Seq. No.	195992
Contig ID	21501_1.R1039
5'-most EST	LIB3145-053-Q1-K1-D3
Method	BLASTX
NCBI GI	g2281334
BLAST score	803
E value	7.0e-86
Match length	255
% identity	60
NCBI Description	(U83619) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	195993
Contig ID	21503_1.R1039
5'-most EST	uC-gsronu33B129g11b1
Method	BLASTX
NCBI GI	g3287695
BLAST score	555
E value	7.0e-57
Match length	161
% identity	64
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb|1729503 from C. elegans cosmid gb|Z83220. [Arabidopsis thaliana]

Seq. No.	195994
Contig ID	21505_1.R1039
5'-most EST	LIB3272-055-P1-K1-E4

Seq. No.	195995
Contig ID	21510_1.R1039
5'-most EST	LIB3146-011-Q1-K1-D4

Seq. No.	195996

Contig ID	21515_1.R1039
5'-most EST	LIB3145-053-Q1-K1-D7
Method	BLASTX
NCBI GI	g4558591
BLAST score	531
E value	4.0e-54
Match length	135
% identity	76
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	195997
Contig ID	21516_1.R1039
5'-most EST	g5046919
Method	BLASTX
NCBI GI	g2583081
BLAST score	287
E value	2.0e-25
Match length	140
% identity	45
NCBI Description	(AF026977) microsomal glutathione S-transferase 3 [Homo sapiens]

Seq. No.	195998
Contig ID	21517_1.R1039
5'-most EST	LIB3165-002-Q1-K1-H7
Method	BLASTX
NCBI GI	g4490321
BLAST score	460
E value	5.0e-46
Match length	105
% identity	85
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	195999
Contig ID	21523_1.R1039
5'-most EST	LIB3145-053-Q1-K1-E3
Method	BLASTX
NCBI GI	g2736387
BLAST score	199
E value	3.0e-15
Match length	160
% identity	34
NCBI Description	(AF039041) No definition line found [Caenorhabditis elegans]

Seq. No.	196000
Contig ID	21528_1.R1039
5'-most EST	LIB3147-001-Q1-K2-C7
Method	BLASTN
NCBI GI	g2828187
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	196001
Contig ID	21536_1.R1039
5'-most EST	LIB3145-053-Q1-K1-F6

Seq. No.	196002
Contig ID	21537_1.R1039
5'-most EST	LIB3146-008-Q1-K1-H5

Seq. No.	196003
Contig ID	21539_1.R1039
5'-most EST	uC-gsronu33B153f03b2
Method	BLASTX
NCBI GI	g3461848
BLAST score	1368
E value	1.0e-152
Match length	306
% identity	86
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	196004
Contig ID	21541_1.R1039
5'-most EST	g3326575
Method	BLASTX
NCBI GI	g4262174
BLAST score	312
E value	3.0e-28
Match length	73
% identity	78
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	196005
Contig ID	21557_1.R1039
5'-most EST	uC-gsronu33B166c04b2
Method	BLASTX
NCBI GI	g1708425
BLAST score	359
E value	8.0e-34
Match length	185
% identity	43
NCBI Description	ISOFLAVONE REDUCTASE (IFR) (NADPH:ISOFLAVONE OXIDOREDUCTASE) >gi|99878|pir||S17830 2'-hydroxyisoflavone reductase (EC 1.3.1.45) - chickpea >gi|17949|emb|CAA43167| (X60755) NADPH:isoflavone oxidoreductase [Cicer arietinum]

Seq. No.	196006
Contig ID	21562_1.R1039
5'-most EST	LIB3145-054-Q1-K1-A10

Seq. No.	196007
Contig ID	21573_1.R1039
5'-most EST	LIB3166-049-P1-K1-C6
Method	BLASTX
NCBI GI	g4102600
BLAST score	715
E value	2.0e-75
Match length	188

% identity	78
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.	196008
Contig ID	21577_1.R1039
5'-most EST	LIB3165-056-P1-K1-F10
Seq. No.	196009
Contig ID	21585_1.R1039
5'-most EST	LIB3149-028-Q1-K1-G2
Seq. No.	196010
Contig ID	21588_1.R1039
5'-most EST	LIB3148-058-Q1-K1-B10
Method	BLASTX
NCBI GI	g4049401
BLAST score	205
E value	4.0e-16
Match length	60
% identity	63
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]
Seq. No.	196011
Contig ID	21596_1.R1039
5'-most EST	LIB3145-054-Q1-K1-D6
Method	BLASTX
NCBI GI	g3608127
BLAST score	351
E value	3.0e-33
Match length	70
% identity	80
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	196012
Contig ID	21598_1.R1039
5'-most EST	uC-gsflmaxxa046g07b1
Method	BLASTX
NCBI GI	g2498732
BLAST score	562
E value	1.0e-57
Match length	247
% identity	61
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi|1362014|pir||S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi|886430|emb|CAA89262| (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.	196013
Contig ID	21601_1.R1039
5'-most EST	LIB3149-027-Q1-K1-D4
Method	BLASTX
NCBI GI	g4559388
BLAST score	321
E value	1.0e-29
Match length	90
% identity	58

NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196014
Contig ID	21604_1.R1039
5'-most EST	LIB3145-054-Q1-K1-E4
Method	BLASTX
NCBI GI	g3334259
BLAST score	331
E value	6.0e-31
Match length	67
% identity	90
NCBI Description	WD-40 REPEAT PROTEIN MSI4 >gi|2599092 (AF028711) WD-40 repeat protein MSI4 [Arabidopsis thaliana]
Seq. No.	196015
Contig ID	21607_1.R1039
5'-most EST	LIB3146-043-Q1-K1-E11
Method	BLASTX
NCBI GI	g1619300
BLAST score	567
E value	3.0e-58
Match length	159
% identity	65
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]
Seq. No.	196016
Contig ID	21609_1.R1039
5'-most EST	uC-gsronu33B150e04b1
Seq. No.	196017
Contig ID	21610_1.R1039
5'-most EST	LIB3148-029-Q1-K1-E8
Seq. No.	196018
Contig ID	21615_1.R1039
5'-most EST	LIB3166-050-P1-K1-E8
Seq. No.	196019
Contig ID	21616_1.R1039
5'-most EST	LIB3149-044-Q1-K1-H7
Method	BLASTX
NCBI GI	g2961358
BLAST score	617
E value	3.0e-64
Match length	137
% identity	87
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]
Seq. No.	196020
Contig ID	21620_1.R1039
5'-most EST	uC-gsronu33B129b07b1
Seq. No.	196021
Contig ID	21623_1.R1039
5'-most EST	LIB3197-035-Q1-M1-D4
Method	BLASTX

NCBI GI	g4454051
BLAST score	1390
E value	1.0e-154
Match length	321
% identity	78
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	196022
Contig ID	21635_1.R1039
5'-most EST	LIB3145-055-Q1-K1-A3

Seq. No.	196023
Contig ID	21638_1.R1039
5'-most EST	LIB3146-024-Q1-K1-C10
Method	BLASTX
NCBI GI	g2673917
BLAST score	1016
E value	1.0e-111
Match length	248
% identity	50
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	196024
Contig ID	21640_1.R1039
5'-most EST	uC-gsflnu33B142e10b1
Method	BLASTX
NCBI GI	g4572679
BLAST score	458
E value	1.0e-45
Match length	121
% identity	71
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	196025
Contig ID	21640_2.R1039
5'-most EST	uC-gsronu33B178d08b1
Method	BLASTX
NCBI GI	g3281869
BLAST score	444
E value	7.0e-44
Match length	179
% identity	55
NCBI Description	(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi|3435094 (AF033586) 9G8-like SR protein [Arabidopsis thaliana]

Seq. No.	196026
Contig ID	21642_1.R1039
5'-most EST	LIB3148-056-Q1-K1-F4
Method	BLASTX
NCBI GI	g480450
BLAST score	820
E value	4.0e-88
Match length	187

% identity	84
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi|402552|emb|CAA49506| (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	196027
Contig ID	21647_1.R1039
5'-most EST	uC-gsflnu33B046a01b1

Seq. No.	196028
Contig ID	21647_2.R1039
5'-most EST	uC-gsflmaxxa026b04b1

Seq. No.	196029
Contig ID	21665_1.R1039
5'-most EST	LIB3145-055-Q1-K1-D2

Seq. No.	196030
Contig ID	21678_1.R1039
5'-most EST	g5048883
Method	BLASTX
NCBI GI	g4467128
BLAST score	438
E value	3.0e-43
Match length	146
% identity	55
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	196031
Contig ID	21684_1.R1039
5'-most EST	g3326298
Method	BLASTX
NCBI GI	g2702269
BLAST score	230
E value	1.0e-18
Match length	142
% identity	42
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196032
Contig ID	21689_1.R1039
5'-most EST	LIB3145-055-Q1-K1-G10
Method	BLASTX
NCBI GI	g3552013
BLAST score	207
E value	2.0e-16
Match length	71
% identity	65
NCBI Description	(AF086759) proline-rich protein precursor [Glycine max]

Seq. No.	196033
Contig ID	21697_1.R1039
5'-most EST	LIB3145-055-Q1-K1-H11
Method	BLASTX
NCBI GI	g3757520
BLAST score	205
E value	5.0e-16

Match length	65
% identity	65
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	196034
Contig ID	21700_1.R1039
5'-most EST	LIB3145-055-Q1-K1-H4
Method	BLASTX
NCBI GI	g533256
BLAST score	371
E value	1.0e-35
Match length	125
% identity	58
NCBI Description	(L27101) pectinesterase [Petunia inflata]

Seq. No.	196035
Contig ID	21709_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A2

Seq. No.	196036
Contig ID	21710_1.R1039
5'-most EST	LIB3145-056-Q1-K1-A4
Method	BLASTX
NCBI GI	g3860797
BLAST score	303
E value	3.0e-27
Match length	148
% identity	44
NCBI Description	(AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia prowazekii]

Seq. No.	196037
Contig ID	21727_1.R1039
5'-most EST	uC-gsflnu33B015b10b1
Method	BLASTX
NCBI GI	g266346
BLAST score	1484
E value	1.0e-165
Match length	326
% identity	87
NCBI Description	KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE) >gi|81509|pir||S17180 ketol-acid reductoisomerase (EC 1.1.1.86) precursor - spinach >gi|21234|emb|CAA40356| (X57073) ketol-acid reductoisomerase [Spinacia oleracea]

Seq. No.	196038
Contig ID	21731_1.R1039
5'-most EST	uC-gsflnu33B130f11b1

Seq. No.	196039
Contig ID	21733_1.R1039
5'-most EST	LIB3145-056-Q1-K1-C3

Seq. No.	196040
Contig ID	21736_1.R1039

5'-most EST	LIB3145-056-Q1-K1-C6
Method	BLASTX
NCBI GI	g3559816
BLAST score	242
E value	2.0e-20
Match length	63
% identity	73
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	196041
Contig ID	21737_1.R1039
5'-most EST	LIB3145-056-Q1-K1-C7

Seq. No.	196042
Contig ID	21749_1.R1039
5'-most EST	LIB3145-056-Q1-K1-D8
Method	BLASTX
NCBI GI	g2982251
BLAST score	290
E value	7.0e-26
Match length	76
% identity	71
NCBI Description	(AF051208) putative RNA-binding protein [Picea mariana]

Seq. No.	196043
Contig ID	21753_1.R1039
5'-most EST	LIB3145-056-Q1-K1-E11
Method	BLASTX
NCBI GI	g2245394
BLAST score	291
E value	3.0e-26
Match length	146
% identity	45
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	196044
Contig ID	21768_1.R1039
5'-most EST	LIB3147-018-Q1-K1-A9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	196045
Contig ID	21777_1.R1039
5'-most EST	LIB3145-056-Q1-K1-H12
Method	BLASTX
NCBI GI	g1352316
BLAST score	340
E value	2.0e-32
Match length	82
% identity	77
NCBI Description	DR1 PROTEIN HOMOLOG >gi|633026|dbj|BAA07288| (D38110) Dr1 [Arabidopsis thaliana]

Seq. No.	196046
Contig ID	21778_1.R1039
5'-most EST	LIB3197-054-Q1-M1-E9
Method	BLASTX
NCBI GI	g3549681
BLAST score	1066
E value	1.0e-116
Match length	345
% identity	59
NCBI Description	(AL031394) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	196047
Contig ID	21783_1.R1039
5'-most EST	LIB3145-056-Q1-K1-H8
Method	BLASTX
NCBI GI	g4105097
BLAST score	683
E value	5.0e-72
Match length	168
% identity	77
NCBI Description	(AF043255) MADS box protein 26 [Cucumis sativus]

Seq. No.	196048
Contig ID	21793_1.R1039
5'-most EST	uC-gsronu33B178h03b1

Seq. No.	196049
Contig ID	21798_1.R1039
5'-most EST	LIB3145-057-Q1-K1-B2

Seq. No.	196050
Contig ID	21804_1.R1039
5'-most EST	LIB3145-057-Q1-K1-B9
Method	BLASTX
NCBI GI	g133085
BLAST score	183
E value	1.0e-13
Match length	110
% identity	45
NCBI Description	50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12) >gi|71136|pir||R7SP12 ribosomal protein L12, chloroplast - spinach >gi|170115 (J02849) ribosomal L12 precursor [Spinacia oleracea]

Seq. No.	196051
Contig ID	21811_1.R1039
5'-most EST	uC-gsflnu33B018d01b1

Seq. No.	196052
Contig ID	21813_1.R1039
5'-most EST	LIB3149-017-Q1-K1-E5
Method	BLASTN
NCBI GI	g899609
BLAST score	38
E value	1.0e-11

Match length	82
% identity	87
NCBI Description	Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA, complete cds

Seq. No.	196053
Contig ID	21813_2.R1039
5'-most EST	LIB3196-041-P1-M1-D2
Method	BLASTX
NCBI GI	g2431771
BLAST score	252
E value	3.0e-21
Match length	113
% identity	48
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	196054
Contig ID	21814_1.R1039
5'-most EST	g5044429
Method	BLASTX
NCBI GI	g1362093
BLAST score	777
E value	9.0e-83
Match length	219
% identity	68
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi|924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	196055
Contig ID	21814_2.R1039
5'-most EST	LIB3166-040-P1-K1-A8
Method	BLASTX
NCBI GI	g1362093
BLAST score	552
E value	1.0e-56
Match length	132
% identity	76
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi|924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	196056
Contig ID	21814_3.R1039
5'-most EST	LIB3166-034-P1-K1-A9
Method	BLASTX
NCBI GI	g1362093
BLAST score	160
E value	7.0e-11
Match length	37
% identity	84
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi|924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	196057
Contig ID	21816_1.R1039
5'-most EST	LIB3196-044-P1-M1-E9

Seq. No.	196058

Contig ID	21823_1.R1039
5'-most EST	LIB3145-057-Q1-K1-D6
Method	BLASTX
NCBI GI	g3915083
BLAST score	709
E value	3.0e-75
Match length	143
% identity	92
NCBI Description	TUBULIN BETA CHAIN >gi|1403143|emb|CAA67056| (X98406) beta-tubulin [Cicer arietinum]

Seq. No.	196059
Contig ID	21832_1.R1039
5'-most EST	LIB3148-040-Q1-K1-F3
Method	BLASTN
NCBI GI	g2570118
BLAST score	55
E value	4.0e-22
Match length	83
% identity	92
NCBI Description	S.latifolia mRNA, clone CCLS

Seq. No.	196060
Contig ID	21844_1.R1039
5'-most EST	uC-gsflnu33B107e02b1
Method	BLASTX
NCBI GI	g2088822
BLAST score	201
E value	2.0e-15
Match length	135
% identity	35
NCBI Description	(AF003384) K07B1.4 gene product [Caenorhabditis elegans]

Seq. No.	196061
Contig ID	21849_1.R1039
5'-most EST	LIB3166-035-P1-K1-D2
Method	BLASTX
NCBI GI	g2088651
BLAST score	709
E value	9.0e-75
Match length	240
% identity	58
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	196062
Contig ID	21851_1.R1039
5'-most EST	LIB3145-057-Q1-K1-G11

Seq. No.	196063
Contig ID	21854_1.R1039
5'-most EST	LIB3189-050-P1-K1-F8
Method	BLASTX
NCBI GI	g4038034
BLAST score	344
E value	2.0e-32
Match length	87

% identity	75
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	196064
Contig ID	21857_1.R1039
5'-most EST	uC-gsflnu33B011c08b1
Method	BLASTX
NCBI GI	g1723832
BLAST score	174
E value	3.0e-12
Match length	81
% identity	44
NCBI Description	HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION >gi|2132531|pir||S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) >gi|1322550|emb|CAA96756| (Z72576) ORF YGL054c [Saccharomyces cerevisiae]

Seq. No.	196065
Contig ID	21860_1.R1039
5'-most EST	LIB3145-057-Q1-K1-H4

Seq. No.	196066
Contig ID	21863_1.R1039
5'-most EST	LIB3196-036-P1-M1-A8

Seq. No.	196067
Contig ID	21868_1.R1039
5'-most EST	uC-gsflnu33B131c11b1
Method	BLASTX
NCBI GI	g122003
BLAST score	343
E value	7.0e-32
Match length	95
% identity	74
NCBI Description	HISTONE H2A >gi|82089|pir||JQ1182 histone H2A.1 - tomato

Seq. No.	196068
Contig ID	21882_1.R1039
5'-most EST	g5046229
Method	BLASTX
NCBI GI	g3341694
BLAST score	417
E value	1.0e-40
Match length	131
% identity	59
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	196069
Contig ID	21882_2.R1039
5'-most EST	LIB3197-028-Q1-M1-A4

Seq. No.	196070
Contig ID	21882_3.R1039
5'-most EST	LIB3272-055-P1-K1-C12

Seq. No.	196071
Contig ID	21885_1.R1039

5'-most EST	uC-gsflnu33B131g05b1
Seq. No.	196072
Contig ID	21888_1.R1039
5'-most EST	uC-gsronu33B168b02b1
Seq. No.	196073
Contig ID	21890_1.R1039
5'-most EST	LIB3165-053-Q1-K1-D2
Seq. No.	196074
Contig ID	21891_1.R1039
5'-most EST	uC-gsflnu33B114a11b1
Method	BLASTX
NCBI GI	g1742951
BLAST score	1094
E value	1.0e-120
Match length	232
% identity	87
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	196075
Contig ID	21896_1.R1039
5'-most EST	LIB3145-058-Q1-K1-C8
Seq. No.	196076
Contig ID	21904_1.R1039
5'-most EST	LIB3145-058-Q1-K1-D4
Method	BLASTX
NCBI GI	g4163997
BLAST score	459
E value	2.0e-70
Match length	226
% identity	62
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]
Seq. No.	196077
Contig ID	21906_1.R1039
5'-most EST	LIB3145-058-Q1-K1-D6
Seq. No.	196078
Contig ID	21907_1.R1039
5'-most EST	LIB3166-050-P1-K1-C2
Method	BLASTX
NCBI GI	g125568
BLAST score	529
E value	4.0e-54
Match length	133
% identity	76
NCBI Description	PROTEIN KINASE PVPK-1 >gi|100013|pir||A30311 protein kinase C (EC 2.7.1.-) homolog - kidney bean >gi|169361 (J04555) PVPK-1 protein [Phaseolus vulgaris]
Seq. No.	196079
Contig ID	21918_1.R1039
5'-most EST	g5049039

Method	BLASTX
NCBI GI	g1620970
BLAST score	936
E value	1.0e-101
Match length	222
% identity	83
NCBI Description	(Y08887) L-lactate dehydrogenase [Lycopersicon esculentum] >gi|1806117|emb|CAA71611| (Y10602) L-lactate dehydrogenase [Lycopersicon esculentum]

Seq. No.	196080
Contig ID	21921_1.R1039
5'-most EST	LIB3145-058-Q1-K1-F2
Method	BLASTN
NCBI GI	g2564046
BLAST score	41
E value	2.0e-13
Match length	227
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	196081
Contig ID	21935_1.R1039
5'-most EST	LIB3145-058-Q1-K1-G9
Method	BLASTX
NCBI GI	g100010
BLAST score	376
E value	3.0e-36
Match length	117
% identity	58
NCBI Description	pectinesterase (EC 3.1.1.11) - kidney bean (fragment) >gi|21062|emb|CAA48169| (X68028) pectinesterase [Phaseolus vulgaris]

Seq. No.	196082
Contig ID	21941_1.R1039
5'-most EST	LIB3145-058-Q1-K1-H4

Seq. No.	196083
Contig ID	21946_1.R1039
5'-most EST	LIB3147-010-Q1-K1-C8
Method	BLASTX
NCBI GI	g729051
BLAST score	551
E value	1.0e-56
Match length	115
% identity	59
NCBI Description	CALTRACTIN (CENTRIN) >gi|444342|prf||1906390A caltractin-like protein [Atriplex nummularia]

Seq. No.	196084
Contig ID	21959_1.R1039
5'-most EST	LIB3146-021-Q1-K1-A7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36

E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	196085
Contig ID	21961_1.R1039
5'-most EST	g5044298
Method	BLASTX
NCBI GI	g4539291
BLAST score	612
E value	2.0e-63
Match length	247
% identity	53
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	196086
Contig ID	21965_1.R1039
5'-most EST	uC-gsflnu33B049h11b1
Method	BLASTX
NCBI GI	g2529662
BLAST score	511
E value	7.0e-52
Match length	107
% identity	93
NCBI Description	(AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi|3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

Seq. No.	196087
Contig ID	21969_1.R1039
5'-most EST	g5045152
Method	BLASTX
NCBI GI	g3355474
BLAST score	893
E value	2.0e-96
Match length	197
% identity	85
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	196088
Contig ID	21972_1.R1039
5'-most EST	LIB3189-001-P1-K1-A3
Method	BLASTX
NCBI GI	g3063467
BLAST score	417
E value	9.0e-41
Match length	127
% identity	65
NCBI Description	(AC003981) F22O13.29 [Arabidopsis thaliana]

Seq. No.	196089
Contig ID	21983_1.R1039
5'-most EST	LIB3146-023-Q1-K1-C10
Method	BLASTX
NCBI GI	g3953471

BLAST score	587
E value	1.0e-60
Match length	163
% identity	64
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	196090
Contig ID	21987_1.R1039
5'-most EST	uC-gsflnu33B136c07b1

Seq. No.	196091
Contig ID	21988_1.R1039
5'-most EST	LIB3165-006-P1-K2-H7
Method	BLASTX
NCBI GI	g4103635
BLAST score	334
E value	3.0e-38
Match length	162
% identity	56
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	196092
Contig ID	21991_1.R1039
5'-most EST	LIB3146-038-P1-K1-E1
Method	BLASTX
NCBI GI	g629735
BLAST score	248
E value	4.0e-21
Match length	71
% identity	66
NCBI Description	fil1 protein - garden snapdragon >gi|406309|emb|CAA40553| (X57296) FIL1 [Antirrhinum majus]

Seq. No.	196093
Contig ID	21995_1.R1039
5'-most EST	g5049647
Method	BLASTX
NCBI GI	g4567262
BLAST score	362
E value	4.0e-34
Match length	165
% identity	47
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No.	196094
Contig ID	22002_1.R1039
5'-most EST	LIB3146-001-P1-K2-F10
Method	BLASTX
NCBI GI	g2388577
BLAST score	182
E value	2.0e-13
Match length	102
% identity	41
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb|AC002329). [Arabidopsis thaliana]

Seq. No. 196095

Contig ID	22007_1.R1039
5'-most EST	LIB3146-061-Q1-K1-H2
Method	BLASTX
NCBI GI	g3738290
BLAST score	455
E value	4.0e-45
Match length	186
% identity	49
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	196096
Contig ID	22020_1.R1039
5'-most EST	uC-gsflnu33B146e12b1
Method	BLASTX
NCBI GI	g3367519
BLAST score	404
E value	2.0e-39
Match length	103
% identity	72
NCBI Description	(AC004392) Contains similarity to gb|U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	196097
Contig ID	22034_1.R1039
5'-most EST	LIB3146-009-Q1-K1-C5
Method	BLASTX
NCBI GI	g2760837
BLAST score	335
E value	4.0e-31
Match length	193
% identity	39
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	196098
Contig ID	22038_1.R1039
5'-most EST	LIB3146-002-P1-K2-A9

Seq. No.	196099
Contig ID	22039_1.R1039
5'-most EST	LIB3146-002-P1-K2-B10
Method	BLASTX
NCBI GI	g3355486
BLAST score	501
E value	1.0e-50
Match length	174
% identity	60
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	196100
Contig ID	22042_1.R1039
5'-most EST	uC-gsflnu33B127d03b1

Seq. No.	196101
Contig ID	22044_1.R1039
5'-most EST	LIB3272-031-P1-K1-C4
Method	BLASTX

NCBI GI	g3355477
BLAST score	394
E value	4.0e-38
Match length	139
% identity	41
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	196102
Contig ID	22059_1.R1039
5'-most EST	LIB3165-021-P1-K1-F10

Seq. No.	196103
Contig ID	22062_1.R1039
5'-most EST	LIB3149-018-Q1-K1-A11
Method	BLASTX
NCBI GI	g3702331
BLAST score	213
E value	5.0e-17
Match length	110
% identity	49
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196104
Contig ID	22064_1.R1039
5'-most EST	LIB3189-030-P1-K1-F1
Method	BLASTX
NCBI GI	g3355617
BLAST score	481
E value	4.0e-48
Match length	113
% identity	78
NCBI Description	(AJ000229) unnamed protein product [Hordeum vulgare]

Seq. No.	196105
Contig ID	22065_1.R1039
5'-most EST	uC-gsflmaxxa076f06b1
Method	BLASTX
NCBI GI	g3395938
BLAST score	556
E value	1.0e-104
Match length	355
% identity	52
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	196106
Contig ID	22077_1.R1039
5'-most EST	LIB3197-050-Q1-M1-B3
Method	BLASTX
NCBI GI	g4538939
BLAST score	534
E value	1.0e-129
Match length	296
% identity	82
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	196107
Contig ID	22077_2.R1039
5'-most EST	LIB3146-002-P1-K2-F11
Method	BLASTX
NCBI GI	g4538939
BLAST score	425
E value	2.0e-41
Match length	117
% identity	72
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	196108
Contig ID	22077_3.R1039
5'-most EST	uC-gsflnu33B114f07b1
Method	BLASTX
NCBI GI	g4538939
BLAST score	335
E value	4.0e-31
Match length	189
% identity	43
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	196109
Contig ID	22079_1.R1039
5'-most EST	LIB3146-002-P1-K2-F2

Seq. No.	196110
Contig ID	22084_1.R1039
5'-most EST	LIB3272-046-P1-K1-H4
Method	BLASTX
NCBI GI	g1155261
BLAST score	681
E value	1.0e-71
Match length	146
% identity	89
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	196111
Contig ID	22085_1.R1039
5'-most EST	LIB3146-002-P1-K2-F8
Method	BLASTX
NCBI GI	g2529707
BLAST score	567
E value	3.0e-58
Match length	227
% identity	48
NCBI Description	(AF001434) Hpast [Homo sapiens]

Seq. No.	196112
Contig ID	22090_1.R1039
5'-most EST	LIB3146-002-P1-K2-G3

Seq. No.	196113

Contig ID	22091_1.R1039
5'-most EST	LIB3196-038-P1-M1-D10
Seq. No.	196114
Contig ID	22098_2.R1039
5'-most EST	LIB3196-044-P1-M1-B6
Seq. No.	196115
Contig ID	22106_1.R1039
5'-most EST	LIB3146-003-P1-K1-A3
Seq. No.	196116
Contig ID	22113_1.R1039
5'-most EST	LIB3196-042-P1-M1-C4
Method	BLASTX
NCBI GI	g3176726
BLAST score	383
E value	8.0e-37
Match length	145
% identity	51
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]
Seq. No.	196117
Contig ID	22114_1.R1039
5'-most EST	LIB3146-020-Q1-K1-B12
Seq. No.	196118
Contig ID	22118_1.R1039
5'-most EST	LIB3146-003-P1-K1-B5
Seq. No.	196119
Contig ID	22141_1.R1039
5'-most EST	LIB3196-037-P1-M1-H11
Method	BLASTX
NCBI GI	g3643608
BLAST score	296
E value	2.0e-26
Match length	213
% identity	32
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196120
Contig ID	22142_1.R1039
5'-most EST	g3325759
Method	BLASTN
NCBI GI	g3449321
BLAST score	43
E value	1.0e-14
Match length	83
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.	196121
Contig ID	22149_1.R1039
5'-most EST	LIB3146-003-P1-K1-F6

Method	BLASTX
NCBI GI	g4006827
BLAST score	650
E value	6.0e-68
Match length	243
% identity	54
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	196122
Contig ID	22157_1.R1039
5'-most EST	uC-gsronu33B080f06b1

Seq. No.	196123
Contig ID	22180_1.R1039
5'-most EST	LIB3146-004-P1-K1-B12

Seq. No.	196124
Contig ID	22185_1.R1039
5'-most EST	uC-gsflnu33B016d07b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	568
E value	4.0e-58
Match length	289
% identity	43
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	196125
Contig ID	22195_1.R1039
5'-most EST	LIB3146-004-P1-K1-D2

Seq. No.	196126
Contig ID	22199_1.R1039
5'-most EST	LIB3165-019-P1-K1-H12
Method	BLASTX
NCBI GI	g2708749
BLAST score	348
E value	9.0e-33
Match length	111
% identity	58
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	196127
Contig ID	22203_1.R1039
5'-most EST	uC-gsronu33B039a05b1

Seq. No.	196128
Contig ID	22211_1.R1039
5'-most EST	LIB3146-004-P1-K1-F1

Seq. No.	196129
Contig ID	22213_1.R1039
5'-most EST	LIB3166-021-P1-K1-B3
Method	BLASTX
NCBI GI	g4126399
BLAST score	833

E value	2.0e-89
Match length	216
% identity	77
NCBI Description	(AB011794) chalcone isomerase [Citrus sinensis]

Seq. No.	196130
Contig ID	22216_1.R1039
5'-most EST	g5046203
Method	BLASTX
NCBI GI	g1708971
BLAST score	349
E value	1.0e-32
Match length	174
% identity	40
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi|421871|pir||S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi|288116|emb|CAA51194| (X72617) mandelonitrile lyase [Prunus serotina] >gi|1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi|1090776|prf||2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	196131
Contig ID	22218_1.R1039
5'-most EST	LIB3166-040-P1-K1-F2
Method	BLASTX
NCBI GI	g2462754
BLAST score	844
E value	1.0e-90
Match length	303
% identity	58
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	196132
Contig ID	22220_1.R1039
5'-most EST	LIB3146-004-P1-K1-F9

Seq. No.	196133
Contig ID	22227_1.R1039
5'-most EST	LIB3149-007-Q1-K1-F6
Method	BLASTX
NCBI GI	g4468050
BLAST score	431
E value	2.0e-42
Match length	169
% identity	47
NCBI Description	(X87099) S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase [Vanilla planifolia]

Seq. No.	196134
Contig ID	22228_1.R1039
5'-most EST	LIB3146-004-P1-K1-H1
Method	BLASTX
NCBI GI	g3386618
BLAST score	308
E value	4.0e-28

Match length 128
% identity 54
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196135
Contig ID 22232_1.R1039
5'-most EST LIB3146-004-P1-K1-H4
Method BLASTX
NCBI GI g2708743
BLAST score 148
E value 2.0e-09
Match length 103
% identity 32
NCBI Description (AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No. 196136
Contig ID 22233_1.R1039
5'-most EST LIB3148-052-Q1-K1-A4
Method BLASTX
NCBI GI g3695021
BLAST score 707
E value 9.0e-75
Match length 202
% identity 71
NCBI Description (AF055849) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196137
Contig ID 22235_1.R1039
5'-most EST LIB3166-055-P1-K1-D12
Method BLASTX
NCBI GI g4335750
BLAST score 252
E value 2.0e-21
Match length 75
% identity 56
NCBI Description (AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 196138
Contig ID 22239_1.R1039
5'-most EST uC-gsflnu33B089f10b1

Seq. No. 196139
Contig ID 22248_1.R1039
5'-most EST LIB3146-005-Q1-K1-B12
Method BLASTX
NCBI GI g2980788
BLAST score 244
E value 2.0e-20
Match length 122
% identity 52
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 196140
Contig ID 22250_1.R1039
5'-most EST LIB3146-005-Q1-K1-B3

Method	BLASTX
NCBI GI	g4539345
BLAST score	571
E value	8.0e-59
Match length	178
% identity	64
NCBI Description	(AL035539) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196141
Contig ID	22251_1.R1039
5'-most EST	uC-gsronu33B004f12b1
Method	BLASTX
NCBI GI	g3763916
BLAST score	680
E value	2.0e-71
Match length	243
% identity	53
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi|4531439|gb|AAD22124.1|AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	196142
Contig ID	22259_1.R1039
5'-most EST	LIB3146-005-Q1-K1-C3
Method	BLASTX
NCBI GI	g2961358
BLAST score	217
E value	2.0e-17
Match length	50
% identity	84
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	196143
Contig ID	22268_1.R1039
5'-most EST	LIB3146-005-Q1-K1-D2

Seq. No.	196144
Contig ID	22270_1.R1039
5'-most EST	LIB3146-005-Q1-K1-D4
Method	BLASTX
NCBI GI	g3702641
BLAST score	214
E value	4.0e-17
Match length	88
% identity	44
NCBI Description	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]

Seq. No.	196145
Contig ID	22278_1.R1039
5'-most EST	LIB3166-026-P1-K1-G1
Method	BLASTX
NCBI GI	g2244926
BLAST score	154
E value	4.0e-10
Match length	84

% identity	38
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	196146
Contig ID	22279_1.R1039
5'-most EST	LIB3189-048-P1-K1-F6
Method	BLASTX
NCBI GI	g2062167
BLAST score	657
E value	2.0e-68
Match length	304
% identity	42
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	196147
Contig ID	22285_1.R1039
5'-most EST	LIB3148-039-Q1-K1-D9
Method	BLASTX
NCBI GI	g4455172
BLAST score	286
E value	2.0e-25
Match length	80
% identity	68
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	196148
Contig ID	22288_1.R1039
5'-most EST	LIB3147-049-Q1-K1-H2
Method	BLASTN
NCBI GI	g3399678
BLAST score	43
E value	1.0e-14
Match length	156
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	196149
Contig ID	22289_1.R1039
5'-most EST	g5047380
Method	BLASTX
NCBI GI	g2462748
BLAST score	914
E value	6.0e-99
Match length	196
% identity	88
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	196150
Contig ID	22292_1.R1039
5'-most EST	g5050572
Method	BLASTX
NCBI GI	g3128168
BLAST score	871
E value	9.0e-94

Match length 197
% identity 75
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 196151
Contig ID 22298_1.R1039
5'-most EST LIB3146-005-Q1-K1-H3
Method BLASTX
NCBI GI g3128192
BLAST score 440
E value 2.0e-43
Match length 109
% identity 72
NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 196152
Contig ID 22305_1.R1039
5'-most EST LIB3146-006-Q1-K1-A12

Seq. No. 196153
Contig ID 22310_1.R1039
5'-most EST LIB3149-046-Q1-K1-E11
Method BLASTX
NCBI GI g1931655
BLAST score 855
E value 4.0e-92
Match length 196
% identity 82
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No. 196154
Contig ID 22312_1.R1039
5'-most EST LIB3146-006-Q1-K1-B10
Method BLASTX
NCBI GI g3687235
BLAST score 470
E value 4.0e-47
Match length 125
% identity 75
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No. 196155
Contig ID 22328_1.R1039
5'-most EST LIB3146-006-Q1-K1-C7
Method BLASTX
NCBI GI g4138583
BLAST score 338
E value 2.0e-31
Match length 72
% identity 90
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No. 196156
Contig ID 22335_1.R1039
5'-most EST LIB3166-038-P1-K1-G3

Method	BLASTX
NCBI GI	g3287695
BLAST score	535
E value	1.0e-54
Match length	161
% identity	65
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb|1729503 from C. elegans cosmid gb|Z83220. [Arabidopsis thaliana]

Seq. No.	196157
Contig ID	22339_1.R1039
5'-most EST	LIB3149-037-Q1-K1-G6
Method	BLASTX
NCBI GI	g2632061
BLAST score	383
E value	4.0e-42
Match length	124
% identity	75
NCBI Description	(AJ002597) membrane-associated salt-inducible protein like [Arabidopsis thaliana]

Seq. No.	196158
Contig ID	22344_1.R1039
5'-most EST	LIB3146-006-Q1-K1-E10

Seq. No.	196159
Contig ID	22350_1.R1039
5'-most EST	g5044583
Method	BLASTX
NCBI GI	g4008159
BLAST score	785
E value	8.0e-84
Match length	195
% identity	76
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	196160
Contig ID	22351_1.R1039
5'-most EST	LIB3146-006-Q1-K1-E7
Method	BLASTX
NCBI GI	g4490342
BLAST score	445
E value	5.0e-44
Match length	153
% identity	67
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	196161
Contig ID	22352_1.R1039
5'-most EST	LIB3197-001-P1-M1-F11

Seq. No.	196162
Contig ID	22358_1.R1039
5'-most EST	LIB3147-027-Q1-K1-F9
Method	BLASTX
NCBI GI	g2275635

BLAST score 176
E value 2.0e-12
Match length 186
% identity 28
NCBI Description (AF014940) similar to the EMP24/GP25L family of membrane proteins [Caenorhabditis elegans]

Seq. No. 196163
Contig ID 22369_1.R1039
5'-most EST LIB3146-006-Q1-K1-H4

Seq. No. 196164
Contig ID 22377_1.R1039
5'-most EST uC-gsflnu33B144c03b1

Seq. No. 196165
Contig ID 22379_1.R1039
5'-most EST LIB3146-024-Q1-K1-F4

Seq. No. 196166
Contig ID 22379_2.R1039
5'-most EST LIB3165-031-P1-K1-C11

Seq. No. 196167
Contig ID 22381_1.R1039
5'-most EST LIB3196-003-P1-M1-H8
Method BLASTX
NCBI GI g4091117
BLAST score 319
E value 4.0e-29
Match length 217
% identity 42
NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. 196168
Contig ID 22384_1.R1039
5'-most EST LIB3146-007-Q1-K1-A7

Seq. No. 196169
Contig ID 22390_2.R1039
5'-most EST uC-gsflmaxxa054d12b1
Method BLASTX
NCBI GI g1293688
BLAST score 719
E value 6.0e-76
Match length 269
% identity 50
NCBI Description (U53827) STA1-2 [Silene latifolia ssp. alba] >gi|1293692 (U53829) STA1-18 [Silene latifolia ssp. alba]

Seq. No. 196170
Contig ID 22400_2.R1039
5'-most EST LIB3146-007-Q1-K1-C7

Seq. No. 196171
Contig ID 22402_1.R1039
5'-most EST uC-gsflnu33B101d07b1

Method	BLASTX
NCBI GI	g4204761
BLAST score	611
E value	1.0e-114
Match length	294
% identity	72
NCBI Description	(U51192) peroxidase precursor [Glycine max]

Seq. No.	196172
Contig ID	22412_1.R1039
5'-most EST	g5046557
Method	BLASTX
NCBI GI	g4262182
BLAST score	164
E value	5.0e-11
Match length	39
% identity	72
NCBI Description	(AC005508) 44123 [Arabidopsis thaliana]

Seq. No.	196173
Contig ID	22417_1.R1039
5'-most EST	LIB3189-005-P1-K1-F12

Seq. No.	196174
Contig ID	22418_1.R1039
5'-most EST	LIB3146-001-P1-K2-H4

Seq. No.	196175
Contig ID	22429_1.R1039
5'-most EST	g5044780
Method	BLASTX
NCBI GI	g544184
BLAST score	875
E value	3.0e-94
Match length	217
% identity	76
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi|322785|pir||A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi|296692|emb|CAA48630| (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No.	196176
Contig ID	22432_1.R1039
5'-most EST	LIB3146-003-P1-K1-D3
Method	BLASTX
NCBI GI	g2760606
BLAST score	616
E value	4.0e-64
Match length	129
% identity	87
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi|3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi|4539451|emb|CAB39931.1| (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	196177
Contig ID	22442_1.R1039
5'-most EST	LIB3165-023-P1-K1-B1
Method	BLASTX
NCBI GI	g544437
BLAST score	461
E value	6.0e-51
Match length	164
% identity	74
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi|296358|emb|CAA47018| (X66377) CIT-SAP [Citrus sinensis]

Seq. No.	196178
Contig ID	22442_3.R1039
5'-most EST	LIB3148-017-Q1-K1-F2
Method	BLASTN
NCBI GI	g296357
BLAST score	133
E value	2.0e-68
Match length	389
% identity	84
NCBI Description	C.sinensis mRNA csa for salt-associated protein

Seq. No.	196179
Contig ID	22444_1.R1039
5'-most EST	LIB3196-017-P1-M1-F5
Method	BLASTX
NCBI GI	g3335375
BLAST score	534
E value	2.0e-54
Match length	138
% identity	80
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	196180
Contig ID	22449_1.R1039
5'-most EST	LIB3146-056-Q1-K1-C3
Method	BLASTX
NCBI GI	g1628471
BLAST score	233
E value	2.0e-19
Match length	71
% identity	61
NCBI Description	(Y08780) Men-8 [Silene latifolia]

Seq. No.	196181
Contig ID	22455_1.R1039
5'-most EST	LIB3148-014-Q1-K1-B3

Seq. No.	196182
Contig ID	22459_1.R1039
5'-most EST	LIB3165-049-Q1-K1-E7

Seq. No.	196183
Contig ID	22463_1.R1039
5'-most EST	uC-gsflnu33B114h03b1

Method	BLASTX
NCBI GI	g2191136
BLAST score	613
E value	1.0e-63
Match length	203
% identity	59
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	196184
Contig ID	22465_1.R1039
5'-most EST	LIB3146-007-Q1-K1-D2
Method	BLASTX
NCBI GI	g2245127
BLAST score	217
E value	9.0e-18
Match length	78
% identity	55
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196185
Contig ID	22469_1.R1039
5'-most EST	LIB3148-012-Q1-K1-H11
Method	BLASTX
NCBI GI	g1710587
BLAST score	249
E value	3.0e-21
Match length	91
% identity	56
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi|1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	196186
Contig ID	22479_1.R1039
5'-most EST	uC-gsronu33B082a01b1
Method	BLASTX
NCBI GI	g2618693
BLAST score	148
E value	4.0e-09
Match length	104
% identity	30
NCBI Description	(AC002510) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	196187
Contig ID	22479_2.R1039
5'-most EST	LIB3148-054-Q1-K1-B12

Seq. No.	196188
Contig ID	22487_1.R1039
5'-most EST	LIB3146-007-Q1-K1-F8

Seq. No.	196189
Contig ID	22496_1.R1039
5'-most EST	g5047413

Seq. No.	196190
Contig ID	22497_1.R1039
5'-most EST	uC-gsflmaxxa003e08b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	602
E value	3.0e-62
Match length	250
% identity	52
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	196191
Contig ID	22513_1.R1039
5'-most EST	LIB3197-055-Q1-M1-E6
Method	BLASTX
NCBI GI	g2443875
BLAST score	215
E value	5.0e-17
Match length	156
% identity	29
NCBI Description	(AC002294) amino acid permease [Arabidopsis thaliana]

Seq. No.	196192
Contig ID	22524_1.R1039
5'-most EST	LIB3146-028-Q1-K1-A1
Method	BLASTX
NCBI GI	g4107099
BLAST score	513
E value	3.0e-52
Match length	148
% identity	64
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi|4156245|dbj|BAA37112| (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	196193
Contig ID	22529_1.R1039
5'-most EST	LIB3146-008-Q1-K1-C9
Method	BLASTX
NCBI GI	g2245069
BLAST score	501
E value	7.0e-51
Match length	134
% identity	66
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196194
Contig ID	22530_1.R1039
5'-most EST	LIB3146-008-Q1-K1-D1

Seq. No.	196195
Contig ID	22533_1.R1039
5'-most EST	LIB3146-008-Q1-K1-D3

Seq. No.	196196
Contig ID	22534_1.R1039

5'-most EST	uC-gsflnu33B064g10b1
Method	BLASTX
NCBI GI	g2499611
BLAST score	975
E value	1.0e-178
Match length	368
% identity	84
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi|629548|pir||S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi|457406|dbj|BAA04870| (D21843) MAP kinase [Arabidopsis thaliana]

Seq. No.	196197
Contig ID	22547_1.R1039
5'-most EST	uC-gsflnu33B055b07b1
Method	BLASTX
NCBI GI	g1076274
BLAST score	491
E value	1.0e-49
Match length	153
% identity	59
NCBI Description	cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No.	196198
Contig ID	22554_1.R1039
5'-most EST	LIB3146-008-Q1-K1-G2
Method	BLASTX
NCBI GI	g4139041
BLAST score	157
E value	5.0e-10
Match length	248
% identity	6
NCBI Description	(AF072274) resistance protein candidate RGC20 [Lactuca sativa]

Seq. No.	196199
Contig ID	22558_1.R1039
5'-most EST	LIB3146-008-Q1-K1-G7
Method	BLASTX
NCBI GI	g1899175
BLAST score	584
E value	3.0e-60
Match length	132
% identity	84
NCBI Description	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No.	196200
Contig ID	22559_1.R1039
5'-most EST	LIB3146-008-Q1-K1-H1
Method	BLASTX
NCBI GI	g2129552
BLAST score	619
E value	2.0e-64
Match length	142
% identity	87

NCBI Description	calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)
Seq. No.	196201
Contig ID	22564_1.R1039
5'-most EST	LIB3146-008-Q1-K1-H4
Method	BLASTX
NCBI GI	g2130017
BLAST score	436
E value	3.0e-43
Match length	95
% identity	81
NCBI Description	hypothetical protein - common sunflower >gi|1040729|emb|CAA60621| (X87143) cytochrome b5 containing fusion protein [Helianthus annuus]
Seq. No.	196202
Contig ID	22571_1.R1039
5'-most EST	LIB3272-036-P1-K1-H6
Method	BLASTX
NCBI GI	g3269284
BLAST score	431
E value	2.0e-42
Match length	125
% identity	71
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.	196203
Contig ID	22571_2.R1039
5'-most EST	LIB3166-040-P1-K1-D12
Method	BLASTX
NCBI GI	g3269284
BLAST score	417
E value	7.0e-41
Match length	122
% identity	70
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.	196204
Contig ID	22571_3.R1039
5'-most EST	LIB3149-051-Q1-K1-F4
Method	BLASTX
NCBI GI	g3269284
BLAST score	426
E value	6.0e-42
Match length	126
% identity	70
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.	196205
Contig ID	22572_1.R1039
5'-most EST	LIB3146-027-Q1-K1-C3
Seq. No.	196206
Contig ID	22586_1.R1039
5'-most EST	LIB3148-005-Q1-K1-A1

Seq. No.	196207
Contig ID	22601_1.R1039
5'-most EST	LIB3196-006-P1-M1-F5
Method	BLASTX
NCBI GI	g3885334
BLAST score	1664
E value	0.0e+00
Match length	380
% identity	82
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	196208
Contig ID	22605_1.R1039
5'-most EST	uC-gsflnu33B026g01b1
Method	BLASTX
NCBI GI	g3980254
BLAST score	510
E value	9.0e-52
Match length	135
% identity	69
NCBI Description	(AJ006053) peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	196209
Contig ID	22617_1.R1039
5'-most EST	LIB3146-060-Q1-K1-H9
Method	BLASTX
NCBI GI	g1698548
BLAST score	524
E value	2.0e-53
Match length	157
% identity	69
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	196210
Contig ID	22630_1.R1039
5'-most EST	g5045678
Method	BLASTX
NCBI GI	g2865175
BLAST score	732
E value	1.0e-77
Match length	177
% identity	76
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No.	196211
Contig ID	22635_1.R1039
5'-most EST	LIB3146-010-Q1-K1-B8
Method	BLASTX
NCBI GI	g3128168
BLAST score	567
E value	3.0e-58
Match length	167
% identity	57
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 196212
Contig ID 22640_1.R1039
5'-most EST uC-gsflmaxxa041c07b1
Method BLASTX
NCBI GI g2344898
BLAST score 401
E value 1.0e-38
Match length 113
% identity 70
NCBI Description (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana]

Seq. No. 196213
Contig ID 22640_2.R1039
5'-most EST g5045458
Method BLASTX
NCBI GI g2344898
BLAST score 468
E value 6.0e-50
Match length 165
% identity 61
NCBI Description (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana]

Seq. No. 196214
Contig ID 22650_1.R1039
5'-most EST LIB3146-014-Q1-K1-B3

Seq. No. 196215
Contig ID 22666_1.R1039
5'-most EST LIB3146-010-Q1-K1-E4

Seq. No. 196216
Contig ID 22669_1.R1039
5'-most EST LIB3146-010-Q1-K1-E7
Method BLASTX
NCBI GI g4263722
BLAST score 425
E value 7.0e-42
Match length 133
% identity 57
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 196217
Contig ID 22675_1.R1039
5'-most EST LIB3147-004-Q1-K1-G7
Method BLASTX
NCBI GI g3183207
BLAST score 204
E value 6.0e-16
Match length 59
% identity 59
NCBI Description HYPOTHETICAL PROTEIN KIAA0017 >gi|285999|dbj|BAA02805| (D13642) KIAA0017 [Homo sapiens]

Seq. No. 196218

Contig ID	22677_1.R1039
5'-most EST	LIB3146-041-Q1-K1-E4
Method	BLASTX
NCBI GI	g2281635
BLAST score	279
E value	2.0e-24
Match length	64
% identity	83
NCBI Description	(AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]

Seq. No.	196219
Contig ID	22678_1.R1039
5'-most EST	LIB3146-010-Q1-K1-F5
Method	BLASTX
NCBI GI	g2344901
BLAST score	650
E value	4.0e-68
Match length	168
% identity	77
NCBI Description	(AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

Seq. No.	196220
Contig ID	22680_1.R1039
5'-most EST	LIB3146-010-Q1-K1-F7
Method	BLASTN
NCBI GI	g3420042
BLAST score	58
E value	1.0e-23
Match length	265
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	196221
Contig ID	22691_1.R1039
5'-most EST	LIB3196-050-P1-M1-H11
Method	BLASTX
NCBI GI	g4335750
BLAST score	265
E value	1.0e-22
Match length	82
% identity	59
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	196222
Contig ID	22696_1.R1039
5'-most EST	LIB3146-010-Q1-K1-H10
Method	BLASTX
NCBI GI	g2499931
BLAST score	268
E value	2.0e-23
Match length	65
% identity	80
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)

>gi|2129534|pir||S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana
>gi|1321681|emb|CAA65609| (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	196223
Contig ID	22698_1.R1039
5'-most EST	uC-gsronu33B080c05b1

Seq. No.	196224
Contig ID	22699_1.R1039
5'-most EST	LIB3146-010-Q1-K1-H3

Seq. No.	196225
Contig ID	22707_1.R1039
5'-most EST	LIB3197-048-Q1-M1-D11
Method	BLASTX
NCBI GI	g3894193
BLAST score	158
E value	2.0e-10
Match length	54
% identity	57
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	196226
Contig ID	22712_1.R1039
5'-most EST	LIB3149-006-Q1-K1-H8

Seq. No.	196227
Contig ID	22715_1.R1039
5'-most EST	LIB3146-011-Q1-K1-A7
Method	BLASTX
NCBI GI	g4512676
BLAST score	263
E value	8.0e-35
Match length	186
% identity	46
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	196228
Contig ID	22716_2.R1039
5'-most EST	LIB3166-019-P1-K1-G6

Seq. No.	196229
Contig ID	22718_1.R1039
5'-most EST	LIB3146-011-Q1-K1-B1

Seq. No.	196230
Contig ID	22720_1.R1039
5'-most EST	LIB3146-011-Q1-K1-B11

Seq. No.	196231
Contig ID	22739_1.R1039
5'-most EST	uC-gsronu33B114d04b1
Method	BLASTX
NCBI GI	g4415933

BLAST score	856
E value	4.0e-92
Match length	222
% identity	73
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi|4559390|gb|AAD23050.1|AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	196232
Contig ID	22748_1.R1039
5'-most EST	LIB3146-011-Q1-K1-D5
Method	BLASTX
NCBI GI	g1665817
BLAST score	155
E value	4.0e-10
Match length	52
% identity	52
NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	196233
Contig ID	22752_1.R1039
5'-most EST	LIB3149-040-Q1-K1-C2

Seq. No.	196234
Contig ID	22757_1.R1039
5'-most EST	LIB3146-011-Q1-K1-E2
Method	BLASTX
NCBI GI	g3355311
BLAST score	527
E value	7.0e-54
Match length	141
% identity	79
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	196235
Contig ID	22761_1.R1039
5'-most EST	g5046975
Method	BLASTX
NCBI GI	g1707018
BLAST score	544
E value	2.0e-55
Match length	167
% identity	68
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]

Seq. No.	196236
Contig ID	22761_2.R1039
5'-most EST	uC-gsflmaxxa009h04b1
Method	BLASTX
NCBI GI	g1707018
BLAST score	318
E value	3.0e-29
Match length	106

% identity	64
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]

Seq. No.	196237
Contig ID	22768_1.R1039
5'-most EST	LIB3146-011-Q1-K1-F3
Method	BLASTX
NCBI GI	g166949
BLAST score	208
E value	2.0e-16
Match length	163
% identity	33
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No.	196238
Contig ID	22775_1.R1039
5'-most EST	uC-gsronu33B136d09b1

Seq. No.	196239
Contig ID	22776_1.R1039
5'-most EST	uC-gsflnu33B018f06b1
Method	BLASTX
NCBI GI	g1742951
BLAST score	477
E value	2.0e-66
Match length	160
% identity	85
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	196240
Contig ID	22778_1.R1039
5'-most EST	LIB3146-011-Q1-K1-G5

Seq. No.	196241
Contig ID	22788_1.R1039
5'-most EST	LIB3147-001-Q1-K2-H9
Method	BLASTX
NCBI GI	g2146729
BLAST score	198
E value	2.0e-15
Match length	109
% identity	39
NCBI Description	cystathionine-gamma-synthase (EC 4.2.99.9) 1 - Arabidopsis thaliana

Seq. No.	196242
Contig ID	22789_1.R1039
5'-most EST	LIB3146-023-Q1-K1-A2

Seq. No.	196243
Contig ID	22802_1.R1039
5'-most EST	LIB3166-048-P1-K1-D4
Method	BLASTX
NCBI GI	g4263711
BLAST score	366
E value	5.0e-58

Match length 159
% identity 72
NCBI Description (AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No. 196244
Contig ID 22807_1.R1039
5'-most EST LIB3146-012-Q1-K1-B3

Seq. No. 196245
Contig ID 22811_1.R1039
5'-most EST uC-gsronu33b023g11b1
Method BLASTX
NCBI GI g4033365
BLAST score 748
E value 2.0e-79
Match length 149
% identity 93
NCBI Description (AJ223499) ATP sulfurylase [Brassica juncea]

Seq. No. 196246
Contig ID 22811_2.R1039
5'-most EST LIB3165-043-Q1-K1-C11
Method BLASTX
NCBI GI g1527219
BLAST score 347
E value 1.0e-32
Match length 76
% identity 83
NCBI Description (U68218) ATP sulphurylase [Brassica napus]

Seq. No. 196247
Contig ID 22821_1.R1039
5'-most EST LIB3166-034-P1-K1-D10
Method BLASTX
NCBI GI g3080437
BLAST score 178
E value 9.0e-13
Match length 50
% identity 76
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 196248
Contig ID 22823_1.R1039
5'-most EST g5045415
Method BLASTX
NCBI GI g4567246
BLAST score 525
E value 4.0e-53
Match length 179
% identity 63
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 196249
Contig ID 22832_1.R1039
5'-most EST LIB3146-012-Q1-K1-D5
Method BLASTX

NCBI GI	g3142300
BLAST score	236
E value	1.0e-19
Match length	118
% identity	43
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb|L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158, gb|N38703 and gb|AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	196250
Contig ID	22840_1.R1039
5'-most EST	LIB3146-012-Q1-K1-E2
Method	BLASTX
NCBI GI	g1769887
BLAST score	284
E value	2.0e-25
Match length	61
% identity	82
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	196251
Contig ID	22864_1.R1039
5'-most EST	uC-gsflmaxxa089h08b1
Method	BLASTN
NCBI GI	g4580365
BLAST score	43
E value	1.0e-14
Match length	129
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	196252
Contig ID	22870_1.R1039
5'-most EST	uC-gsronu33B168b08b1
Method	BLASTX
NCBI GI	g2407800
BLAST score	514
E value	3.0e-52
Match length	110
% identity	93
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	196253
Contig ID	22870_2.R1039
5'-most EST	LIB3146-012-Q1-K1-H10
Method	BLASTX
NCBI GI	g2407800
BLAST score	337
E value	1.0e-31
Match length	78
% identity	87
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	196254
Contig ID	22871_1.R1039

5'-most EST	LIB3146-012-Q1-K1-H2
Seq. No.	196255
Contig ID	22877_1.R1039
5'-most EST	LIB3197-024-Q1-M1-F4
Method	BLASTX
NCBI GI	g1518059
BLAST score	303
E value	2.0e-27
Match length	96
% identity	56
NCBI Description	(U65650) blue-copper binging protein III [Arabidopsis thaliana] >gi|3395770 (AF039404) uclacyanin 3 [Arabidopsis thaliana]
Seq. No.	196256
Contig ID	22897_1.R1039
5'-most EST	LIB3146-023-Q1-K1-H3
Method	BLASTX
NCBI GI	g2981131
BLAST score	599
E value	3.0e-62
Match length	147
% identity	81
NCBI Description	(AF052570) AGAMOUS homolog [Populus balsamifera subsp. trichocarpa]
Seq. No.	196257
Contig ID	22903_1.R1039
5'-most EST	g5050726
Method	BLASTX
NCBI GI	g3298540
BLAST score	808
E value	2.0e-86
Match length	174
% identity	87
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.	196258
Contig ID	22908_1.R1039
5'-most EST	LIB3196-037-P1-M1-G1
Seq. No.	196259
Contig ID	22911_1.R1039
5'-most EST	g5046935
Method	BLASTX
NCBI GI	g3785977
BLAST score	338
E value	3.0e-31
Match length	135
% identity	48
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]
Seq. No.	196260
Contig ID	22914_1.R1039
5'-most EST	uC-gsflmaxxa042h05b1

Method	BLASTX
NCBI GI	g2695931
BLAST score	358
E value	7.0e-34
Match length	169
% identity	51
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	196261
Contig ID	22923_1.R1039
5'-most EST	LIB3146-013-Q1-K1-G11
Method	BLASTX
NCBI GI	g2492772
BLAST score	150
E value	1.0e-09
Match length	32
% identity	81
NCBI Description	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH) (FALDH) (GSH-FDH) >gi|1498024 (U63931) glutathione-dependent formaldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	196262
Contig ID	22928_1.R1039
5'-most EST	g3326577
Method	BLASTX
NCBI GI	g1176658
BLAST score	175
E value	3.0e-21
Match length	122
% identity	48
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi|726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	196263
Contig ID	22929_1.R1039
5'-most EST	LIB3146-013-Q1-K1-H7
Method	BLASTX
NCBI GI	g3702608
BLAST score	386
E value	1.0e-37
Match length	79
% identity	90
NCBI Description	(AJ224165) shaggy kinase 7 [Petunia x hybrida]

Seq. No.	196264
Contig ID	22938_1.R1039
5'-most EST	LIB3146-014-Q1-K1-A4
Method	BLASTX
NCBI GI	g2618731
BLAST score	382
E value	1.0e-36
Match length	102
% identity	71
NCBI Description	(U49077) IAA21 [Arabidopsis thaliana]

Seq. No.	196265
Contig ID	22940_1.R1039
5'-most EST	g3325881
Method	BLASTX
NCBI GI	g3881976
BLAST score	841
E value	2.0e-90
Match length	222
% identity	71
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	196266
Contig ID	22940_2.R1039
5'-most EST	LIB3148-059-Q1-K1-H8
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	7.0e-09
Match length	48
% identity	51
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	196267
Contig ID	22943_1.R1039
5'-most EST	LIB3166-038-P1-K1-B10
Method	BLASTN
NCBI GI	g2351065
BLAST score	46
E value	2.0e-16
Match length	389
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	196268
Contig ID	22946_1.R1039
5'-most EST	LIB3146-014-Q1-K1-B12
Method	BLASTX
NCBI GI	g4097585
BLAST score	231
E value	4.0e-19
Match length	70
% identity	73
NCBI Description	(U64925) NTGP4 [Nicotiana tabacum]

Seq. No.	196269
Contig ID	22957_1.R1039
5'-most EST	uC-gsronu33B117g08b1

Seq. No.	196270
Contig ID	22962_1.R1039
5'-most EST	uC-gsflnu33B128d12b1

Seq. No.	196271
Contig ID	22968_1.R1039
5'-most EST	g5046806
Method	BLASTX

NCBI GI	g2911072
BLAST score	662
E value	2.0e-75
Match length	241
% identity	64
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	196272
Contig ID	22976_1.R1039
5'-most EST	LIB3148-023-Q1-K1-H3
Method	BLASTX
NCBI GI	g1762634
BLAST score	554
E value	5.0e-57
Match length	120
% identity	83
NCBI Description	(U64789) AROGP2 [Lycopersicon esculentum]

Seq. No.	196273
Contig ID	22988_1.R1039
5'-most EST	LIB3147-015-Q1-K1-C10
Method	BLASTX
NCBI GI	g4432855
BLAST score	649
E value	8.0e-68
Match length	257
% identity	58
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	196274
Contig ID	23001_1.R1039
5'-most EST	LIB3147-026-Q1-K1-H1
Method	BLASTN
NCBI GI	g18731
BLAST score	43
E value	7.0e-15
Match length	119
% identity	84
NCBI Description	Soybean RPB1-B1 gene for the largest subunit of RNA polymerase II (EC 2.7.7.6)

Seq. No.	196275
Contig ID	23009_1.R1039
5'-most EST	uC-gsflnu33B128c01b1
Method	BLASTX
NCBI GI	g3851670
BLAST score	215
E value	7.0e-21
Match length	82
% identity	67
NCBI Description	(AF099906) J8 [Arabidopsis thaliana]

Seq. No.	196276
Contig ID	23012_1.R1039
5'-most EST	uC-gsflnu33B126d02b1
Method	BLASTX
NCBI GI	g122106

BLAST score	410
E value	7.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi|70771|pir||HSZM4 histone H4 - maize >gi|81642|pir||S06904 histone H4 - Arabidopsis thaliana >gi|2119028|pir||S60475 histone H4 - garden pea >gi|21795|emb|CAA24924| (X00043) histone H4 [Triticum aestivum] >gi|166740 (M17132) histone H4 [Arabidopsis thaliana] >gi|166742 (M17133) histone H4 [Arabidopsis thaliana] >gi|168499 (M36659) histone H4 (H4C13) [Zea mays] >gi|168501 (M13370) histone H4 [Zea mays] >gi|168503 (M13377) histone H4 [Zea mays] >gi|498898 (U10042) histone H4 homolog [Pisum sativum] >gi|1806285|emb|CAB01914| (Z79638) histone H4 homologue [Sesbania rostrata] >gi|3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi|4580385|gb|AAD24364.1|AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi|225838|prf||1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	196277
Contig ID	23012_2.R1039
5'-most EST	uC-gsflnu33B060g09b1
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	6.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi|70771|pir||HSZM4 histone H4 - maize >gi|81642|pir||S06904 histone H4 - Arabidopsis thaliana >gi|2119028|pir||S60475 histone H4 - garden pea >gi|21795|emb|CAA24924| (X00043) histone H4 [Triticum aestivum] >gi|166740 (M17132) histone H4 [Arabidopsis thaliana] >gi|166742 (M17133) histone H4 [Arabidopsis thaliana] >gi|168499 (M36659) histone H4 (H4C13) [Zea mays] >gi|168501 (M13370) histone H4 [Zea mays] >gi|168503 (M13377) histone H4 [Zea mays] >gi|498898 (U10042) histone H4 homolog [Pisum sativum] >gi|1806285|emb|CAB01914| (Z79638) histone H4 homologue [Sesbania rostrata] >gi|3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi|4580385|gb|AAD24364.1|AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi|225838|prf||1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	196278
Contig ID	23019_1.R1039
5'-most EST	LIB3146-015-Q1-K1-A1
Method	BLASTX
NCBI GI	g2505870
BLAST score	121
E value	3.0e-09
Match length	60
% identity	46
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196279

Contig ID	23028_1.R1039
5'-most EST	LIB3272-047-P1-K1-C5
Method	BLASTX
NCBI GI	g4127456
BLAST score	602
E value	2.0e-62
Match length	187
% identity	42
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	196280
Contig ID	23028_2.R1039
5'-most EST	LIB3166-014-P1-K1-G5
Method	BLASTX
NCBI GI	g4127456
BLAST score	433
E value	1.0e-42
Match length	151
% identity	36
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	196281
Contig ID	23029_1.R1039
5'-most EST	uC-gsflnu33B024a11b1
Method	BLASTX
NCBI GI	g4056506
BLAST score	546
E value	8.0e-56
Match length	212
% identity	51
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	196282
Contig ID	23034_2.R1039
5'-most EST	uC-gsflmaxxa097b02b1

Seq. No.	196283
Contig ID	23038_1.R1039
5'-most EST	LIB3146-015-Q1-K1-C10
Method	BLASTX
NCBI GI	g3335378
BLAST score	590
E value	5.0e-61
Match length	174
% identity	68
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	196284
Contig ID	23065_1.R1039
5'-most EST	LIB3146-015-Q1-K1-E7
Method	BLASTN
NCBI GI	g2264309
BLAST score	35
E value	6.0e-10
Match length	107
% identity	83

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	196285
Contig ID	23070_1.R1039
5'-most EST	uC-gsflmaxxa045g05b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	355
E value	2.0e-33
Match length	179
% identity	44
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	196286
Contig ID	23075_1.R1039
5'-most EST	uC-gsflnu33B111a10b1
Method	BLASTX
NCBI GI	g3603473
BLAST score	474
E value	3.0e-47
Match length	145
% identity	63
NCBI Description	(AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No.	196287
Contig ID	23077_1.R1039
5'-most EST	LIB3196-054-P1-M1-H11
Method	BLASTX
NCBI GI	g4206122
BLAST score	811
E value	1.0e-86
Match length	188
% identity	82
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	196288
Contig ID	23081_1.R1039
5'-most EST	LIB3165-021-P1-K1-G8
Method	BLASTX
NCBI GI	g4049399
BLAST score	203
E value	1.0e-15
Match length	165
% identity	30
NCBI Description	(Y09581) FRO2 [Arabidopsis thaliana]

Seq. No.	196289
Contig ID	23089_1.R1039
5'-most EST	g3325679
Method	BLASTX
NCBI GI	g4006921
BLAST score	529
E value	1.0e-107
Match length	253

% identity	75
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	196290
Contig ID	23100_1.R1039
5'-most EST	LIB3149-027-Q1-K1-G11
Method	BLASTX
NCBI GI	g2266949
BLAST score	672
E value	1.0e-70
Match length	141
% identity	92
NCBI Description	(AF008940) phosphoenolpyruvate carboxylase 2 [Gossypium hirsutum]

Seq. No.	196291
Contig ID	23101_1.R1039
5'-most EST	LIB3146-016-Q1-K1-A7
Method	BLASTX
NCBI GI	g2979544
BLAST score	145
E value	8.0e-12
Match length	135
% identity	38
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	196292
Contig ID	23107_1.R1039
5'-most EST	LIB3146-016-Q1-K1-B11

Seq. No.	196293
Contig ID	23117_1.R1039
5'-most EST	LIB3146-016-Q1-K1-C10

Seq. No.	196294
Contig ID	23138_1.R1039
5'-most EST	LIB3189-043-P1-K1-F1

Seq. No.	196295
Contig ID	23149_1.R1039
5'-most EST	LIB3146-016-Q1-K1-F4
Method	BLASTX
NCBI GI	g2569938
BLAST score	708
E value	6.0e-75
Match length	168
% identity	77
NCBI Description	(Y15193) GAI [Arabidopsis thaliana]

Seq. No.	196296
Contig ID	23151_1.R1039
5'-most EST	LIB3146-016-Q1-K1-F8
Method	BLASTX
NCBI GI	g1255852
BLAST score	225
E value	2.0e-18
Match length	122

% identity	35
NCBI Description	(U53339) simmilar to enoyl-CoA hydratases [Caenorhabditis elegans]

Seq. No.	196297
Contig ID	23159_1.R1039
5'-most EST	uC-gsflnu33B058h05b1
Method	BLASTX
NCBI GI	g3600039
BLAST score	813
E value	3.0e-87
Match length	188
% identity	79
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	196298
Contig ID	23162_1.R1039
5'-most EST	LIB3146-016-Q1-K1-H3

Seq. No.	196299
Contig ID	23163_1.R1039
5'-most EST	LIB3146-016-Q1-K1-H4

Seq. No.	196300
Contig ID	23167_1.R1039
5'-most EST	uC-gsronu33B018b05b1
Method	BLASTX
NCBI GI	g1946355
BLAST score	487
E value	5.0e-49
Match length	175
% identity	50
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi|2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	196301
Contig ID	23175_1.R1039
5'-most EST	LIB3146-043-Q1-K1-D11
Method	BLASTX
NCBI GI	g3122228
BLAST score	320
E value	2.0e-29
Match length	84
% identity	75
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi|2129837|pir||S65049 low molecular weight heat shock protein precursor (clone Hsp23.9) - soybean >gi|710432 (U21722) Hsp23.9 [Glycine max]

Seq. No.	196302
Contig ID	23196_1.R1039
5'-most EST	LIB3146-017-Q1-K1-C6
Method	BLASTX
NCBI GI	g4138265
BLAST score	165

E value	9.0e-12
Match length	42
% identity	64
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	196303
Contig ID	23198_2.R1039
5'-most EST	LIB3146-017-Q1-K1-C8
Method	BLASTX
NCBI GI	g2981131
BLAST score	181
E value	6.0e-15
Match length	67
% identity	73
NCBI Description	(AF052570) AGAMOUS homolog [Populus balsamifera subsp. trichocarpa]

Seq. No.	196304
Contig ID	23237_1.R1039
5'-most EST	g5050590
Method	BLASTX
NCBI GI	g2244807
BLAST score	412
E value	4.0e-40
Match length	202
% identity	35
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196305
Contig ID	23246_1.R1039
5'-most EST	uC-gsronu33B007a01b1
Method	BLASTX
NCBI GI	g4539350
BLAST score	249
E value	4.0e-21
Match length	67
% identity	64
NCBI Description	(AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	196306
Contig ID	23253_1.R1039
5'-most EST	uC-gsronu33B169f10b1
Method	BLASTX
NCBI GI	g2281090
BLAST score	500
E value	8.0e-60
Match length	176
% identity	72
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196307
Contig ID	23259_1.R1039
5'-most EST	g5046982
Method	BLASTN
NCBI GI	g2281081
BLAST score	36

E value	1.0e-10
Match length	165
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	196308
Contig ID	23263_1.R1039
5'-most EST	uC-gsronu33B049e01b1
Method	BLASTX
NCBI GI	g1684851
BLAST score	283
E value	3.0e-25
Match length	113
% identity	53
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	196309
Contig ID	23289_1.R1039
5'-most EST	LIB3146-018-Q1-K1-E12
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	2.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	196310
Contig ID	23296_1.R1039
5'-most EST	uC-gsflnu33B130f03b1

Seq. No.	196311
Contig ID	23306_1.R1039
5'-most EST	g3326188
Method	BLASTX
NCBI GI	g1653513
BLAST score	195
E value	2.0e-19
Match length	95
% identity	50
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	196312
Contig ID	23313_1.R1039
5'-most EST	LIB3146-018-Q1-K1-G6
Method	BLASTX
NCBI GI	g166949
BLAST score	469
E value	9.0e-47
Match length	214
% identity	44
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No.	196313
Contig ID	23317_1.R1039

5'-most EST	LIB3146-018-Q1-K1-H5
Seq. No.	196314
Contig ID	23318_1.R1039
5'-most EST	LIB3166-053-P1-K1-H3
Method	BLASTX
NCBI GI	g3367515
BLAST score	381
E value	1.0e-36
Match length	97
% identity	72
NCBI Description	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
Seq. No.	196315
Contig ID	23324_1.R1039
5'-most EST	LIB3146-018-Q1-K1-H9
Method	BLASTX
NCBI GI	g4539437
BLAST score	352
E value	2.0e-33
Match length	129
% identity	55
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]
Seq. No.	196316
Contig ID	23331_1.R1039
5'-most EST	LIB3148-019-Q1-K1-H9
Seq. No.	196317
Contig ID	23351_1.R1039
5'-most EST	g3325873
Method	BLASTX
NCBI GI	g4490737
BLAST score	569
E value	3.0e-58
Match length	203
% identity	51
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	196318
Contig ID	23357_1.R1039
5'-most EST	LIB3146-023-Q1-K1-G8
Method	BLASTX
NCBI GI	g2281115
BLAST score	642
E value	4.0e-67
Match length	181
% identity	79
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]
Seq. No.	196319
Contig ID	23365_1.R1039
5'-most EST	uC-gsflnu33B059b11b1

Seq. No.	196320
Contig ID	23384_1.R1039
5'-most EST	LIB3146-019-Q1-K1-F9
Method	BLASTX
NCBI GI	g1236961
BLAST score	402
E value	6.0e-39
Match length	131
% identity	56
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	196321
Contig ID	23398_1.R1039
5'-most EST	g5050129
Method	BLASTX
NCBI GI	g872116
BLAST score	929
E value	1.0e-100
Match length	207
% identity	38
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	196322
Contig ID	23399_1.R1039
5'-most EST	LIB3272-051-P1-K1-D7

Seq. No.	196323
Contig ID	23406_1.R1039
5'-most EST	LIB3146-020-Q1-K1-A6

Seq. No.	196324
Contig ID	23406_2.R1039
5'-most EST	LIB3146-032-Q1-K1-C11
Method	BLASTX
NCBI GI	g1771261
BLAST score	158
E value	2.0e-10
Match length	124
% identity	37
NCBI Description	(X77012) 1,4-alpha-glucan branching enzyme [Manihot esculenta]

Seq. No.	196325
Contig ID	23413_1.R1039
5'-most EST	LIB3146-020-Q1-K1-B2
Method	BLASTX
NCBI GI	g3219271
BLAST score	616
E value	4.0e-64
Match length	201
% identity	64
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No.	196326
Contig ID	23414_1.R1039
5'-most EST	LIB3147-029-Q1-K1-C9
Method	BLASTX

NCBI GI	g4006899
BLAST score	399
E value	1.0e-38
Match length	109
% identity	62
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	196327
Contig ID	23430_1.R1039
5'-most EST	LIB3149-050-Q1-K1-B7
Method	BLASTN
NCBI GI	g2943791
BLAST score	89
E value	6.0e-42
Match length	593
% identity	82
NCBI Description	Cucurbita sp. mRNA for PV72, complete cds

Seq. No.	196328
Contig ID	23436_1.R1039
5'-most EST	g5049681
Method	BLASTX
NCBI GI	g3738332
BLAST score	508
E value	2.0e-51
Match length	208
% identity	51
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	196329
Contig ID	23448_1.R1039
5'-most EST	uC-gsflnu33B101a04b1
Method	BLASTX
NCBI GI	g2244993
BLAST score	501
E value	1.0e-50
Match length	168
% identity	60
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	196330
Contig ID	23462_1.R1039
5'-most EST	LIB3166-046-P1-K1-D1
Method	BLASTX
NCBI GI	g4490297
BLAST score	315
E value	6.0e-29
Match length	150
% identity	43
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	196331
Contig ID	23464_1.R1039
5'-most EST	uC-gsronu33B179b04b1
Method	BLASTN

NCBI GI	g433664
BLAST score	42
E value	3.0e-14
Match length	136
% identity	87
NCBI Description	A.thaliana for Sec61 beta-subunit homolog

Seq. No.	196332
Contig ID	23465_1.R1039
5'-most EST	LIB3146-020-Q1-K1-F7
Method	BLASTX
NCBI GI	g1237250
BLAST score	808
E value	1.0e-86
Match length	198
% identity	76
NCBI Description	(X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No.	196333
Contig ID	23472_1.R1039
5'-most EST	LIB3146-020-Q1-K1-G4

Seq. No.	196334
Contig ID	23475_1.R1039
5'-most EST	LIB3146-020-Q1-K1-G7
Method	BLASTX
NCBI GI	g2191165
BLAST score	388
E value	2.0e-37
Match length	132
% identity	58
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No.	196335
Contig ID	23480_1.R1039
5'-most EST	LIB3146-020-Q1-K1-H2

Seq. No.	196336
Contig ID	23494_1.R1039
5'-most EST	uC-gsronu33B171b08b1
Method	BLASTX
NCBI GI	g2462749
BLAST score	428
E value	6.0e-42
Match length	192
% identity	44
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	196337
Contig ID	23501_1.R1039
5'-most EST	LIB3166-028-P1-K1-E5
Method	BLASTX
NCBI GI	g1621268
BLAST score	293
E value	3.0e-26

Match length	63
% identity	90
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	196338
Contig ID	23510_1.R1039
5'-most EST	LIB3146-057-Q1-K1-E3

Seq. No.	196339
Contig ID	23514_1.R1039
5'-most EST	LIB3147-006-Q1-K1-G2
Method	BLASTX
NCBI GI	g4263779
BLAST score	559
E value	2.0e-57
Match length	185
% identity	61
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196340
Contig ID	23517_1.R1039
5'-most EST	LIB3146-021-Q1-K1-C8
Method	BLASTX
NCBI GI	g2462749
BLAST score	161
E value	4.0e-11
Match length	114
% identity	38
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	196341
Contig ID	23532_1.R1039
5'-most EST	g5044510
Method	BLASTX
NCBI GI	g3688174
BLAST score	603
E value	2.0e-62
Match length	166
% identity	70
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	196342
Contig ID	23535_1.R1039
5'-most EST	uC-gsflnu33B145d06b1
Method	BLASTX
NCBI GI	g4262154
BLAST score	209
E value	2.0e-16
Match length	102
% identity	47
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	196343
Contig ID	23539_1.R1039
5'-most EST	LIB3146-026-Q1-K2-G4

Method	BLASTX
NCBI GI	g4322948
BLAST score	235
E value	1.0e-19
Match length	51
% identity	84
NCBI Description	(AF097180) cystathionine gamma-synthase precursor [Nicotiana tabacum]

Seq. No.	196344
Contig ID	23559_1.R1039
5'-most EST	LIB3197-050-Q1-M1-D4
Method	BLASTX
NCBI GI	g4467158
BLAST score	173
E value	3.0e-12
Match length	156
% identity	33
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	196345
Contig ID	23562_1.R1039
5'-most EST	LIB3165-016-P1-K1-C2

Seq. No.	196346
Contig ID	23564_1.R1039
5'-most EST	LIB3146-024-Q1-K1-F7

Seq. No.	196347
Contig ID	23573_1.R1039
5'-most EST	LIB3166-021-P1-K1-C3
Method	BLASTX
NCBI GI	g2947063
BLAST score	176
E value	2.0e-12
Match length	76
% identity	43
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	196348
Contig ID	23579_1.R1039
5'-most EST	LIB3146-022-Q1-K1-A2
Method	BLASTX
NCBI GI	g1707857
BLAST score	641
E value	3.0e-67
Match length	135
% identity	90
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	196349
Contig ID	23584_1.R1039
5'-most EST	LIB3147-043-Q1-K1-B8
Method	BLASTX
NCBI GI	g225267

BLAST score	583
E value	4.0e-60
Match length	244
% identity	52
NCBI Description	ORF 1244 [Nicotiana tabacum]

Seq. No.	196350
Contig ID	23600_1.R1039
5'-most EST	LIB3196-064-P1-M1-B12
Method	BLASTX
NCBI GI	g2160160
BLAST score	198
E value	1.0e-32
Match length	101
% identity	72
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	196351
Contig ID	23605_1.R1039
5'-most EST	LIB3148-012-Q1-K1-G10

Seq. No.	196352
Contig ID	23606_1.R1039
5'-most EST	LIB3146-022-Q1-K1-C8
Method	BLASTX
NCBI GI	g2462671
BLAST score	284
E value	5.0e-25
Match length	206
% identity	38
NCBI Description	(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]

Seq. No.	196353
Contig ID	23608_1.R1039
5'-most EST	LIB3166-032-P1-K1-F12
Method	BLASTX
NCBI GI	g1361979
BLAST score	959
E value	1.0e-104
Match length	258
% identity	74
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi|1350550|dbj|BAA12843| (D85624) serine acetyltransferase [Citrullus lanatus] >gi|1841312|dbj|BAA08479| (D49535) serine acetyltransferase. [Citrullus lanatus] >gi|2337772|dbj|BAA21827| (AB006530) serine acetyltransferase [Citrullus lanatus]

Seq. No.	196354
Contig ID	23608_2.R1039
5'-most EST	LIB3146-022-Q1-K1-D1
Method	BLASTX
NCBI GI	g1361979
BLAST score	543
E value	2.0e-65
Match length	142

% identity	86
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi|1350550|dbj|BAA12843| (D85624) serine acetyltransferase [Citrullus lanatus] >gi|1841312|dbj|BAA08479| (D49535) serine acetyltransferase. [Citrullus lanatus] >gi|2337772|dbj|BAA21827| (AB006530) serine acetyltransferase [Citrullus lanatus]
Seq. No.	196355
Contig ID	23609_1.R1039
5'-most EST	LIB3166-024-P1-K1-B6
Seq. No.	196356
Contig ID	23610_1.R1039
5'-most EST	LIB3146-044-Q1-K1-E11
Seq. No.	196357
Contig ID	23630_1.R1039
5'-most EST	uC-gsflnu33B126h06b1
Method	BLASTX
NCBI GI	g4559330
BLAST score	429
E value	2.0e-42
Match length	98
% identity	83
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.	196358
Contig ID	23637_1.R1039
5'-most EST	LIB3165-044-Q1-K1-F9
Method	BLASTX
NCBI GI	g3776005
BLAST score	279
E value	2.0e-36
Match length	92
% identity	91
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.	196359
Contig ID	23642_1.R1039
5'-most EST	uC-gsronu33B017c02b1
Method	BLASTX
NCBI GI	g3860250
BLAST score	688
E value	1.0e-72
Match length	150
% identity	90
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]
Seq. No.	196360
Contig ID	23650_2.R1039
5'-most EST	LIB3148-006-Q1-K1-D8
Seq. No.	196361
Contig ID	23655_1.R1039
5'-most EST	LIB3146-022-Q1-K1-H5

Method	BLASTX
NCBI GI	g3659907
BLAST score	455
E value	4.0e-45
Match length	112
% identity	79
NCBI Description	(AF091857) protein translation factor SUI1 homolog [Pimpinella brachycarpa]

Seq. No.	196362
Contig ID	23656_1.R1039
5'-most EST	uC-gsronu33B001g10b1

Seq. No.	196363
Contig ID	23673_1.R1039
5'-most EST	LIB3146-023-Q1-K1-B10

Seq. No.	196364
Contig ID	23678_2.R1039
5'-most EST	LIB3272-053-P1-K1-G8
Method	BLASTN
NCBI GI	g3513725
BLAST score	34
E value	2.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	196365
Contig ID	23689_1.R1039
5'-most EST	LIB3146-023-Q1-K1-C4

Seq. No.	196366
Contig ID	23693_1.R1039
5'-most EST	LIB3146-023-Q1-K1-C8
Method	BLASTX
NCBI GI	g2244914
BLAST score	213
E value	6.0e-17
Match length	102
% identity	54
NCBI Description	(Z97339) similarity to probable splicing factor Ceprp21 [Arabidopsis thaliana]

Seq. No.	196367
Contig ID	23694_1.R1039
5'-most EST	LIB3146-024-Q1-K1-C11
Method	BLASTX
NCBI GI	g1086147
BLAST score	485
E value	1.0e-48
Match length	132
% identity	66
NCBI Description	protein S2 - Phalaris coerulescens >gi|556833|emb|CAA57520| (X81992) S2 [Phalaris coerulescens]

Seq. No. 196368

Contig ID	23702_1.R1039
5'-most EST	LIB3146-023-Q1-K1-D7

Seq. No.	196369
Contig ID	23707_1.R1039
5'-most EST	LIB3146-023-Q1-K1-E11
Method	BLASTX
NCBI GI	g2462746
BLAST score	721
E value	2.0e-76
Match length	165
% identity	84
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	196370
Contig ID	23708_1.R1039
5'-most EST	LIB3166-030-P1-K1-B7
Method	BLASTX
NCBI GI	g584794
BLAST score	800
E value	1.0e-85
Match length	193
% identity	80
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi|282953|pir||A41779 H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi|170289 (M80489) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]

Seq. No.	196371
Contig ID	23709_1.R1039
5'-most EST	LIB3165-036-P1-K1-H7

Seq. No.	196372
Contig ID	23745_1.R1039
5'-most EST	uC-gsronu33B172c02b1

Seq. No.	196373
Contig ID	23755_1.R1039
5'-most EST	LIB3146-024-Q1-K1-A5
Method	BLASTX
NCBI GI	g2108252
BLAST score	333
E value	5.0e-31
Match length	158
% identity	22
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi|2108254|emb|CAA71276| (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi|4538925|emb|CAB39661.1| (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	196374
Contig ID	23764_1.R1039
5'-most EST	LIB3146-024-Q1-K1-B2
Method	BLASTX
NCBI GI	g1653655
BLAST score	296

E value	8.0e-27
Match length	132
% identity	50
NCBI Description	(D90915) ATP-dependent Clp protease proteolytic subunit [Synechocystis sp.]

Seq. No.	196375
Contig ID	23765_1.R1039
5'-most EST	LIB3147-059-Q1-K1-F8
Method	BLASTX
NCBI GI	g2464852
BLAST score	254
E value	2.0e-21
Match length	157
% identity	44
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	196376
Contig ID	23770_1.R1039
5'-most EST	LIB3146-024-Q1-K1-B8
Method	BLASTX
NCBI GI	g2392895
BLAST score	701
E value	4.0e-74
Match length	154
% identity	88
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	196377
Contig ID	23789_1.R1039
5'-most EST	uC-gsflnu33B110d08b1
Method	BLASTX
NCBI GI	g416641
BLAST score	657
E value	2.0e-68
Match length	190
% identity	69
NCBI Description	INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4 >gi|287568|dbj|BAA03309| (D14413) ORF [Vigna radiata]

Seq. No.	196378
Contig ID	23790_1.R1039
5'-most EST	g5049399
Method	BLASTX
NCBI GI	g2190550
BLAST score	1297
E value	1.0e-143
Match length	329
% identity	77
NCBI Description	(AC001229) ESTs gb|T45673,gb|N37512 come from this gene. [Arabidopsis thaliana]

Seq. No.	196379
Contig ID	23796_1.R1039
5'-most EST	g5048995
Method	BLASTX

NCBI GI	g1001263
BLAST score	369
E value	9.0e-44
Match length	182
% identity	54
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	196380
Contig ID	23806_1.R1039
5'-most EST	LIB3146-024-Q1-K1-F1

Seq. No.	196381
Contig ID	23808_1.R1039
5'-most EST	uC-gsflmaxxa088f11b1
Method	BLASTX
NCBI GI	g112972
BLAST score	1541
E value	1.0e-172
Match length	403
% identity	68
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi|167546 (M92660) aspartate aminotransferase [Daucus carota] >gi|445587|prf||1909339A Asp aminotransferase [Daucus carota]

Seq. No.	196382
Contig ID	23816_1.R1039
5'-most EST	LIB3197-005-P1-M1-B11
Method	BLASTX
NCBI GI	g4371285
BLAST score	781
E value	4.0e-83
Match length	362
% identity	48
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196383
Contig ID	23825_1.R1039
5'-most EST	LIB3147-009-Q1-K1-D5

Seq. No.	196384
Contig ID	23826_1.R1039
5'-most EST	LIB3197-023-Q1-M1-A8
Method	BLASTX
NCBI GI	g4580394
BLAST score	1103
E value	1.0e-121
Match length	372
% identity	55
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	196385
Contig ID	23838_1.R1039
5'-most EST	LIB3197-013-P1-M1-A9

Seq. No.	196386

Contig ID	23842_1.R1039
5'-most EST	LIB3272-014-P1-K1-C8
Method	BLASTX
NCBI GI	g2352492
BLAST score	549
E value	3.0e-56
Match length	182
% identity	61
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi|2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	196387
Contig ID	23843_1.R1039
5'-most EST	LIB3146-053-Q1-K1-G4
Method	BLASTX
NCBI GI	g3341684
BLAST score	322
E value	2.0e-29
Match length	135
% identity	53
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196388
Contig ID	23847_1.R1039
5'-most EST	uC-gsflmaxxa089d12b1
Method	BLASTX
NCBI GI	g3599386
BLAST score	160
E value	2.0e-10
Match length	93
% identity	42
NCBI Description	(AF083071) peptidyl-prolyl cis/trans isomerase [Cenarchaeum symbiosum]

Seq. No.	196389
Contig ID	23848_1.R1039
5'-most EST	LIB3146-026-Q1-K2-A8
Method	BLASTX
NCBI GI	g3721926
BLAST score	563
E value	4.0e-58
Match length	127
% identity	89
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	196390
Contig ID	23849_1.R1039
5'-most EST	LIB3146-026-Q1-K2-A7

Seq. No.	196391
Contig ID	23852_1.R1039
5'-most EST	g3326463
Method	BLASTX
NCBI GI	g3550661
BLAST score	713
E value	3.0e-75

Match length	249
% identity	42
NCBI Description	(AJ001310) 39 kDa EF-Hand containing protein [Solanum tuberosum]

Seq. No.	196392
Contig ID	23856_1.R1039
5'-most EST	LIB3146-026-Q1-K2-B6

Seq. No.	196393
Contig ID	23858_1.R1039
5'-most EST	LIB3146-025-Q1-K1-B8
Method	BLASTX
NCBI GI	g2245077
BLAST score	692
E value	3.0e-73
Match length	148
% identity	85
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	196394
Contig ID	23860_1.R1039
5'-most EST	LIB3149-060-Q1-K1-D6

Seq. No.	196395
Contig ID	23861_1.R1039
5'-most EST	LIB3189-042-P1-K1-H2
Method	BLASTX
NCBI GI	g3150415
BLAST score	1292
E value	1.0e-143
Match length	301
% identity	77
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi|3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	196396
Contig ID	23864_1.R1039
5'-most EST	LIB3146-025-Q1-K1-C3
Method	BLASTX
NCBI GI	g2970556
BLAST score	623
E value	4.0e-65
Match length	141
% identity	83
NCBI Description	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]

Seq. No.	196397
Contig ID	23867_1.R1039
5'-most EST	g5046400
Method	BLASTX
NCBI GI	g1076715
BLAST score	210
E value	2.0e-16
Match length	85

% identity	43
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi|404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	196398
Contig ID	23867_3.R1039
5'-most EST	LIB3148-018-Q1-K1-H5
Method	BLASTX
NCBI GI	g1076715
BLAST score	203
E value	7.0e-16
Match length	88
% identity	41
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi|404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	196399
Contig ID	23869_1.R1039
5'-most EST	LIB3146-025-Q1-K1-C8

Seq. No.	196400
Contig ID	23871_1.R1039
5'-most EST	LIB3146-056-Q1-K1-E2

Seq. No.	196401
Contig ID	23875_1.R1039
5'-most EST	LIB3147-058-Q1-K1-B8
Method	BLASTX
NCBI GI	g1173187
BLAST score	708
E value	9.0e-75
Match length	142
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi|643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	196402
Contig ID	23880_1.R1039
5'-most EST	uC-gsflmaxxa028c04b1
Method	BLASTX
NCBI GI	g1938424
BLAST score	490
E value	3.0e-49
Match length	170
% identity	57
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No.	196403
Contig ID	23883_1.R1039
5'-most EST	LIB3146-026-Q1-K2-E11
Method	BLASTX
NCBI GI	g3169180
BLAST score	994
E value	1.0e-108

Match length	197
% identity	93
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	196404
Contig ID	23885_1.R1039
5'-most EST	LIB3146-026-Q1-K2-E2

Seq. No.	196405
Contig ID	23886_1.R1039
5'-most EST	uC-gsronu33B078g11b1
Method	BLASTN
NCBI GI	g22116
BLAST score	134
E value	6.0e-69
Match length	334
% identity	85
NCBI Description	Z.mays ZMACK2 mRNA for casein kinase II alpha subunit

Seq. No.	196406
Contig ID	23890_1.R1039
5'-most EST	uC-gsflnu33B127c02b1
Method	BLASTX
NCBI GI	g2911052
BLAST score	171
E value	4.0e-12
Match length	65
% identity	60
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	196407
Contig ID	23893_1.R1039
5'-most EST	LIB3146-058-Q1-K1-B10

Seq. No.	196408
Contig ID	23894_1.R1039
5'-most EST	LIB3189-005-P1-K1-F6
Method	BLASTX
NCBI GI	g3928142
BLAST score	1178
E value	1.0e-130
Match length	250
% identity	32
NCBI Description	(AJ131045) protein phosphatase [Cicer arietinum]

Seq. No.	196409
Contig ID	23897_1.R1039
5'-most EST	LIB3146-025-Q1-K1-F4
Method	BLASTX
NCBI GI	g2135842
BLAST score	216
E value	2.0e-17
Match length	75
% identity	59
NCBI Description	nucleolar phosphoprotein p130 - human >gi|663008|emb|CAA84063| (Z34289) nucleolar phosphoprotein

p130 [Homo sapiens]

Seq. No.	196410
Contig ID	23899_1.R1039
5'-most EST	LIB3146-025-Q1-K1-F7
Method	BLASTX
NCBI GI	g4104931
BLAST score	144
E value	6.0e-09
Match length	27
% identity	93
NCBI Description	(AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No.	196411
Contig ID	23901_1.R1039
5'-most EST	LIB3189-027-P1-K1-H6
Method	BLASTX
NCBI GI	g2677830
BLAST score	758
E value	1.0e-80
Match length	166
% identity	89
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	196412
Contig ID	23903_1.R1039
5'-most EST	LIB3146-026-Q1-K2-G12

Seq. No.	196413
Contig ID	23907_1.R1039
5'-most EST	LIB3146-025-Q1-K1-G5

Seq. No.	196414
Contig ID	23910_1.R1039
5'-most EST	LIB3166-018-P1-K1-D4
Method	BLASTX
NCBI GI	g1943751
BLAST score	610
E value	2.0e-63
Match length	134
% identity	86
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi|2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	196415
Contig ID	23911_1.R1039
5'-most EST	LIB3146-025-Q1-K1-H1

Seq. No.	196416
Contig ID	23912_1.R1039
5'-most EST	LIB3197-058-Q1-M1-C9

Seq. No.	196417
Contig ID	23913_1.R1039
5'-most EST	LIB3146-026-Q1-K2-H11

Seq. No.	196418
Contig ID	23914_1.R1039
5'-most EST	LIB3149-013-Q1-K1-F10
Method	BLASTX
NCBI GI	g3242785
BLAST score	722
E value	2.0e-76
Match length	190
% identity	75
NCBI Description	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]

Seq. No.	196419
Contig ID	23919_1.R1039
5'-most EST	LIB3146-025-Q1-K1-H7

Seq. No.	196420
Contig ID	23924_1.R1039
5'-most EST	LIB3146-025-Q1-K2-A12

Seq. No.	196421
Contig ID	23927_1.R1039
5'-most EST	uC-gsflnu33B081d08b1
Method	BLASTX
NCBI GI	g481818
BLAST score	838
E value	5.0e-90
Match length	158
% identity	94
NCBI Description	coproporphyrinogen oxidase - soybean

Seq. No.	196422
Contig ID	23931_1.R1039
5'-most EST	LIB3146-025-Q1-K2-B1
Method	BLASTX
NCBI GI	g2245136
BLAST score	664
E value	7.0e-70
Match length	164
% identity	76
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	196423
Contig ID	23934_1.R1039
5'-most EST	uC-gsflmaxxa067b11b1
Method	BLASTX
NCBI GI	g2507617
BLAST score	585
E value	1.0e-109
Match length	283
% identity	70
NCBI Description	(U90341) chalcone synthase homolog PrChS1 [Pinus radiata]

Seq. No.	196424
Contig ID	23936_1.R1039
5'-most EST	LIB3272-019-P1-K1-C8

Method	BLASTX
NCBI GI	g3860255
BLAST score	325
E value	3.0e-30
Match length	140
% identity	50
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196425
Contig ID	23949_1.R1039
5'-most EST	LIB3146-025-Q1-K2-C5
Method	BLASTX
NCBI GI	g3860258
BLAST score	145
E value	7.0e-09
Match length	38
% identity	68
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	196426
Contig ID	23952_1.R1039
5'-most EST	LIB3146-025-Q1-K2-F7

Seq. No.	196427
Contig ID	23956_1.R1039
5'-most EST	LIB3146-025-Q1-K2-D4

Seq. No.	196428
Contig ID	23958_1.R1039
5'-most EST	LIB3189-040-P1-K1-D9

Seq. No.	196429
Contig ID	23961_1.R1039
5'-most EST	LIB3165-041-Q1-K1-B9

Seq. No.	196430
Contig ID	23968_1.R1039
5'-most EST	LIB3146-036-P1-K1-H4
Method	BLASTX
NCBI GI	g1708971
BLAST score	207
E value	2.0e-16
Match length	74
% identity	53
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi|421871|pir||S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi|288116|emb|CAA51194| (X72617) mandelonitrile lyase [Prunus serotina] >gi|1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi|1090776|prf||2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	196431
Contig ID	23984_1.R1039
5'-most EST	LIB3146-025-Q1-K2-G7
Method	BLASTX

NCBI GI	g4567275
BLAST score	147
E value	4.0e-09
Match length	187
% identity	29
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196432
Contig ID	24005_1.R1039
5'-most EST	LIB3146-026-Q1-K2-B11
Method	BLASTX
NCBI GI	g1082801
BLAST score	545
E value	1.0e-55
Match length	238
% identity	46
NCBI Description	splicing factor SF3a60 - human >gi|551450|emb|CAA57388| (X81789) splicing factor SF3a60 [Homo sapiens]

Seq. No.	196433
Contig ID	24055_1.R1039
5'-most EST	LIB3146-026-Q1-K2-G1
Method	BLASTX
NCBI GI	g3894171
BLAST score	509
E value	2.0e-51
Match length	209
% identity	48
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	196434
Contig ID	24080_1.R1039
5'-most EST	LIB3146-027-Q1-K1-H7

Seq. No.	196435
Contig ID	24088_1.R1039
5'-most EST	g5044301
Method	BLASTX
NCBI GI	g4490739
BLAST score	497
E value	4.0e-50
Match length	173
% identity	63
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	196436
Contig ID	24091_1.R1039
5'-most EST	LIB3272-007-P1-K1-H2
Method	BLASTX
NCBI GI	g4314390
BLAST score	144
E value	1.0e-08
Match length	52
% identity	62
NCBI Description	(AC006232) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	196437
Contig ID	24094_1.R1039
5'-most EST	LIB3146-027-Q1-K1-C4
Method	BLASTX
NCBI GI	g3860321
BLAST score	267
E value	6.0e-30
Match length	98
% identity	73
NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No.	196438
Contig ID	24098_1.R1039
5'-most EST	g5046166
Method	BLASTX
NCBI GI	g2961390
BLAST score	432
E value	2.0e-72
Match length	161
% identity	80
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	196439
Contig ID	24098_2.R1039
5'-most EST	uC-gsronu33B169c03b1
Method	BLASTN
NCBI GI	g3860320
BLAST score	63
E value	9.0e-27
Match length	151
% identity	85
NCBI Description	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5

Seq. No.	196440
Contig ID	24100_1.R1039
5'-most EST	LIB3146-027-Q1-K1-C12
Method	BLASTX
NCBI GI	g857397
BLAST score	935
E value	1.0e-101
Match length	203
% identity	86
NCBI Description	(D50870) mitotic cyclin a2-type [Glycine max]

Seq. No.	196441
Contig ID	24130_1.R1039
5'-most EST	LIB3148-051-Q1-K1-D11
Method	BLASTX
NCBI GI	g3913518
BLAST score	205
E value	7.0e-16
Match length	54
% identity	81
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE

(3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi|1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	196442
Contig ID	24132_1.R1039
5'-most EST	LIB3197-044-Q1-M1-E5
Method	BLASTX
NCBI GI	g2895576
BLAST score	220
E value	2.0e-17
Match length	237
% identity	24
NCBI Description	(AF041337) vacuolar proton pump subunit SFD beta isoform [Bos taurus]

Seq. No.	196443
Contig ID	24139_1.R1039
5'-most EST	LIB3146-027-Q1-K1-G6
Method	BLASTX
NCBI GI	g2832625
BLAST score	289
E value	3.0e-44
Match length	170
% identity	50
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	196444
Contig ID	24179_1.R1039
5'-most EST	LIB3166-053-P1-K1-H12

Seq. No.	196445
Contig ID	24190_1.R1039
5'-most EST	LIB3165-060-Q1-K1-H12
Method	BLASTX
NCBI GI	g1255954
BLAST score	465
E value	2.0e-46
Match length	110
% identity	76
NCBI Description	(Z70677) thioredoxin [Ricinus communis]

Seq. No.	196446
Contig ID	24192_1.R1039
5'-most EST	LIB3148-054-Q1-K1-H10
Method	BLASTX
NCBI GI	g3914449
BLAST score	1626
E value	0.0e+00
Match length	313
% identity	100
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi|3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	196447
Contig ID	24195_1.R1039

5'-most EST	LIB3146-028-Q1-K1-E1
Seq. No.	196448
Contig ID	24206_1.R1039
5'-most EST	LIB3146-028-Q1-K1-E6
Method	BLASTX
NCBI GI	g3204125
BLAST score	345
E value	2.0e-32
Match length	83
% identity	81
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]
Seq. No.	196449
Contig ID	24207_1.R1039
5'-most EST	g5046521
Method	BLASTX
NCBI GI	g2224731
BLAST score	542
E value	2.0e-55
Match length	152
% identity	70
NCBI Description	(AB004932) Aux22d [Vigna radiata]
Seq. No.	196450
Contig ID	24207_2.R1039
5'-most EST	uC-gsronu33B170g03b1
Method	BLASTX
NCBI GI	g1168607
BLAST score	248
E value	2.0e-35
Match length	103
% identity	72
NCBI Description	AUXIN-INDUCED PROTEIN AUX2-11 >gi|16197|emb|CAA37526| (X53435) Aux2-11 protein [Arabidopsis thaliana] >gi|454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]
Seq. No.	196451
Contig ID	24210_1.R1039
5'-most EST	LIB3166-001-Q1-K1-A7
Seq. No.	196452
Contig ID	24212_1.R1039
5'-most EST	LIB3146-028-Q1-K1-F11
Method	BLASTX
NCBI GI	g3738092
BLAST score	548
E value	4.0e-56
Match length	126
% identity	83
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]
Seq. No.	196453
Contig ID	24213_1.R1039
5'-most EST	LIB3165-022-P1-K1-C11

Method	BLASTX
NCBI GI	g3560264
BLAST score	332
E value	2.0e-30
Match length	191
% identity	43
NCBI Description	(AL031535) sol1 family protein [Schizosaccharomyces pombe]

Seq. No.	196454
Contig ID	24215_1.R1039
5'-most EST	uC-gsflmaxxa048b05b1

Seq. No.	196455
Contig ID	24224_1.R1039
5'-most EST	LIB3189-026-P1-K1-A11
Method	BLASTX
NCBI GI	g3415117
BLAST score	251
E value	2.0e-21
Match length	71
% identity	66
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	196456
Contig ID	24238_1.R1039
5'-most EST	LIB3146-028-Q1-K1-H8
Method	BLASTX
NCBI GI	g4467124
BLAST score	278
E value	1.0e-24
Match length	100
% identity	60
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196457
Contig ID	24242_1.R1039
5'-most EST	g3326335
Method	BLASTX
NCBI GI	g4512667
BLAST score	532
E value	4.0e-54
Match length	159
% identity	64
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	196458
Contig ID	24242_2.R1039
5'-most EST	LIB3147-055-Q1-K1-F3

Seq. No.	196459
Contig ID	24248_1.R1039
5'-most EST	LIB3146-030-Q1-K1-A7
Method	BLASTX
NCBI GI	g2737894
BLAST score	670
E value	2.0e-70
Match length	169

% identity	72
NCBI Description	(U59151) Cbf5p homolog [Homo sapiens]

Seq. No.	196460
Contig ID	24251_1.R1039
5'-most EST	uC-gsronu33B179b12b1
Method	BLASTX
NCBI GI	g3249096
BLAST score	332
E value	8.0e-31
Match length	100
% identity	68
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb|Y14616 from A. thaliana. ESTs gb|N96440, gb|N37503, gb|N37498 and gb|T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	196461
Contig ID	24252_1.R1039
5'-most EST	LIB3146-030-Q1-K1-B10
Method	BLASTX
NCBI GI	g3355480
BLAST score	148
E value	2.0e-09
Match length	58
% identity	47
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	196462
Contig ID	24256_1.R1039
5'-most EST	g5045402
Method	BLASTN
NCBI GI	g4220636
BLAST score	37
E value	5.0e-11
Match length	109
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	196463
Contig ID	24258_1.R1039
5'-most EST	g5048293

Seq. No.	196464
Contig ID	24258_2.R1039
5'-most EST	g5049542

Seq. No.	196465
Contig ID	24260_1.R1039
5'-most EST	g5050858

Seq. No.	196466
Contig ID	24264_1.R1039
5'-most EST	LIB3147-015-Q1-K1-A9

Seq. No.	196467
Contig ID	24267_1.R1039
5'-most EST	uC-gsflnu33B129d10b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	51
E value	1.0e-19
Match length	160
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	196468
Contig ID	24269_1.R1039
5'-most EST	uC-gsflnu33B114g05b1

Seq. No.	196469
Contig ID	24275_1.R1039
5'-most EST	uC-gsflnu33B109c01b1
Method	BLASTX
NCBI GI	g142742
BLAST score	1392
E value	1.0e-155
Match length	261
% identity	99
NCBI Description	(M73248) cryIA(c)3 [Bacillus thuringiensis]

Seq. No.	196470
Contig ID	24277_1.R1039
5'-most EST	LIB3146-030-Q1-K1-D6
Method	BLASTX
NCBI GI	g1076515
BLAST score	221
E value	5.0e-18
Match length	110
% identity	44
NCBI Description	pectinesterase precursor - kidney bean >gi|732913|emb|CAA59482| (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No.	196471
Contig ID	24280_1.R1039
5'-most EST	LIB3146-030-Q1-K1-E1
Method	BLASTN
NCBI GI	g3258636
BLAST score	92
E value	4.0e-44
Match length	296
% identity	83
NCBI Description	Populus tremuloides clone Pt4CL2 4-coumarate:CoA ligase mRNA, complete cds

Seq. No.	196472
Contig ID	24283_1.R1039
5'-most EST	LIB3197-046-Q1-M1-E6
Method	BLASTX
NCBI GI	g3608137

BLAST score 316
E value 6.0e-29
Match length 119
% identity 51
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 196473
Contig ID 24290_1.R1039
5'-most EST LIB3146-030-Q1-K1-E8

Seq. No. 196474
Contig ID 24291_1.R1039
5'-most EST uC-gsronu33B168e07b1
Method BLASTX
NCBI GI g3892057
BLAST score 903
E value 1.0e-97
Match length 206
% identity 45
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196475
Contig ID 24295_2.R1039
5'-most EST LIB3146-030-Q1-K1-F2

Seq. No. 196476
Contig ID 24297_1.R1039
5'-most EST uC-gsflnu33B145e06b1
Method BLASTX
NCBI GI g1172597
BLAST score 226
E value 2.0e-18
Match length 47
% identity 91
NCBI Description WOUND-INDUCED BASIC PROTEIN >gi|81888|pir||JS0731 wound-inducible basic protein - kidney bean >gi|169365 (L00625) basic protein [Phaseolus vulgaris] >gi|217989|dbj|BAA02299| (D12914) 5.8 kb basic protein [Phaseolus vulgaris]

Seq. No. 196477
Contig ID 24301_1.R1039
5'-most EST g3220217

Seq. No. 196478
Contig ID 24308_1.R1039
5'-most EST LIB3165-023-P1-K1-D7

Seq. No. 196479
Contig ID 24317_1.R1039
5'-most EST uC-gsronu33B114d05b1

Seq. No. 196480
Contig ID 24325_1.R1039
5'-most EST LIB3146-032-Q1-K1-A2

Seq. No. 196481

Contig ID	24331_1.R1039
5'-most EST	LIB3146-032-Q1-K1-A9
Method	BLASTX
NCBI GI	g2618698
BLAST score	871
E value	7.0e-94
Match length	257
% identity	67
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	196482
Contig ID	24334_1.R1039
5'-most EST	g5046729
Method	BLASTN
NCBI GI	g2618683
BLAST score	42
E value	5.0e-14
Match length	121
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	196483
Contig ID	24339_1.R1039
5'-most EST	uC-gsflnu33B006h10b1
Method	BLASTX
NCBI GI	g2983537
BLAST score	147
E value	2.0e-09
Match length	55
% identity	53
NCBI Description	(AE000720) phosphate transport ATP binding protein [Aquifex aeolicus]

Seq. No.	196484
Contig ID	24353_1.R1039
5'-most EST	LIB3147-015-Q1-K1-G4
Method	BLASTX
NCBI GI	g4325372
BLAST score	290
E value	9.0e-26
Match length	148
% identity	51
NCBI Description	(AF128396) contains similarity to protein disulfide isomerases [Arabidopsis thaliana]

Seq. No.	196485
Contig ID	24369_1.R1039
5'-most EST	LIB3146-032-Q1-K1-E3

Seq. No.	196486
Contig ID	24370_1.R1039
5'-most EST	LIB3146-032-Q1-K1-E4

Seq. No.	196487
Contig ID	24379_1.R1039
5'-most EST	LIB3146-032-Q1-K1-F2

Method	BLASTX
NCBI GI	g3021485
BLAST score	429
E value	4.0e-42
Match length	87
% identity	100
NCBI Description	(AJ224932) histone H2B-3 [Lycopersicon esculentum]

Seq. No.	196488
Contig ID	24382_1.R1039
5'-most EST	uC-gsronu33B162b07b2
Method	BLASTX
NCBI GI	g139780
BLAST score	210
E value	1.0e-19
Match length	97
% identity	55
NCBI Description	WOUND-INDUCED PROTEIN 1 >gi|82293|pir||JQ0398 wun1 protein - potato

Seq. No.	196489
Contig ID	24390_1.R1039
5'-most EST	LIB3146-032-Q1-K1-G4
Method	BLASTX
NCBI GI	g4454009
BLAST score	201
E value	2.0e-15
Match length	128
% identity	38
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	196490
Contig ID	24391_1.R1039
5'-most EST	uC-gsflmaxxa097e06b1
Method	BLASTX
NCBI GI	g3860333
BLAST score	389
E value	1.0e-37
Match length	97
% identity	70
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	196491
Contig ID	24392_1.R1039
5'-most EST	uC-gsflmaxxa054e12b1
Method	BLASTX
NCBI GI	g4539371
BLAST score	239
E value	1.0e-25
Match length	191
% identity	41
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	196492
Contig ID	24399_1.R1039
5'-most EST	g5048222
Method	BLASTX

NCBI GI	g4454011
BLAST score	291
E value	6.0e-26
Match length	107
% identity	58
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	196493
Contig ID	24413_1.R1039
5'-most EST	LIB3147-060-Q1-K1-C10
Method	BLASTX
NCBI GI	g3219939
BLAST score	173
E value	2.0e-12
Match length	141
% identity	35
NCBI Description	HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I >gi|2094864|emb|CAB08603| (Z95334) unknown [Schizosaccharomyces pombe]

Seq. No.	196494
Contig ID	24415_1.R1039
5'-most EST	LIB3146-052-Q1-K1-E8
Method	BLASTX
NCBI GI	g1708971
BLAST score	297
E value	1.0e-26
Match length	142
% identity	40
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi|421871|pir||S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi|288116|emb|CAA51194| (X72617) mandelonitrile lyase [Prunus serotina] >gi|1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi|1090776|prf||2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	196495
Contig ID	24425_1.R1039
5'-most EST	LIB3146-033-Q1-K1-C1
Method	BLASTX
NCBI GI	g3540195
BLAST score	1157
E value	1.0e-127
Match length	242
% identity	46
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	196496
Contig ID	24431_1.R1039
5'-most EST	LIB3146-033-Q1-K1-C6
Method	BLASTX
NCBI GI	g320565
BLAST score	179
E value	2.0e-13
Match length	73

% identity	49
NCBI Description	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
Seq. No.	196497
Contig ID	24434_1.R1039
5'-most EST	LIB3197-041-Q1-M1-G1
Method	BLASTX
NCBI GI	g3395427
BLAST score	267
E value	4.0e-23
Match length	143
% identity	47
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.	196498
Contig ID	24438_1.R1039
5'-most EST	LIB3146-033-Q1-K1-D12
Method	BLASTX
NCBI GI	g3482918
BLAST score	366
E value	5.0e-35
Match length	94
% identity	77
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]
Seq. No.	196499
Contig ID	24451_1.R1039
5'-most EST	LIB3146-033-Q1-K1-E2
Seq. No.	196500
Contig ID	24466_2.R1039
5'-most EST	LIB3146-033-Q1-K1-F6
Method	BLASTX
NCBI GI	g1684851
BLAST score	232
E value	4.0e-19
Match length	81
% identity	57
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]
Seq. No.	196501
Contig ID	24472_1.R1039
5'-most EST	LIB3146-033-Q1-K1-G12
Seq. No.	196502
Contig ID	24478_1.R1039
5'-most EST	g5044813
Seq. No.	196503
Contig ID	24479_1.R1039
5'-most EST	LIB3146-033-Q1-K1-G8
Method	BLASTX
NCBI GI	g1703200
BLAST score	821
E value	4.0e-88
Match length	185

% identity	83
NCBI Description	PROTEIN KINASE AFC2 >gi|601789 (U16177) protein kinase [Arabidopsis thaliana] >gi|642130|dbj|BAA08214| (D45353) protein kinase [Arabidopsis thaliana] >gi|4220516|emb|CAA22989| (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]
Seq. No.	196504
Contig ID	24481_1.R1039
5'-most EST	uC-gsflnu33B009e12b1
Seq. No.	196505
Contig ID	24489_1.R1039
5'-most EST	LIB3146-033-Q1-K1-H6
Method	BLASTN
NCBI GI	g2911279
BLAST score	78
E value	1.0e-35
Match length	429
% identity	80
NCBI Description	Nicotiana tabacum PK12 protein kinase (PK12) mRNA, complete cds
Seq. No.	196506
Contig ID	24498_1.R1039
5'-most EST	LIB3146-034-Q1-K1-A3
Method	BLASTX
NCBI GI	g2245139
BLAST score	270
E value	2.0e-23
Match length	107
% identity	54
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196507
Contig ID	24506_1.R1039
5'-most EST	LIB3146-050-Q1-K1-A3
Method	BLASTX
NCBI GI	g2493321
BLAST score	248
E value	5.0e-21
Match length	55
% identity	85
NCBI Description	L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO) >gi|2129952|pir||S66353 L-ascorbate oxidase (EC 1.10.3.3) precursor - common tobacco >gi|599594|dbj|BAA07734| (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
Seq. No.	196508
Contig ID	24507_1.R1039
5'-most EST	LIB3146-034-Q1-K1-B12
Seq. No.	196509
Contig ID	24519_1.R1039
5'-most EST	uC-gsflmaxxa028a09b1
Seq. No.	196510

Contig ID	24520_1.R1039
5'-most EST	LIB3146-034-Q1-K1-C3
Method	BLASTX
NCBI GI	g2244835
BLAST score	359
E value	4.0e-34
Match length	132
% identity	52
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	196511
Contig ID	24527_1.R1039
5'-most EST	LIB3146-034-Q1-K1-D12
Method	BLASTX
NCBI GI	g3298443
BLAST score	272
E value	5.0e-24
Match length	111
% identity	47
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	196512
Contig ID	24536_1.R1039
5'-most EST	LIB3165-030-P1-K1-E4
Method	BLASTX
NCBI GI	g4262223
BLAST score	176
E value	2.0e-12
Match length	54
% identity	52
NCBI Description	(AC006200) RING-H2 finger protein RHA2b [Arabidopsis thaliana]

Seq. No.	196513
Contig ID	24537_1.R1039
5'-most EST	LIB3146-034-Q1-K1-E6

Seq. No.	196514
Contig ID	24543_1.R1039
5'-most EST	LIB3147-011-Q1-K1-D2
Method	BLASTX
NCBI GI	g4510383
BLAST score	1143
E value	1.0e-125
Match length	324
% identity	71
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	196515
Contig ID	24555_2.R1039
5'-most EST	uC-gsronu33B143c12b1
Method	BLASTX
NCBI GI	g4220514
BLAST score	305
E value	7.0e-40
Match length	117

% identity	69
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	196516
Contig ID	24559_1.R1039
5'-most EST	uC-gsflnu33B130e07b1
Method	BLASTX
NCBI GI	g1174583
BLAST score	257
E value	8.0e-22
Match length	200
% identity	34
NCBI Description	TRANSALDOLASE >gi|1074653|pir||D64167 hypothetical protein HI1125 - Haemophilus influenzae (strain Rd KW20) >gi|1574680 (U32792) transaldolase B (talB) [Haemophilus influenzae Rd]

Seq. No.	196517
Contig ID	24561_1.R1039
5'-most EST	LIB3146-034-Q1-K1-H10

Seq. No.	196518
Contig ID	24562_1.R1039
5'-most EST	LIB3147-031-Q1-K1-B2
Method	BLASTX
NCBI GI	g3947614
BLAST score	126
E value	4.0e-11
Match length	97
% identity	40
NCBI Description	(AL023828) cDNA EST yk491f8.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	196519
Contig ID	24570_1.R1039
5'-most EST	LIB3272-036-P1-K1-D10
Method	BLASTX
NCBI GI	g2462758
BLAST score	377
E value	3.0e-36
Match length	126
% identity	60
NCBI Description	(AC002292) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	196520
Contig ID	24576_1.R1039
5'-most EST	g5047901
Method	BLASTX
NCBI GI	g549750
BLAST score	262
E value	1.0e-22
Match length	175
% identity	35
NCBI Description	HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION >gi|539221|pir||S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi|486369|emb|CAA82052|

(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No.	196521
Contig ID	24579_1.R1039
5'-most EST	uC-gsflmaxxa014c03b1
Method	BLASTX
NCBI GI	g4263791
BLAST score	540
E value	6.0e-70
Match length	151
% identity	88
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	196522
Contig ID	24579_2.R1039
5'-most EST	uC-gsflmaxxa014c09b1
Method	BLASTX
NCBI GI	g4263791
BLAST score	432
E value	2.0e-42
Match length	114
% identity	77
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	196523
Contig ID	24586_1.R1039
5'-most EST	LIB3196-025-P1-M1-C3
Method	BLASTX
NCBI GI	g3176965
BLAST score	494
E value	5.0e-50
Match length	120
% identity	84
NCBI Description	(AF067967) pyrroline-5-carboxylate synthetase [Mesembryanthemum crystallinum]

Seq. No.	196524
Contig ID	24589_1.R1039
5'-most EST	LIB3146-035-P1-K1-G5
Method	BLASTN
NCBI GI	g3176964
BLAST score	72
E value	3.0e-32
Match length	268
% identity	82
NCBI Description	Mesembryanthemum crystallinum pyrroline-5-carboxylate synthetase (P5CS) mRNA, complete cds

Seq. No.	196525
Contig ID	24597_1.R1039
5'-most EST	LIB3146-036-P1-K1-B1

Seq. No.	196526
Contig ID	24605_1.R1039
5'-most EST	LIB3146-036-P1-K1-D4

Method	BLASTX
NCBI GI	g3023436
BLAST score	1179
E value	1.0e-130
Match length	248
% identity	90
NCBI Description	CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi|857578 (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus tremuloides]

Seq. No.	196527
Contig ID	24605_2.R1039
5'-most EST	uC-gsronu33B155c01b2
Method	BLASTX
NCBI GI	g684942
BLAST score	501
E value	9.0e-51
Match length	97
% identity	94
NCBI Description	(U20736) S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase [Medicago sativa subsp. sativa]

Seq. No.	196528
Contig ID	24613_4.R1039
5'-most EST	LIB3149-003-P1-K1-A5
Method	BLASTX
NCBI GI	g3600030
BLAST score	167
E value	1.0e-11
Match length	134
% identity	37
NCBI Description	(AF080119) contains similarity to ankyrin repeats (Pfam: ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis thaliana]

Seq. No.	196529
Contig ID	24614_1.R1039
5'-most EST	LIB3146-036-P1-K1-F1
Method	BLASTX
NCBI GI	g1175252
BLAST score	144
E value	5.0e-09
Match length	92
% identity	37
NCBI Description	HYPOTHETICAL PROTEIN HI0488 >gi|1074418|pir||D64008 hypothetical protein HI0488 - Haemophilus influenzae (strain Rd KW20) >gi|1573468 (U32731) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No.	196530
Contig ID	24619_1.R1039
5'-most EST	LIB3146-036-P1-K1-F6

Seq. No.	196531
Contig ID	24635_1.R1039
5'-most EST	LIB3146-037-P1-K1-A1

Method	BLASTX
NCBI GI	g3540180
BLAST score	441
E value	1.0e-43
Match length	156
% identity	46
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	196532
Contig ID	24637_1.R1039
5'-most EST	LIB3146-060-Q1-K1-E4

Seq. No.	196533
Contig ID	24640_1.R1039
5'-most EST	LIB3165-045-Q1-K1-A2

Seq. No.	196534
Contig ID	24646_1.R1039
5'-most EST	LIB3146-037-P1-K1-B1

Seq. No.	196535
Contig ID	24654_1.R1039
5'-most EST	LIB3146-037-P1-K1-B8

Seq. No.	196536
Contig ID	24657_1.R1039
5'-most EST	LIB3146-037-P1-K1-C11

Seq. No.	196537
Contig ID	24658_1.R1039
5'-most EST	LIB3146-038-P1-K1-C11
Method	BLASTX
NCBI GI	g3551247
BLAST score	486
E value	5.0e-49
Match length	144
% identity	68
NCBI Description	(AB012703) 181 [Daucus carota]

Seq. No.	196538
Contig ID	24665_1.R1039
5'-most EST	LIB3146-038-P1-K1-C9

Seq. No.	196539
Contig ID	24669_1.R1039
5'-most EST	LIB3166-017-P1-K1-B11
Method	BLASTX
NCBI GI	g3927838
BLAST score	485
E value	1.0e-48
Match length	121
% identity	78
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	196540
Contig ID	24677_1.R1039
5'-most EST	uC-gsronu33B041f11b1

Method	BLASTX
NCBI GI	g1934730
BLAST score	528
E value	7.0e-54
Match length	128
% identity	75
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	196541
Contig ID	24683_1.R1039
5'-most EST	LIB3197-041-Q1-M1-E3

Seq. No.	196542
Contig ID	24685_1.R1039
5'-most EST	uC-gsronu33B080d06b1
Method	BLASTX
NCBI GI	g1881585
BLAST score	264
E value	8.0e-23
Match length	90
% identity	58
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	196543
Contig ID	24687_1.R1039
5'-most EST	LIB3146-037-P1-K1-E9

Seq. No.	196544
Contig ID	24688_1.R1039
5'-most EST	LIB3197-007-P1-M1-D1
Method	BLASTX
NCBI GI	g3746069
BLAST score	159
E value	2.0e-10
Match length	119
% identity	32
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	196545
Contig ID	24704_1.R1039
5'-most EST	uC-gsronu33B162c01b2
Method	BLASTX
NCBI GI	g1169012
BLAST score	946
E value	1.0e-103
Match length	198
% identity	89
NCBI Description	COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1) >gi|402685 (L24437) regulatory protein [Arabidopsis thaliana]

Seq. No.	196546
Contig ID	24706_1.R1039
5'-most EST	uC-gsflnu33B115b07b1

Seq. No.	196547
Contig ID	24709_1.R1039

5'-most EST	LIB3146-061-Q1-K1-G3
Method	BLASTX
NCBI GI	g1498053
BLAST score	514
E value	7.0e-80
Match length	196
% identity	85
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	196548
Contig ID	24710_1.R1039
5'-most EST	LIB3146-037-P1-K1-H4

Seq. No.	196549
Contig ID	24717_2.R1039
5'-most EST	LIB3196-029-P1-M1-G7

Seq. No.	196550
Contig ID	24718_1.R1039
5'-most EST	LIB3146-038-P1-K1-A12
Method	BLASTX
NCBI GI	g2462834
BLAST score	237
E value	7.0e-20
Match length	87
% identity	54
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196551
Contig ID	24720_1.R1039
5'-most EST	uC-gsflnu33B093b02b1
Method	BLASTX
NCBI GI	g2894611
BLAST score	386
E value	6.0e-37
Match length	270
% identity	43
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	196552
Contig ID	24725_1.R1039
5'-most EST	LIB3146-038-P1-K1-A9
Method	BLASTX
NCBI GI	g2443751
BLAST score	811
E value	5.0e-87
Match length	177
% identity	88
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi|2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No.	196553
Contig ID	24736_1.R1039
5'-most EST	uC-gsflmaxxa045f10b1
Method	BLASTX
NCBI GI	g2827551
BLAST score	344

E value	8.0e-32
Match length	207
% identity	50
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	196554
Contig ID	24738_1.R1039
5'-most EST	LIB3146-038-P1-K1-C1
Method	BLASTX
NCBI GI	g2370232
BLAST score	251
E value	1.0e-42
Match length	123
% identity	72
NCBI Description	(AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No.	196555
Contig ID	24744_1.R1039
5'-most EST	LIB3146-038-P1-K1-C5

Seq. No.	196556
Contig ID	24749_1.R1039
5'-most EST	LIB3146-038-P1-K1-D1

Seq. No.	196557
Contig ID	24770_1.R1039
5'-most EST	LIB3146-038-P1-K1-F1
Method	BLASTX
NCBI GI	g4263790
BLAST score	588
E value	1.0e-60
Match length	133
% identity	88
NCBI Description	(AC006068) putative ch-TOG protein [Arabidopsis thaliana]

Seq. No.	196558
Contig ID	24775_1.R1039
5'-most EST	LIB3148-004-Q1-K1-G8
Method	BLASTX
NCBI GI	g2894598
BLAST score	256
E value	6.0e-22
Match length	97
% identity	46
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	196559
Contig ID	24775_2.R1039
5'-most EST	LIB3166-052-P1-K1-G1
Method	BLASTX
NCBI GI	g2662469
BLAST score	222
E value	5.0e-18
Match length	50
% identity	86
NCBI Description	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	196560
Contig ID	24793_1.R1039
5'-most EST	LIB3146-039-Q1-K1-A1
Method	BLASTX
NCBI GI	g3687250
BLAST score	411
E value	2.0e-74
Match length	177
% identity	80
NCBI Description	(AC005169) putative arginine n-methyltransferase [Arabidopsis thaliana]

Seq. No.	196561
Contig ID	24794_1.R1039
5'-most EST	LIB3197-029-Q1-M1-D10

Seq. No.	196562
Contig ID	24797_1.R1039
5'-most EST	LIB3272-019-P1-K1-C6
Method	BLASTX
NCBI GI	g1213069
BLAST score	1050
E value	1.0e-115
Match length	230
% identity	83
NCBI Description	(X79675) dihydrodipicolinate synthase [Nicotiana tabacum]

Seq. No.	196563
Contig ID	24809_1.R1039
5'-most EST	LIB3146-039-Q1-K1-B5
Method	BLASTX
NCBI GI	g3451075
BLAST score	177
E value	1.0e-12
Match length	122
% identity	41
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	196564
Contig ID	24814_1.R1039
5'-most EST	g5049411
Method	BLASTX
NCBI GI	g3249096
BLAST score	1669
E value	0.0e+00
Match length	383
% identity	53
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb|Y14616 from A. thaliana. ESTs gb|N96440, gb|N37503, gb|N37498 and gb|T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	196565
Contig ID	24817_1.R1039
5'-most EST	LIB3146-039-Q1-K1-C4

Seq. No.	196566

Contig ID	24823_1.R1039
5'-most EST	LIB3146-039-Q1-K1-D12
Method	BLASTX
NCBI GI	g1351791
BLAST score	460
E value	5.0e-46
Match length	139
% identity	19
NCBI Description	HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION >gi|83249|pir||S19487 hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae) >gi|1907211|emb|CAA42270| (X59720) YCR072c, len:515 [Saccharomyces cerevisiae]

Seq. No.	196567
Contig ID	24826_1.R1039
5'-most EST	g5049702
Method	BLASTX
NCBI GI	g2129726
BLAST score	919
E value	1.0e-122
Match length	268
% identity	82
NCBI Description	RNA polymerase II third largest chain RPB35.5A - Arabidopsis thaliana >gi|514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi|4544370|gb|AAD22281.1|AC006920_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No.	196568
Contig ID	24828_1.R1039
5'-most EST	uC-gsflmaxxa045a11b1
Method	BLASTX
NCBI GI	g4126405
BLAST score	525
E value	3.0e-53
Match length	117
% identity	91
NCBI Description	(AB011798) homolog to defender against apoptotic death 1 [Citrus unshiu]

Seq. No.	196569
Contig ID	24836_1.R1039
5'-most EST	LIB3148-058-Q1-K1-G5
Method	BLASTX
NCBI GI	g4204804
BLAST score	455
E value	3.0e-45
Match length	124
% identity	67
NCBI Description	(U52520) cyclin [Pisum sativum]

Seq. No.	196570
Contig ID	24845_1.R1039
5'-most EST	LIB3146-039-Q1-K1-F3
Method	BLASTX
NCBI GI	g2760322

BLAST score 484
E value 7.0e-49
Match length 126
% identity 71
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 196571
Contig ID 24853_1.R1039
5'-most EST LIB3146-039-Q1-K1-G11
Method BLASTX
NCBI GI g3953471
BLAST score 531
E value 3.0e-54
Match length 146
% identity 62
NCBI Description (AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 196572
Contig ID 24862_1.R1039
5'-most EST uC-gsronu33B002f12b1
Method BLASTX
NCBI GI g2244826
BLAST score 387
E value 3.0e-37
Match length 88
% identity 76
NCBI Description (Z97336) replication control protein homolog [Arabidopsis thaliana]

Seq. No. 196573
Contig ID 24876_1.R1039
5'-most EST LIB3148-047-Q1-K1-A1
Method BLASTX
NCBI GI g3335366
BLAST score 218
E value 1.0e-17
Match length 65
% identity 55
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 196574
Contig ID 24882_1.R1039
5'-most EST LIB3146-040-Q1-K1-B4
Method BLASTX
NCBI GI g477430
BLAST score 317
E value 2.0e-29
Match length 99
% identity 62
NCBI Description nucleolar protein p120 - mouse (fragment)

Seq. No. 196575
Contig ID 24888_1.R1039
5'-most EST uC-gsflnu33B005f01b1

Seq. No. 196576
Contig ID 24918_1.R1039

5'-most EST	LIB3189-023-P1-K1-F2
Method	BLASTX
NCBI GI	g4098129
BLAST score	559
E value	2.0e-57
Match length	115
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	196577
Contig ID	24918_2.R1039
5'-most EST	LIB3149-013-Q1-K1-A2
Method	BLASTX
NCBI GI	g4098129
BLAST score	242
E value	2.0e-20
Match length	49
% identity	96
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	196578
Contig ID	24930_1.R1039
5'-most EST	g5047761
Method	BLASTX
NCBI GI	g1176485
BLAST score	153
E value	1.0e-09
Match length	104
% identity	37
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN IME2-MEF2 INTERGENIC REGION >gi|1078244|pir||S53383 probable membrane protein YJL104w - yeast (Saccharomyces cerevisiae) >gi|728706|emb|CAA59390| (X85021) orf 8 [Saccharomyces cerevisiae] >gi|1009450|emb|CAA89399| (Z49379) ORF YJL104w [Saccharomyces cerevisiae]

Seq. No.	196579
Contig ID	24932_1.R1039
5'-most EST	LIB3272-039-P1-K1-H2
Method	BLASTX
NCBI GI	g3738302
BLAST score	220
E value	1.0e-17
Match length	109
% identity	44
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi|4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	196580
Contig ID	24934_1.R1039
5'-most EST	LIB3146-041-Q1-K1-A10
Method	BLASTX
NCBI GI	g549893
BLAST score	187
E value	5.0e-14
Match length	43

% identity	84
NCBI Description	(U09342) homeobox protein [Arabidopsis thaliana]

Seq. No.	196581
Contig ID	24937_1.R1039
5'-most EST	LIB3146-041-Q1-K1-A2
Method	BLASTX
NCBI GI	g3551257
BLAST score	288
E value	5.0e-26
Match length	96
% identity	21
NCBI Description	(AB012708) 98b [Daucus carota]

Seq. No.	196582
Contig ID	24956_1.R1039
5'-most EST	uC-gsronu33B061h11b1
Method	BLASTX
NCBI GI	g3281855
BLAST score	164
E value	4.0e-11
Match length	111
% identity	38
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196583
Contig ID	24961_1.R1039
5'-most EST	LIB3146-041-Q1-K1-C6
Method	BLASTX
NCBI GI	g2275199
BLAST score	466
E value	1.0e-46
Match length	142
% identity	71
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196584
Contig ID	24962_1.R1039
5'-most EST	LIB3197-053-Q1-M1-D8
Method	BLASTX
NCBI GI	g2244826
BLAST score	820
E value	5.0e-88
Match length	197
% identity	79
NCBI Description	(Z97336) replication control protein homolog [Arabidopsis thaliana]

Seq. No.	196585
Contig ID	24967_1.R1039
5'-most EST	g5050347
Method	BLASTX
NCBI GI	g4158230
BLAST score	330
E value	1.0e-30
Match length	108
% identity	57

NCBI Description	(Y18625) amylogenin [Triticum aestivum]
Seq. No.	196586
Contig ID	24977_1.R1039
5'-most EST	uC-gsflmaxxa096g07b1
Method	BLASTX
NCBI GI	g2529668
BLAST score	925
E value	1.0e-100
Match length	211
% identity	82
NCBI Description	(AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi|3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana]
Seq. No.	196587
Contig ID	24981_1.R1039
5'-most EST	LIB3146-041-Q1-K1-E6
Seq. No.	196588
Contig ID	24993_1.R1039
5'-most EST	uC-gsronu33B032b12b1
Method	BLASTX
NCBI GI	g3738331
BLAST score	251
E value	2.0e-21
Match length	55
% identity	76
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.	196589
Contig ID	25000_1.R1039
5'-most EST	LIB3165-044-Q1-K1-G2
Seq. No.	196590
Contig ID	25004_1.R1039
5'-most EST	LIB3146-049-Q1-K1-A1
Method	BLASTX
NCBI GI	g99749
BLAST score	333
E value	5.0e-31
Match length	100
% identity	72
NCBI Description	probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana >gi|217843|dbj|BAA01731| (D10937) protein kinase [Arabidopsis thaliana]
Seq. No.	196591
Contig ID	25011_1.R1039
5'-most EST	uC-gsronu33B044d04b1
Method	BLASTX
NCBI GI	g2979565
BLAST score	367
E value	4.0e-35
Match length	84

% identity	83
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	196592
Contig ID	25015_1.R1039
5'-most EST	LIB3189-024-P1-K1-B3

Seq. No.	196593
Contig ID	25020_1.R1039
5'-most EST	LIB3146-042-Q1-K1-A4
Method	BLASTX
NCBI GI	g3044218
BLAST score	384
E value	4.0e-37
Match length	93
% identity	76
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	196594
Contig ID	25021_1.R1039
5'-most EST	LIB3147-057-Q1-K1-G2

Seq. No.	196595
Contig ID	25049_1.R1039
5'-most EST	uC-gsronu33B134a08b1

Seq. No.	196596
Contig ID	25066_1.R1039
5'-most EST	LIB3146-042-Q1-K1-G5
Method	BLASTX
NCBI GI	g2632252
BLAST score	198
E value	2.0e-20
Match length	154
% identity	41
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	196597
Contig ID	25068_1.R1039
5'-most EST	uC-gsronu33B101d11b1
Method	BLASTX
NCBI GI	g3334756
BLAST score	551
E value	3.0e-56
Match length	111
% identity	95
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No.	196598
Contig ID	25068_2.R1039
5'-most EST	uC-gsflnu33B144c09b1
Method	BLASTX
NCBI GI	g3334756
BLAST score	466
E value	1.0e-46

Match length	113
% identity	81
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No.	196599
Contig ID	25076_1.R1039
5'-most EST	LIB3146-042-Q1-K1-H8

Seq. No.	196600
Contig ID	25078_1.R1039
5'-most EST	LIB3272-026-P1-K1-D2

Seq. No.	196601
Contig ID	25084_1.R1039
5'-most EST	LIB3147-006-Q1-K1-E6

Seq. No.	196602
Contig ID	25089_2.R1039
5'-most EST	LIB3146-054-Q1-K1-D11
Method	BLASTX
NCBI GI	g2191171
BLAST score	152
E value	8.0e-10
Match length	80
% identity	45
NCBI Description	(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No.	196603
Contig ID	25090_1.R1039
5'-most EST	LIB3197-003-P1-M1-B3

Seq. No.	196604
Contig ID	25102_1.R1039
5'-most EST	uC-gsronu33B116c03b1
Method	BLASTN
NCBI GI	g2558961
BLAST score	78
E value	9.0e-36
Match length	210
% identity	86
NCBI Description	Gossypium hirsutum histone H2B1 mRNA, complete cds

Seq. No.	196605
Contig ID	25111_1.R1039
5'-most EST	LIB3189-037-P1-K1-A12
Method	BLASTX
NCBI GI	g2583130
BLAST score	109
E value	4.0e-12
Match length	162
% identity	32
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	196606

Contig ID 25115_1.R1039
5'-most EST LIB3166-050-P1-K1-A5
Method BLASTX
NCBI GI g1345787
BLAST score 1018
E value 1.0e-111
Match length 202
% identity 96
NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2) >gi|567937|dbj|BAA05641| (D26594) chalcone synthase [Camellia sinensis]

Seq. No. 196607
Contig ID 25127_1.R1039
5'-most EST LIB3272-031-P1-K1-C10
Method BLASTX
NCBI GI g1483218
BLAST score 219
E value 2.0e-17
Match length 100
% identity 50
NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 196608
Contig ID 25128_1.R1039
5'-most EST LIB3146-043-Q1-K1-E5
Method BLASTX
NCBI GI g4580575
BLAST score 417
E value 1.0e-40
Match length 142
% identity 59
NCBI Description (AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No. 196609
Contig ID 25142_1.R1039
5'-most EST LIB3147-023-Q1-K1-A3

Seq. No. 196610
Contig ID 25145_1.R1039
5'-most EST LIB3146-043-Q1-K1-G12

Seq. No. 196611
Contig ID 25163_1.R1039
5'-most EST LIB3149-056-Q1-K1-C9
Method BLASTX
NCBI GI g2253442
BLAST score 206
E value 7.0e-16
Match length 56
% identity 62
NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 196612
Contig ID 25175_1.R1039
5'-most EST uC-gsronu33B164e02b2

Method	BLASTX
NCBI GI	g3213227
BLAST score	218
E value	2.0e-17
Match length	139
% identity	35
NCBI Description	(AF035209) putative v-SNARE Vti1a [Mus musculus] >gi|3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No.	196613
Contig ID	25182_1.R1039
5'-most EST	LIB3146-044-Q1-K1-B5

Seq. No.	196614
Contig ID	25186_1.R1039
5'-most EST	LIB3146-044-Q1-K1-C1
Method	BLASTN
NCBI GI	g2828184
BLAST score	39
E value	2.0e-12
Match length	79
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	196615
Contig ID	25187_1.R1039
5'-most EST	LIB3146-044-Q1-K1-C10

Seq. No.	196616
Contig ID	25189_1.R1039
5'-most EST	LIB3165-018-P1-K1-G8

Seq. No.	196617
Contig ID	25199_1.R1039
5'-most EST	LIB3272-018-P1-K1-H2
Method	BLASTX
NCBI GI	g4490728
BLAST score	324
E value	7.0e-30
Match length	99
% identity	64
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	196618
Contig ID	25201_1.R1039
5'-most EST	LIB3146-044-Q1-K1-D2

Seq. No.	196619
Contig ID	25205_1.R1039
5'-most EST	LIB3146-044-Q1-K1-D6
Method	BLASTX
NCBI GI	g3687250
BLAST score	355
E value	1.0e-33
Match length	82
% identity	79

NCBI Description	(AC005169) putative arginine n-methyltransferase [Arabidopsis thaliana]

Seq. No.	196620
Contig ID	25206_1.R1039
5'-most EST	uC-gsflnu33B085c10b1
Method	BLASTX
NCBI GI	g1730171
BLAST score	1594
E value	1.0e-178
Match length	344
% identity	88
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi|1370066|emb|CAA61574| (X89394) glucose-6-phosphate isomerase [Clarkia williamsonii]

Seq. No.	196621
Contig ID	25211_1.R1039
5'-most EST	LIB3146-044-Q1-K1-E12
Method	BLASTX
NCBI GI	g2764941
BLAST score	393
E value	3.0e-38
Match length	90
% identity	73
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	196622
Contig ID	25212_1.R1039
5'-most EST	uC-gsronu33B160d11b1
Method	BLASTX
NCBI GI	g114171
BLAST score	240
E value	5.0e-20
Match length	48
% identity	90
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi|99781|pir||S12744 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape >gi|17815|emb|CAA35839| (X51475) 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]

Seq. No.	196623
Contig ID	25216_1.R1039
5'-most EST	uC-gsflmaxxa096g11b1

Seq. No.	196624
Contig ID	25219_1.R1039
5'-most EST	uC-gsronu33B051e01b1
Method	BLASTX
NCBI GI	g1724114
BLAST score	174

E value	4.0e-12
Match length	63
% identity	62
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	196625
Contig ID	25225_1.R1039
5'-most EST	LIB3146-044-Q1-K1-F6
Method	BLASTX
NCBI GI	g2104446
BLAST score	142
E value	4.0e-22
Match length	107
% identity	59
NCBI Description	(Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	196626
Contig ID	25229_1.R1039
5'-most EST	uC-gsronu33B154g08b2
Method	BLASTX
NCBI GI	g2598049
BLAST score	566
E value	3.0e-58
Match length	126
% identity	87
NCBI Description	(Y15269) chloroplast drought-induced stress protein, 34 kD) [Solanum tuberosum]

Seq. No.	196627
Contig ID	25230_1.R1039
5'-most EST	LIB3146-044-Q1-K1-G11
Method	BLASTX
NCBI GI	g1669341
BLAST score	343
E value	2.0e-32
Match length	131
% identity	53
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	196628
Contig ID	25233_1.R1039
5'-most EST	LIB3146-044-Q1-K1-G4
Method	BLASTX
NCBI GI	g1617206
BLAST score	399
E value	7.0e-39
Match length	122
% identity	66
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	196629
Contig ID	25238_1.R1039
5'-most EST	LIB3196-041-P1-M1-H4
Method	BLASTX
NCBI GI	g3702327
BLAST score	150

E value 1.0e-09
Match length 92
% identity 41
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 196630
Contig ID 25241_1.R1039
5'-most EST LIB3146-044-Q1-K1-H11

Seq. No. 196631
Contig ID 25244_1.R1039
5'-most EST g5048413
Method BLASTX
NCBI GI g4056437
BLAST score 433
E value 3.0e-77
Match length 214
% identity 69
NCBI Description (AC005990) Strong similarity to PFAM PF|00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No. 196632
Contig ID 25256_1.R1039
5'-most EST g5044501
Method BLASTX
NCBI GI g4337175
BLAST score 489
E value 4.0e-49
Match length 143
% identity 67
NCBI Description (AC006416) ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 196633
Contig ID 25265_1.R1039
5'-most EST LIB3165-008-P1-K1-E10

Seq. No. 196634
Contig ID 25270_1.R1039
5'-most EST LIB3197-035-Q1-M1-B6
Method BLASTX
NCBI GI g1617274
BLAST score 754
E value 4.0e-80
Match length 271
% identity 73
NCBI Description (Z72152) AMP-binding protein [Brassica napus]

Seq. No. 196635
Contig ID 25272_1.R1039
5'-most EST LIB3147-027-Q1-K1-E12
Method BLASTX
NCBI GI g4204313
BLAST score 459
E value 4.0e-50

Match length	139
% identity	76
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	196636
Contig ID	25285_1.R1039
5'-most EST	LIB3146-046-Q1-K1-D1
Method	BLASTX
NCBI GI	g3024657
BLAST score	380
E value	2.0e-36
Match length	112
% identity	68
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi|2668740 (AF034944) translation initiation factor; GOS2 [Zea mays]

Seq. No.	196637
Contig ID	25292_1.R1039
5'-most EST	LIB3146-046-Q1-K1-D6
Method	BLASTX
NCBI GI	g4218144
BLAST score	382
E value	1.0e-36
Match length	115
% identity	66
NCBI Description	(AJ132398) glutathione transferase, GST 10b [Arabidopsis thaliana]

Seq. No.	196638
Contig ID	25308_1.R1039
5'-most EST	LIB3146-046-Q1-K1-F11

Seq. No.	196639
Contig ID	25309_1.R1039
5'-most EST	LIB3165-011-P1-K1-G10
Method	BLASTX
NCBI GI	g1483218
BLAST score	205
E value	6.0e-16
Match length	159
% identity	36
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	196640
Contig ID	25311_1.R1039
5'-most EST	LIB3272-030-P1-K1-A3

Seq. No.	196641
Contig ID	25312_1.R1039
5'-most EST	LIB3146-046-Q1-K1-F4

Seq. No.	196642
Contig ID	25315_1.R1039
5'-most EST	uC-gsflmaxxa003h10b1

Seq. No.	196643
Contig ID	25323_1.R1039
5'-most EST	uC-gsflnu33B026c04b1

Seq. No.	196644
Contig ID	25326_1.R1039
5'-most EST	LIB3146-046-Q1-K1-G7
Method	BLASTX
NCBI GI	g3776577
BLAST score	435
E value	7.0e-43
Match length	130
% identity	63
NCBI Description	(AC005388) T22H22.24 [Arabidopsis thaliana]

Seq. No.	196645
Contig ID	25328_1.R1039
5'-most EST	uC-gsronu33B078h04b1
Method	BLASTX
NCBI GI	g4455207
BLAST score	415
E value	1.0e-40
Match length	89
% identity	88
NCBI Description	(AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	196646
Contig ID	25333_1.R1039
5'-most EST	LIB3147-058-Q1-K1-D11

Seq. No.	196647
Contig ID	25334_1.R1039
5'-most EST	LIB3146-046-Q1-K1-H3
Method	BLASTX
NCBI GI	g3334299
BLAST score	189
E value	3.0e-14
Match length	41
% identity	93
NCBI Description	PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi|2315211|emb|CAA74725| (Y14339) proteasome alpha subunit [Lycopersicon esculentum]

Seq. No.	196648
Contig ID	25346_1.R1039
5'-most EST	LIB3146-047-Q1-K1-A8

Seq. No.	196649
Contig ID	25348_1.R1039
5'-most EST	uC-gsflmaxxa096c12b1
Method	BLASTX
NCBI GI	g4049354
BLAST score	844
E value	1.0e-120
Match length	248
% identity	84

NCBI Description	(AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No.	196650
Contig ID	25356_1.R1039
5'-most EST	LIB3146-047-Q1-K1-B7
Method	BLASTX
NCBI GI	g3695061
BLAST score	598
E value	6.0e-62
Match length	208
% identity	64
NCBI Description	(AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No.	196651
Contig ID	25361_1.R1039
5'-most EST	LIB3146-047-Q1-K1-C4
Method	BLASTX
NCBI GI	g2088658
BLAST score	626
E value	4.0e-65
Match length	201
% identity	66
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	196652
Contig ID	25374_1.R1039
5'-most EST	LIB3146-047-Q1-K1-D7

Seq. No.	196653
Contig ID	25375_1.R1039
5'-most EST	LIB3146-047-Q1-K1-D9
Method	BLASTX
NCBI GI	g3668118
BLAST score	740
E value	9.0e-79
Match length	164
% identity	32
NCBI Description	(AJ224078) hypothetical protein [Brassica napus]

Seq. No.	196654
Contig ID	25384_1.R1039
5'-most EST	LIB3148-050-Q1-K1-D5
Method	BLASTX
NCBI GI	g3068704
BLAST score	714
E value	2.0e-75
Match length	172
% identity	40
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	196655
Contig ID	25395_1.R1039
5'-most EST	LIB3148-032-Q1-K1-F12

Seq. No.	196656

Contig ID	25404_1.R1039
5'-most EST	LIB3146-047-Q1-K1-G4
Method	BLASTX
NCBI GI	g100294
BLAST score	497
E value	4.0e-50
Match length	182
% identity	34
NCBI Description	ribonucleoprotein B, 29K - wood tobacco >gi|14135|emb|CAA43428| (X61114) 29kD B ribonucleoprotein [Nicotiana sylvestris]

Seq. No.	196657
Contig ID	25410_1.R1039
5'-most EST	LIB3146-047-Q1-K1-H10
Method	BLASTX
NCBI GI	g3176690
BLAST score	1597
E value	1.0e-179
Match length	339
% identity	91
NCBI Description	(AC003671) Similar to ubiquitin ligase gb|D63905 from S. cerevisiae. EST gb|R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	196658
Contig ID	25422_1.R1039
5'-most EST	uC-gsronu33B049c07b1
Method	BLASTX
NCBI GI	g629670
BLAST score	857
E value	4.0e-92
Match length	242
% identity	69
NCBI Description	hypothetical protein - tomato

Seq. No.	196659
Contig ID	25429_1.R1039
5'-most EST	LIB3146-048-Q1-K1-A8
Method	BLASTX
NCBI GI	g4415931
BLAST score	426
E value	4.0e-42
Match length	121
% identity	67
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi|4559393|gb|AAD23053.1|AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	196660
Contig ID	25438_1.R1039
5'-most EST	LIB3146-048-Q1-K1-B5

Seq. No.	196661
Contig ID	25443_1.R1039
5'-most EST	uC-gsronu33B078f07b1
Method	BLASTX

NCBI GI g3717946
BLAST score 328
E value 3.0e-30
Match length 110
% identity 62
NCBI Description (AJ005901) vag1 [Arabidopsis thaliana]

Seq. No. 196662
Contig ID 25448_1.R1039
5'-most EST LIB3166-042-P1-K1-B2

Seq. No. 196663
Contig ID 25457_1.R1039
5'-most EST LIB3146-048-Q1-K1-D11

Seq. No. 196664
Contig ID 25473_1.R1039
5'-most EST LIB3147-034-Q1-K1-C12
Method BLASTX
NCBI GI g4263702
BLAST score 216
E value 3.0e-17
Match length 55
% identity 71
NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196665
Contig ID 25474_1.R1039
5'-most EST LIB3146-048-Q1-K1-E7

Seq. No. 196666
Contig ID 25479_1.R1039
5'-most EST uC-gsronu33B089g02b1

Seq. No. 196667
Contig ID 25486_1.R1039
5'-most EST LIB3189-030-P1-K1-F3
Method BLASTX
NCBI GI g2924520
BLAST score 907
E value 3.0e-98
Match length 209
% identity 84
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No. 196668
Contig ID 25495_1.R1039
5'-most EST uC-gsflmaxxa014b04b1
Method BLASTX
NCBI GI g577503
BLAST score 514
E value 3.0e-52
Match length 157
% identity 64
NCBI Description (L37790) cationic peroxidase [Stylosanthes humilis]

Seq. No. 196669
Contig ID 25497_1.R1039
5'-most EST uC-gsronu33B132d04b1

Seq. No. 196670
Contig ID 25508_1.R1039
5'-most EST LIB3166-007-P1-K1-B10

Seq. No. 196671
Contig ID 25513_1.R1039
5'-most EST LIB3146-049-Q1-K1-A5
Method BLASTX
NCBI GI g118514
BLAST score 243
E value 1.0e-20
Match length 45
% identity 100
NCBI Description TURGOR-RESPONSIVE PROTEIN 26G >gi|100051|pir||S11863 aldehyde dehydrogenase homolog - garden pea >gi|20681|emb|CAA38243| (X54359) 508 aa peptide [Pisum sativum]

Seq. No. 196672
Contig ID 25516_1.R1039
5'-most EST LIB3149-038-Q1-K1-E1
Method BLASTX
NCBI GI g3122258
BLAST score 512
E value 6.0e-52
Match length 128
% identity 78
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB) >gi|2809383 (AF022229) translation initiation factor 6 [Homo sapiens] >gi|2910997|emb|CAA72243| (Y11435) b4 integrin interactor [Homo sapiens] >gi|3335506 (AF047433) b(2)gcn homolog [Homo sapiens] >gi|4504771|ref|NP_002203.1|pITGB4BP| integrin beta 4 binding protein

Seq. No. 196673
Contig ID 25522_1.R1039
5'-most EST LIB3146-049-Q1-K1-B5

Seq. No. 196674
Contig ID 25541_1.R1039
5'-most EST LIB3166-017-P1-K1-E8

Seq. No. 196675
Contig ID 25542_1.R1039
5'-most EST LIB3166-031-P1-K1-D1
Method BLASTX
NCBI GI g4335755
BLAST score 229
E value 7.0e-19
Match length 111
% identity 47
NCBI Description (AC006284) putative hydroxyproline-rich glycoprotein

[Arabidopsis thaliana]

Seq. No.	196676
Contig ID	25546_1.R1039
5'-most EST	LIB3196-034-P1-M1-A2
Method	BLASTX
NCBI GI	g4415908
BLAST score	392
E value	5.0e-38
Match length	110
% identity	64
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	196677
Contig ID	25549_1.R1039
5'-most EST	LIB3148-017-Q1-K1-H2

Seq. No.	196678
Contig ID	25559_1.R1039
5'-most EST	LIB3146-049-Q1-K1-E9

Seq. No.	196679
Contig ID	25560_1.R1039
5'-most EST	LIB3146-049-Q1-K1-F1

Seq. No.	196680
Contig ID	25576_1.R1039
5'-most EST	LIB3146-049-Q1-K1-G7
Method	BLASTX
NCBI GI	g2911068
BLAST score	752
E value	5.0e-80
Match length	145
% identity	88
NCBI Description	(AL021960) G10 - like protein [Arabidopsis thaliana]

Seq. No.	196681
Contig ID	25583_1.R1039
5'-most EST	LIB3146-049-Q1-K1-H2
Method	BLASTX
NCBI GI	g4455351
BLAST score	172
E value	4.0e-12
Match length	48
% identity	65
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	196682
Contig ID	25596_1.R1039
5'-most EST	LIB3146-050-Q1-K1-B10

Seq. No.	196683
Contig ID	25599_1.R1039
5'-most EST	uC-gsflmaxxa076a05b1
Method	BLASTX
NCBI GI	g629561
BLAST score	267

E value	3.0e-23
Match length	141
% identity	40
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi|479047|emb|CAA55654| (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	196684
Contig ID	25602_1.R1039
5'-most EST	uC-gsflnu33B058b05b1
Method	BLASTX
NCBI GI	g3935169
BLAST score	313
E value	2.0e-28
Match length	68
% identity	88
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No.	196685
Contig ID	25608_1.R1039
5'-most EST	uC-gsronu33B058c04b1
Method	BLASTX
NCBI GI	g4138581
BLAST score	427
E value	4.0e-42
Match length	144
% identity	23
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	196686
Contig ID	25611_1.R1039
5'-most EST	LIB3148-020-Q1-K1-E11
Method	BLASTX
NCBI GI	g2244993
BLAST score	259
E value	2.0e-22
Match length	103
% identity	53
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	196687
Contig ID	25616_1.R1039
5'-most EST	LIB3166-033-P1-K1-E2
Method	BLASTX
NCBI GI	g3249084
BLAST score	826
E value	2.0e-88
Match length	246
% identity	26
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb|X92750 from Mus musculus. ESTs gb|AA712687 and gb|Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	196688
Contig ID	25622_1.R1039

5'-most EST	g5045625
Method	BLASTX
NCBI GI	g121736
BLAST score	672
E value	1.0e-70
Match length	198
% identity	64
NCBI Description	GLUTATHIONE S-TRANSFERASE 1 (SR8) (CLASS-THETA) >gi|99589|pir||S16604 glutathione transferase (EC 2.5.1.18) CARSR8 - clove pink >gi|18330|emb|CAA41279| (X58390) glutathione s-transferase [Dianthus caryophyllus] >gi|167968 (M64268) glutathione transferase [Dianthus caryophyllus]

Seq. No.	196689
Contig ID	25627_1.R1039
5'-most EST	LIB3146-050-Q1-K1-E12

Seq. No.	196690
Contig ID	25630_1.R1039
5'-most EST	LIB3148-051-Q1-K1-F9
Method	BLASTX
NCBI GI	g3738297
BLAST score	159
E value	1.0e-10
Match length	60
% identity	13
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	196691
Contig ID	25631_1.R1039
5'-most EST	LIB3165-051-Q1-K1-D12
Method	BLASTX
NCBI GI	g452357
BLAST score	472
E value	2.0e-47
Match length	95
% identity	97
NCBI Description	(Z29591) guanine nucleotide regulatory protein [Vicia faba] >gi|1098294|prf||2115367B small GTP-binding protein [Vicia faba]

Seq. No.	196692
Contig ID	25633_1.R1039
5'-most EST	LIB3189-023-P1-K1-G11
Method	BLASTX
NCBI GI	g2330739
BLAST score	276
E value	2.0e-24
Match length	78
% identity	63
NCBI Description	(Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]

Seq. No.	196693
Contig ID	25638_1.R1039
5'-most EST	LIB3146-058-Q1-K1-G12

Seq. No.	196694
Contig ID	25638_7.R1039
5'-most EST	LIB3147-041-Q1-K1-B2
Seq. No.	196695
Contig ID	25642_1.R1039
5'-most EST	LIB3147-010-Q1-K1-C5
Seq. No.	196696
Contig ID	25646_1.R1039
5'-most EST	LIB3146-050-Q1-K1-G11
Seq. No.	196697
Contig ID	25647_1.R1039
5'-most EST	LIB3189-036-P1-K1-C1
Method	BLASTX
NCBI GI	g3004560
BLAST score	308
E value	4.0e-36
Match length	98
% identity	74
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]
Seq. No.	196698
Contig ID	25654_1.R1039
5'-most EST	LIB3146-050-Q1-K1-H1
Method	BLASTX
NCBI GI	g2245125
BLAST score	320
E value	3.0e-29
Match length	176
% identity	43
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196699
Contig ID	25657_1.R1039
5'-most EST	LIB3147-036-Q1-K1-G8
Method	BLASTX
NCBI GI	g2642157
BLAST score	505
E value	5.0e-85
Match length	199
% identity	72
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.	196700
Contig ID	25674_1.R1039
5'-most EST	uC-gsronu33B015c11b1
Seq. No.	196701
Contig ID	25685_1.R1039
5'-most EST	LIB3196-041-P1-M1-E1
Seq. No.	196702
Contig ID	25686_1.R1039

5'-most EST	LIB3148-039-Q1-K1-G6
Method	BLASTX
NCBI GI	g285286
BLAST score	258
E value	3.0e-22
Match length	91
% identity	54
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	196703
Contig ID	25687_1.R1039
5'-most EST	uC-gsronu33B108a08b1

Seq. No.	196704
Contig ID	25689_1.R1039
5'-most EST	LIB3146-051-Q1-K1-C12
Method	BLASTX
NCBI GI	g2738998
BLAST score	1051
E value	1.0e-114
Match length	264
% identity	77
NCBI Description	(AF022458) CYP98A2p [Glycine max]

Seq. No.	196705
Contig ID	25697_1.R1039
5'-most EST	LIB3197-046-Q1-M1-D8

Seq. No.	196706
Contig ID	25701_1.R1039
5'-most EST	uC-gsflnu33B110b08b1
Method	BLASTX
NCBI GI	g3540184
BLAST score	572
E value	4.0e-59
Match length	154
% identity	70
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	196707
Contig ID	25705_1.R1039
5'-most EST	g5049155
Method	BLASTX
NCBI GI	g3023713
BLAST score	1537
E value	1.0e-172
Match length	321
% identity	93
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi|780372 (U09450) enolase [Oryza sativa]

Seq. No.	196708
Contig ID	25708_1.R1039
5'-most EST	LIB3147-002-Q1-K1-C10

Seq. No.	196709

Contig ID	25710_1.R1039
5'-most EST	LIB3165-006-P1-K1-H12

Seq. No.	196710
Contig ID	25719_1.R1039
5'-most EST	LIB3149-044-Q1-K1-F7
Method	BLASTX
NCBI GI	g464840
BLAST score	1228
E value	1.0e-136
Match length	240
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi|421781|pir||S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi|296494|emb|CAA48927| (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	196711
Contig ID	25728_1.R1039
5'-most EST	LIB3146-051-Q1-K1-F7
Method	BLASTX
NCBI GI	g3953463
BLAST score	320
E value	2.0e-57
Match length	164
% identity	65
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	196712
Contig ID	25729_1.R1039
5'-most EST	g5050099
Method	BLASTX
NCBI GI	g4097569
BLAST score	382
E value	1.0e-36
Match length	107
% identity	67
NCBI Description	(U64915) GMFP4 [Glycine max]

Seq. No.	196713
Contig ID	25758_1.R1039
5'-most EST	LIB3146-052-Q1-K1-A8
Method	BLASTX
NCBI GI	g2274859
BLAST score	396
E value	2.0e-38
Match length	73
% identity	97
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi|4510420|gb|AAD21506.1| (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	196714
Contig ID	25761_1.R1039
5'-most EST	uC-gsflmaxxa027h08b1
Method	BLASTX

NCBI GI	g2191136
BLAST score	424
E value	1.0e-41
Match length	146
% identity	62
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	196715
Contig ID	25767_1.R1039
5'-most EST	uC-gsronu33B169g04b1

Seq. No.	196716
Contig ID	25769_1.R1039
5'-most EST	LIB3146-052-Q1-K1-C5
Method	BLASTX
NCBI GI	g4539460
BLAST score	165
E value	3.0e-11
Match length	197
% identity	8
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	196717
Contig ID	25777_1.R1039
5'-most EST	g5047827

Seq. No.	196718
Contig ID	25786_1.R1039
5'-most EST	g3325860
Method	BLASTX
NCBI GI	g3204108
BLAST score	259
E value	7.0e-28
Match length	109
% identity	63
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	196719
Contig ID	25790_1.R1039
5'-most EST	LIB3272-010-P1-K1-A12
Method	BLASTX
NCBI GI	g3617770
BLAST score	886
E value	1.0e-95
Match length	211
% identity	78
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	196720
Contig ID	25793_1.R1039
5'-most EST	LIB3272-049-P1-K1-A5
Method	BLASTX
NCBI GI	g3337356

BLAST score	1400
E value	1.0e-156
Match length	293
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	196721
Contig ID	25800_1.R1039
5'-most EST	uC-gsflmaxxa098c08b1

Seq. No.	196722
Contig ID	25817_1.R1039
5'-most EST	LIB3146-053-Q1-K1-A7

Seq. No.	196723
Contig ID	25820_1.R1039
5'-most EST	LIB3165-042-Q1-K1-E12
Method	BLASTX
NCBI GI	g3243234
BLAST score	270
E value	1.0e-23
Match length	123
% identity	44
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	196724
Contig ID	25831_1.R1039
5'-most EST	LIB3189-043-P1-K1-D4
Method	BLASTX
NCBI GI	g1168470
BLAST score	1018
E value	1.0e-111
Match length	228
% identity	84
NCBI Description	PROTEIN KINASE APK1A >gi|282877|pir||S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi|217829|dbj|BAA02092| (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	196725
Contig ID	25835_1.R1039
5'-most EST	LIB3147-033-Q1-K1-B11

Seq. No.	196726
Contig ID	25845_1.R1039
5'-most EST	LIB3196-020-P1-M1-H4
Method	BLASTX
NCBI GI	g416662
BLAST score	609
E value	2.0e-63
Match length	182
% identity	61
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi|99954|pir||S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860|

(X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No.	196727
Contig ID	25867_1.R1039
5'-most EST	uC-gsflmaxxa002e05b1
Method	BLASTX
NCBI GI	g1808590
BLAST score	294
E value	4.0e-26
Match length	79
% identity	67
NCBI Description	(Y10836) HMG-I/Y [Arabidopsis thaliana]

Seq. No.	196728
Contig ID	25870_1.R1039
5'-most EST	uC-gsflnu33B018b11b1

Seq. No.	196729
Contig ID	25877_1.R1039
5'-most EST	LIB3146-053-Q1-K1-G11

Seq. No.	196730
Contig ID	25882_1.R1039
5'-most EST	uC-gsflnu33B027a08b1
Method	BLASTX
NCBI GI	g4101574
BLAST score	254
E value	2.0e-21
Match length	182
% identity	35
NCBI Description	(AF004876) 54TMp [Homo sapiens]

Seq. No.	196731
Contig ID	25887_1.R1039
5'-most EST	LIB3146-053-Q1-K1-H10
Method	BLASTX
NCBI GI	g3650032
BLAST score	196
E value	6.0e-15
Match length	45
% identity	67
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	196732
Contig ID	25896_1.R1039
5'-most EST	LIB3146-053-Q1-K1-H9

Seq. No.	196733
Contig ID	25900_1.R1039
5'-most EST	g3326147

Seq. No.	196734
Contig ID	25902_1.R1039
5'-most EST	LIB3166-055-P1-K1-H9
Method	BLASTX
NCBI GI	g4539348

BLAST score 822
E value 5.0e-88
Match length 241
% identity 61
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 196735
Contig ID 25902_3.R1039
5'-most EST LIB3166-001-Q1-K1-D7
Method BLASTX
NCBI GI g4539348
BLAST score 142
E value 9.0e-09
Match length 50
% identity 80
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 196736
Contig ID 25905_1.R1039
5'-most EST LIB3147-060-Q1-K1-H4
Method BLASTX
NCBI GI g1418127
BLAST score 227
E value 1.0e-18
Match length 55
% identity 80
NCBI Description (D63166) CTP:phosphocholine cytidylyltransferase [Brassica napus]

Seq. No. 196737
Contig ID 25906_1.R1039
5'-most EST g5045489
Method BLASTX
NCBI GI g4454043
BLAST score 940
E value 1.0e-102
Match length 246
% identity 71
NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 196738
Contig ID 25909_1.R1039
5'-most EST g5044299
Method BLASTX
NCBI GI g2344871
BLAST score 328
E value 3.0e-30
Match length 202
% identity 39
NCBI Description (AJ001270) purple acid phosphatase precursor [Phaseolus vulgaris]

Seq. No. 196739
Contig ID 25909_2.R1039
5'-most EST LIB3148-009-Q1-K1-G1
Method BLASTX
NCBI GI g2961389

BLAST score 230
E value 7.0e-19
Match length 71
% identity 54
NCBI Description (AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi|4006925|emb|CAB16853| (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No. 196740
Contig ID 25918_1.R1039
5'-most EST LIB3146-054-Q1-K1-B9

Seq. No. 196741
Contig ID 25930_1.R1039
5'-most EST LIB3166-054-P1-K1-G3

Seq. No. 196742
Contig ID 25939_1.R1039
5'-most EST g5045400
Method BLASTX
NCBI GI g3128228
BLAST score 880
E value 6.0e-95
Match length 178
% identity 92
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi|3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 196743
Contig ID 25939_2.R1039
5'-most EST uC-gsronu33B116h05b1
Method BLASTX
NCBI GI g3128228
BLAST score 879
E value 1.0e-94
Match length 178
% identity 92
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi|3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 196744
Contig ID 25939_3.R1039
5'-most EST LIB3166-025-P1-K1-H10
Method BLASTX
NCBI GI g3128228
BLAST score 358
E value 8.0e-34
Match length 102
% identity 69
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi|3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 196745
Contig ID 25951_1.R1039

5'-most EST	LIB3146-054-Q1-K1-E8
Method	BLASTX
NCBI GI	g3176684
BLAST score	655
E value	1.0e-68
Match length	211
% identity	60
NCBI Description	(AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb|U81375 from Homo sapiens. ESTs gb|N65317, gb|T20785, gb|AA586285 and gb|AA712578 come from this gene. [Arabidopsis thaliana]

Seq. No.	196746
Contig ID	25958_1.R1039
5'-most EST	LIB3146-054-Q1-K1-F4

Seq. No.	196747
Contig ID	25962_1.R1039
5'-most EST	LIB3197-047-Q1-M1-A3
Method	BLASTX
NCBI GI	g2499569
BLAST score	645
E value	3.0e-67
Match length	170
% identity	70
NCBI Description	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi|2129700|pir||S66344 protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) - Arabidopsis thaliana >gi|1322021 (U31288) L-isoaspartyl methyltransferase [Arabidopsis thaliana]

Seq. No.	196748
Contig ID	25966_1.R1039
5'-most EST	uC-gsflmaxxa049d08b1

Seq. No.	196749
Contig ID	25971_1.R1039
5'-most EST	LIB3148-019-Q1-K1-G6

Seq. No.	196750
Contig ID	25975_1.R1039
5'-most EST	g5048802
Method	BLASTX
NCBI GI	g1655653
BLAST score	229
E value	2.0e-18
Match length	149
% identity	37
NCBI Description	(Z81368) hypothetical protein Rv2406c [Mycobacterium tuberculosis]

Seq. No.	196751
Contig ID	25978_1.R1039
5'-most EST	uC-gsronu33B169b05b1
Method	BLASTX

NCBI GI	g3063444
BLAST score	228
E value	1.0e-18
Match length	90
% identity	57
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	196752
Contig ID	25984_1.R1039
5'-most EST	LIB3197-044-Q1-M1-C3
Method	BLASTX
NCBI GI	g282963
BLAST score	421
E value	3.0e-41
Match length	89
% identity	81
NCBI Description	transforming protein (myb) homolog (clone myb.Ph2) - garden petunia >gi|20561|emb|CAA78387| (Z13997) protein 2 [Petunia x hybrida]

Seq. No.	196753
Contig ID	25991_1.R1039
5'-most EST	LIB3149-013-Q1-K1-F5
Method	BLASTX
NCBI GI	g2765091
BLAST score	796
E value	5.0e-85
Match length	261
% identity	57
NCBI Description	(Y10982) putative cytochrome P450 [Glycine max]

Seq. No.	196754
Contig ID	25993_1.R1039
5'-most EST	LIB3146-055-Q1-K1-B1

Seq. No.	196755
Contig ID	26021_1.R1039
5'-most EST	uC-gsronu33B126b10b1
Method	BLASTX
NCBI GI	g556409
BLAST score	159
E value	2.0e-10
Match length	222
% identity	30
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	196756
Contig ID	26027_1.R1039
5'-most EST	LIB3149-047-Q1-K1-B5
Method	BLASTX
NCBI GI	g3877252
BLAST score	412
E value	4.0e-40
Match length	149
% identity	54
NCBI Description	(Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No.	196757
Contig ID	26038_1.R1039
5'-most EST	LIB3272-023-P1-K1-H7
Method	BLASTX
NCBI GI	g1076316
BLAST score	345
E value	7.0e-33
Match length	124
% identity	57
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi|469110|emb|CAA55321| (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	196758
Contig ID	26048_1.R1039
5'-most EST	LIB3146-055-Q1-K1-G3
Method	BLASTX
NCBI GI	g1173638
BLAST score	431
E value	1.0e-42
Match length	129
% identity	64
NCBI Description	(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq. No.	196759
Contig ID	26052_1.R1039
5'-most EST	uC-gsronu33B077e03b1
Method	BLASTX
NCBI GI	g2443329
BLAST score	465
E value	2.0e-46
Match length	105
% identity	80
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	196760
Contig ID	26056_1.R1039
5'-most EST	g5046342

Seq. No.	196761
Contig ID	26059_1.R1039
5'-most EST	uC-gsflnu33B057c03b1
Method	BLASTX
NCBI GI	g4510349
BLAST score	241
E value	5.0e-20
Match length	137
% identity	49
NCBI Description	(AC006921) putative bZIP transcription factor [Arabidopsis thaliana]

Seq. No.	196762
Contig ID	26073_1.R1039
5'-most EST	uC-gsflmaxxa040g10b1
Method	BLASTX
NCBI GI	g2196466

BLAST score	483
E value	1.0e-48
Match length	142
% identity	67
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	196763
Contig ID	26083_1.R1039
5'-most EST	LIB3196-058-P1-M1-E9

Seq. No.	196764
Contig ID	26088_1.R1039
5'-most EST	LIB3146-056-Q1-K1-C10

Seq. No.	196765
Contig ID	26104_1.R1039
5'-most EST	LIB3149-064-Q1-K1-F2
Method	BLASTX
NCBI GI	g1710587
BLAST score	831
E value	4.0e-89
Match length	213
% identity	80
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi|1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	196766
Contig ID	26114_1.R1039
5'-most EST	LIB3146-056-Q1-K1-E6

Seq. No.	196767
Contig ID	26121_1.R1039
5'-most EST	LIB3166-056-P1-K1-B12

Seq. No.	196768
Contig ID	26126_1.R1039
5'-most EST	LIB3146-056-Q1-K1-F9
Method	BLASTX
NCBI GI	g4063751
BLAST score	252
E value	1.0e-21
Match length	141
% identity	35
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi|4510409|gb|AAD21495.1| (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	196769
Contig ID	26131_1.R1039
5'-most EST	LIB3146-056-Q1-K1-G2
Method	BLASTX
NCBI GI	g4220524
BLAST score	243
E value	2.0e-20
Match length	62
% identity	68

NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	196770
Contig ID	26133_1.R1039
5'-most EST	LIB3197-057-Q1-M1-A8
Method	BLASTX
NCBI GI	g2104529
BLAST score	674
E value	5.0e-71
Match length	156
% identity	83
NCBI Description	(AF001308) putative hexose transporter [Arabidopsis thaliana]
Seq. No.	196771
Contig ID	26141_1.R1039
5'-most EST	LIB3196-045-P1-M1-C3
Method	BLASTX
NCBI GI	g4314361
BLAST score	216
E value	3.0e-17
Match length	44
% identity	95
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]
Seq. No.	196772
Contig ID	26144_1.R1039
5'-most EST	LIB3272-031-P1-K1-D10
Method	BLASTX
NCBI GI	g3738285
BLAST score	272
E value	1.0e-23
Match length	151
% identity	40
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	196773
Contig ID	26149_1.R1039
5'-most EST	LIB3146-057-Q1-K1-A1
Method	BLASTX
NCBI GI	g4539408
BLAST score	200
E value	2.0e-15
Match length	86
% identity	51
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]
Seq. No.	196774
Contig ID	26156_1.R1039
5'-most EST	LIB3146-057-Q1-K1-A5
Method	BLASTX
NCBI GI	g529353
BLAST score	241
E value	4.0e-20
Match length	129
% identity	41
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 196775
Contig ID 26158_1.R1039
5'-most EST LIB3146-057-Q1-K1-A7

Seq. No. 196776
Contig ID 26161_1.R1039
5'-most EST uC-gsflnu33B100e08b1
Method BLASTX
NCBI GI g3402711
BLAST score 366
E value 1.0e-34
Match length 82
% identity 41
NCBI Description (AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No. 196777
Contig ID 26166_1.R1039
5'-most EST q5047558
Method BLASTX
NCBI GI g3860250
BLAST score 734
E value 1.0e-77
Match length 226
% identity 63
NCBI Description (AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No. 196778
Contig ID 26167_1.R1039
5'-most EST LIB3146-057-Q1-K1-B4
Method BLASTX
NCBI GI g1143427
BLAST score 657
E value 1.0e-74
Match length 156
% identity 93
NCBI Description (X73961) heat shock protein 70 [Cucumis sativus]

Seq. No. 196779
Contig ID 26181_1.R1039
5'-most EST LIB3146-057-Q1-K1-C6

Seq. No. 196780
Contig ID 26192_1.R1039
5'-most EST LIB3146-057-Q1-K1-D7
Method BLASTX
NCBI GI g1931638
BLAST score 239
E value 8.0e-20
Match length 224
% identity 34
NCBI Description (U95973) transcription factor RUSH-1alpha isolog [Arabidopsis thaliana]

Seq. No. 196781

Contig ID	26210_1.R1039
5'-most EST	LIB3146-057-Q1-K1-F2
Method	BLASTX
NCBI GI	g3894168
BLAST score	233
E value	2.0e-19
Match length	136
% identity	35
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	196782
Contig ID	26214_1.R1039
5'-most EST	LIB3165-018-P1-K1-A4
Method	BLASTX
NCBI GI	g2136011
BLAST score	184
E value	2.0e-13
Match length	64
% identity	48
NCBI Description	protein DS 1, 24K - human >gi|1045059|emb|CAA57387| (X81788) ICT1 protein [Homo sapiens] >gi|4557657|ref|NP_001536.1|pICT1| immature colon carcinoma transcript

Seq. No.	196783
Contig ID	26220_1.R1039
5'-most EST	LIB3146-057-Q1-K1-G11

Seq. No.	196784
Contig ID	26221_1.R1039
5'-most EST	g5045969
Method	BLASTX
NCBI GI	g464806
BLAST score	227
E value	2.0e-18
Match length	225
% identity	31
NCBI Description	SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72) >gi|423182|pir||A40692 signal recognition particle 72K chain - dog >gi|297768|emb|CAA48014| (X67813) signal recognition particle,72 kDa subunit [Canis familiaris]

Seq. No.	196785
Contig ID	26229_1.R1039
5'-most EST	g5050846
Method	BLASTX
NCBI GI	g3152606
BLAST score	154
E value	4.0e-10
Match length	45
% identity	62
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	196786
Contig ID	26277_1.R1039

5'-most EST	uC-gsflnu33B107e04b1
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	196787
Contig ID	26278_1.R1039
5'-most EST	LIB3146-058-Q1-K1-D3

Seq. No.	196788
Contig ID	26299_1.R1039
5'-most EST	LIB3196-013-P1-M1-A6
Method	BLASTX
NCBI GI	g2244990
BLAST score	239
E value	2.0e-34
Match length	120
% identity	62
NCBI Description	(Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No.	196789
Contig ID	26301_1.R1039
5'-most EST	LIB3146-058-Q1-K1-F2
Method	BLASTX
NCBI GI	g1172556
BLAST score	390
E value	1.0e-37
Match length	83
% identity	90
NCBI Description	36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi|629729|pir||S46925 porin II, 36K - potato >gi|1076681|pir||B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi|515360|emb|CAA56600| (X80387) 36kDA porin II [Solanum tuberosum]

Seq. No.	196790
Contig ID	26303_1.R1039
5'-most EST	LIB3146-058-Q1-K1-F4
Method	BLASTX
NCBI GI	g3152618
BLAST score	383
E value	8.0e-37
Match length	108
% identity	67
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi|3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	196791
Contig ID	26307_1.R1039
5'-most EST	LIB3166-002-Q1-K1-E3

Seq. No.	196792
Contig ID	26308_1.R1039
5'-most EST	LIB3146-058-Q1-K1-F9
Method	BLASTX
NCBI GI	g3860258
BLAST score	384
E value	1.0e-36
Match length	117
% identity	62
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	196793
Contig ID	26308_2.R1039
5'-most EST	LIB3165-014-P1-K1-F12
Method	BLASTX
NCBI GI	g3860258
BLAST score	207
E value	4.0e-16
Match length	62
% identity	65
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	196794
Contig ID	26336_1.R1039
5'-most EST	uC-gsflmaxxa060f04b1

Seq. No.	196795
Contig ID	26339_1.R1039
5'-most EST	LIB3166-026-P1-K1-C2

Seq. No.	196796
Contig ID	26345_1.R1039
5'-most EST	LIB3189-035-P1-K1-D12
Method	BLASTX
NCBI GI	g3193301
BLAST score	275
E value	4.0e-50
Match length	146
% identity	69
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	196797
Contig ID	26358_1.R1039
5'-most EST	LIB3147-034-Q1-K1-D9
Method	BLASTX
NCBI GI	g3128173
BLAST score	539
E value	4.0e-55
Match length	119
% identity	86
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196798
Contig ID	26374_1.R1039

5'-most EST	uC-gsflmaxxa098a10b1
Method	BLASTX
NCBI GI	g2462837
BLAST score	501
E value	2.0e-50
Match length	232
% identity	47
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196799
Contig ID	26381_1.R1039
5'-most EST	LIB3146-059-Q1-K1-E9

Seq. No.	196800
Contig ID	26382_1.R1039
5'-most EST	uC-gsronu33B080h07b1
Method	BLASTX
NCBI GI	g2961345
BLAST score	456
E value	3.0e-45
Match length	111
% identity	73
NCBI Description	(AL022140) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196801
Contig ID	26385_1.R1039
5'-most EST	uC-gsflnu33B098c12b1
Method	BLASTX
NCBI GI	g498040
BLAST score	219
E value	6.0e-18
Match length	52
% identity	83
NCBI Description	(L33793) ORF [Senecio odorus]

Seq. No.	196802
Contig ID	26388_1.R1039
5'-most EST	uC-gsflnu33B111c09b1
Method	BLASTX
NCBI GI	g1174470
BLAST score	684
E value	8.0e-72
Match length	207
% identity	64
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi|508543 (L34260) integral membrane protein 1 [Mus musculus] >gi|1588285|prf||2208301A integral membrane protein [Mus musculus]

Seq. No.	196803
Contig ID	26393_1.R1039
5'-most EST	uC-gsflnu33B084e10b1
Method	BLASTX
NCBI GI	g3618214
BLAST score	168
E value	1.0e-11
Match length	161

% identity	29
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	196804
Contig ID	26403_1.R1039
5'-most EST	LIB3147-007-Q1-K1-G11
Method	BLASTX
NCBI GI	g3335361
BLAST score	731
E value	2.0e-77
Match length	150
% identity	89
NCBI Description	(AC003028) putative acyltransferase [Arabidopsis thaliana]

Seq. No.	196805
Contig ID	26406_1.R1039
5'-most EST	LIB3196-020-P1-M1-A8
Method	BLASTX
NCBI GI	g2431767
BLAST score	237
E value	1.0e-19
Match length	120
% identity	42
NCBI Description	(U62751) acidic ribosomal protein P3a [Zea mays]

Seq. No.	196806
Contig ID	26419_1.R1039
5'-most EST	LIB3146-060-Q1-K1-A6
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	6.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	196807
Contig ID	26420_1.R1039
5'-most EST	LIB3146-060-Q1-K1-A8
Method	BLASTX
NCBI GI	g400515
BLAST score	178
E value	8.0e-13
Match length	66
% identity	48
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8) (CI-B8) >gi|346540|pir||S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine >gi|246|emb|CAA44904| (X63219) NADH dehydrogenase [Bos taurus]

Seq. No.	196808
Contig ID	26438_1.R1039
5'-most EST	LIB3146-060-Q1-K1-C4

Seq. No.	196809

Contig ID	26442_1.R1039
5'-most EST	uC-gsflnu33B022g12b1
Method	BLASTX
NCBI GI	g3264778
BLAST score	643
E value	4.0e-67
Match length	245
% identity	55
NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	196810
Contig ID	26444_1.R1039
5'-most EST	LIB3196-008-P1-M1-G3

Seq. No.	196811
Contig ID	26445_1.R1039
5'-most EST	LIB3146-060-Q1-K1-D12

Seq. No.	196812
Contig ID	26457_1.R1039
5'-most EST	uC-gsflnu33B046c09b1
Method	BLASTX
NCBI GI	g4063749
BLAST score	146
E value	5.0e-09
Match length	170
% identity	22
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196813
Contig ID	26463_1.R1039
5'-most EST	LIB3146-060-Q1-K1-E9
Method	BLASTX
NCBI GI	g2980770
BLAST score	393
E value	8.0e-38
Match length	199
% identity	58
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	196814
Contig ID	26465_1.R1039
5'-most EST	LIB3146-060-Q1-K1-F9

Seq. No.	196815
Contig ID	26466_1.R1039
5'-most EST	LIB3146-060-Q1-K1-F11
Method	BLASTX
NCBI GI	g4406771
BLAST score	206
E value	4.0e-16
Match length	140
% identity	37
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 196816

Contig ID	26475_1.R1039
5'-most EST	LIB3272-007-P1-K1-A2
Method	BLASTX
NCBI GI	g4510363
BLAST score	532
E value	3.0e-54
Match length	131
% identity	75
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	196817
Contig ID	26475_2.R1039
5'-most EST	LIB3196-058-P1-M1-F4
Method	BLASTX
NCBI GI	g4510363
BLAST score	401
E value	6.0e-39
Match length	95
% identity	78
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	196818
Contig ID	26484_1.R1039
5'-most EST	LIB3166-028-P1-K1-D4
Method	BLASTX
NCBI GI	g1707032
BLAST score	242
E value	2.0e-20
Match length	125
% identity	42
NCBI Description	(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8

Seq. No.	196819
Contig ID	26517_1.R1039
5'-most EST	uC-gsronu33B111h12b1
Method	BLASTX
NCBI GI	g4324409
BLAST score	219
E value	2.0e-17
Match length	200
% identity	29
NCBI Description	(AF104119) intracellular chloride ion channel protein p64H1 [Rattus norvegicus]

Seq. No.	196820
Contig ID	26523_1.R1039
5'-most EST	uC-gsflnu33B078f05b1
Method	BLASTX
NCBI GI	g3925265
BLAST score	122
E value	1.0e-12

Match length	154
% identity	32
NCBI Description	(Z93394) similar to Probable rabGAP domains [Caenorhabditis elegans]

Seq. No.	196821
Contig ID	26535_1.R1039
5'-most EST	LIB3146-061-Q1-K1-E9
Method	BLASTX
NCBI GI	g3319357
BLAST score	414
E value	1.0e-40
Match length	129
% identity	66
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	196822
Contig ID	26543_1.R1039
5'-most EST	LIB3197-059-Q1-M1-B9
Method	BLASTX
NCBI GI	g3334133
BLAST score	549
E value	8.0e-56
Match length	229
% identity	48
NCBI Description	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi|1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	196823
Contig ID	26582_1.R1039
5'-most EST	LIB3196-029-P1-M1-F7
Method	BLASTN
NCBI GI	g1929413
BLAST score	73
E value	1.0e-32
Match length	511
% identity	81
NCBI Description	N.tabacum mRNA for ribonucleotide reductase R2 protein

Seq. No.	196824
Contig ID	26589_1.R1039
5'-most EST	LIB3147-001-Q1-K1-C3

Seq. No.	196825
Contig ID	26594_1.R1039
5'-most EST	LIB3147-001-Q1-K2-C8
Method	BLASTX
NCBI GI	g2055374
BLAST score	142
E value	8.0e-09
Match length	60
% identity	55
NCBI Description	(U29095) serine-threonine protein kinase [Triticum aestivum]

Seq. No.	196826

Contig ID 26596_1.R1039
5'-most EST LIB3147-001-Q1-K1-D3

Seq. No. 196827
Contig ID 26597_1.R1039
5'-most EST LIB3147-001-Q1-K2-D4
Method BLASTX
NCBI GI g3183219
BLAST score 231
E value 6.0e-19
Match length 161
% identity 39
NCBI Description HYPOTHETICAL PROTEIN KIAA0112 (HA0609)
>gi|434779|dbj|BAA04948| (D25218) KIAA0112 [Homo sapiens]

Seq. No. 196828
Contig ID 26600_1.R1039
5'-most EST LIB3147-001-Q1-K2-D7

Seq. No. 196829
Contig ID 26603_1.R1039
5'-most EST LIB3147-001-Q1-K1-E2

Seq. No. 196830
Contig ID 26607_1.R1039
5'-most EST uC-gsflnu33B029h11b1
Method BLASTX
NCBI GI g3372671
BLAST score 527
E value 1.0e-53
Match length 140
% identity 71
NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No. 196831
Contig ID 26611_1.R1039
5'-most EST uC-gsflmaxxa060g10b1
Method BLASTX
NCBI GI g508304
BLAST score 350
E value 6.0e-33
Match length 79
% identity 80
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 196832
Contig ID 26611_2.R1039
5'-most EST LIB3147-001-Q1-K1-F3
Method BLASTX
NCBI GI g508304
BLAST score 350
E value 5.0e-33
Match length 79
% identity 80
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 196833

Contig ID	26613_1.R1039
5'-most EST	LIB3147-001-Q1-K2-F5
Method	BLASTX
NCBI GI	g4115377
BLAST score	355
E value	1.0e-33
Match length	145
% identity	48
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	196834
Contig ID	26621_1.R1039
5'-most EST	LIB3147-001-Q1-K2-G5

Seq. No.	196835
Contig ID	26626_1.R1039
5'-most EST	LIB3147-001-Q1-K2-H3

Seq. No.	196836
Contig ID	26639_1.R1039
5'-most EST	uC-gsflnu33B022g05b1
Method	BLASTX
NCBI GI	g1730502
BLAST score	345
E value	5.0e-32
Match length	225
% identity	35
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi|110903|pir||A31351 probable transmembrane protein FT27 - mouse >gi|535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	196837
Contig ID	26722_1.R1039
5'-most EST	uC-gsronu33B146h10b1
Method	BLASTX
NCBI GI	g730934
BLAST score	479
E value	6.0e-48
Match length	225
% identity	44
NCBI Description	QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi|2137015|pir||S68430 queuine tRNA-ribosyltransferase (EC 2.4.2.29), 60K chain - rabbit >gi|623547 (L37420) queuine tRNA-ribosyltransferase [Oryctolagus cuniculus]

Seq. No.	196838
Contig ID	26729_1.R1039
5'-most EST	uC-gsronu33B072c02b1
Method	BLASTX
NCBI GI	g2257756
BLAST score	319
E value	5.0e-29
Match length	255
% identity	34
NCBI Description	(U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi|3650466 (AF026917) histone deacetylase HD2-p39 [Zea

mays]

Seq. No.	196839
Contig ID	26744_1.R1039
5'-most EST	LIB3148-001-P1-K1-H10
Method	BLASTX
NCBI GI	g2754816
BLAST score	201
E value	1.0e-15
Match length	139
% identity	35
NCBI Description	(AF021346) non-race specific disease resistance protein [Arabidopsis thaliana]

Seq. No.	196840
Contig ID	26751_1.R1039
5'-most EST	LIB3166-022-P1-K1-G4
Method	BLASTX
NCBI GI	g3451411
BLAST score	789
E value	1.0e-99
Match length	242
% identity	74
NCBI Description	(Z98761) seryl-tRNA synthetase [Helianthus annuus]

Seq. No.	196841
Contig ID	26754_1.R1039
5'-most EST	LIB3148-059-Q1-K1-A10
Method	BLASTX
NCBI GI	g585960
BLAST score	211
E value	7.0e-17
Match length	43
% identity	93
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT >gi|433665|emb|CAA81412| (Z26753) Sec61 beta-subunit homolog [Arabidopsis thaliana]

Seq. No.	196842
Contig ID	26756_1.R1039
5'-most EST	LIB3149-063-Q1-K1-B8
Method	BLASTX
NCBI GI	g2688830
BLAST score	873
E value	6.0e-94
Match length	247
% identity	71
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	196843
Contig ID	26759_1.R1039
5'-most EST	uC-gsflnu33B059d04b1
Method	BLASTN
NCBI GI	g2688829
BLAST score	120
E value	2.0e-60
Match length	572

% identity	83
NCBI Description	Prunus armeniaca putative sugar transporter mRNA, complete cds
Seq. No.	196844
Contig ID	26760_1.R1039
5'-most EST	LIB3147-003-Q1-K1-B10
Seq. No.	196845
Contig ID	26762_1.R1039
5'-most EST	LIB3166-001-Q1-K1-D12
Seq. No.	196846
Contig ID	26771_1.R1039
5'-most EST	g5048188
Method	BLASTX
NCBI GI	g2832241
BLAST score	1063
E value	1.0e-116
Match length	255
% identity	79
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]
Seq. No.	196847
Contig ID	26790_1.R1039
5'-most EST	LIB3147-003-Q1-K1-D9
Seq. No.	196848
Contig ID	26815_1.R1039
5'-most EST	LIB3147-003-Q1-K1-G12
Seq. No.	196849
Contig ID	26820_1.R1039
5'-most EST	LIB3165-022-P1-K1-C6
Method	BLASTX
NCBI GI	g2245125
BLAST score	172
E value	7.0e-12
Match length	45
% identity	64
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196850
Contig ID	26822_1.R1039
5'-most EST	uC-gsflnu33B012a11b1
Method	BLASTX
NCBI GI	g3355472
BLAST score	336
E value	1.0e-31
Match length	94
% identity	71
NCBI Description	(AC004218) disease resistance response protein (206-d) like [Arabidopsis thaliana]
Seq. No.	196851
Contig ID	26830_1.R1039

5'-most EST	LIB3147-003-Q1-K1-H5
Method	BLASTN
NCBI GI	g2804257
BLAST score	34
E value	2.0e-09
Match length	194
% identity	79
NCBI Description	Arabidopsis thaliana DNA for phosphoglycerate dehydrogenase, complete cds

Seq. No.	196852
Contig ID	26840_1.R1039
5'-most EST	LIB3147-004-Q1-K1-A4
Method	BLASTX
NCBI GI	g2827710
BLAST score	412
E value	3.0e-40
Match length	92
% identity	75
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	196853
Contig ID	26842_1.R1039
5'-most EST	LIB3148-044-Q1-K1-F8
Method	BLASTX
NCBI GI	g3834330
BLAST score	150
E value	2.0e-09
Match length	81
% identity	49
NCBI Description	(AC005679) F9K20.17 [Arabidopsis thaliana]

Seq. No.	196854
Contig ID	26852_1.R1039
5'-most EST	LIB3147-004-Q1-K1-B4
Method	BLASTX
NCBI GI	g3250675
BLAST score	505
E value	4.0e-51
Match length	173
% identity	64
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	196855
Contig ID	26855_1.R1039
5'-most EST	uC-gsflnu33B029b05b1

Seq. No.	196856
Contig ID	26874_1.R1039
5'-most EST	LIB3147-004-Q1-K1-D5

Seq. No.	196857
Contig ID	26875_1.R1039
5'-most EST	g5049820
Method	BLASTX
NCBI GI	g3075391

BLAST score 427
E value 5.0e-42
Match length 98
% identity 84
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 196858
Contig ID 26886_1.R1039
5'-most EST uC-gsronu33B089g04b1

Seq. No. 196859
Contig ID 26888_1.R1039
5'-most EST uC-gsflmaxxa003g01b1
Method BLASTX
NCBI GI g3548801
BLAST score 207
E value 7.0e-36
Match length 162
% identity 52
NCBI Description (AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi|4335768|gb|AAD17445| (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 196860
Contig ID 26898_1.R1039
5'-most EST LIB3147-026-Q1-K1-D11
Method BLASTX
NCBI GI g1222552
BLAST score 671
E value 1.0e-70
Match length 141
% identity 87
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No. 196861
Contig ID 26905_1.R1039
5'-most EST LIB3147-004-Q1-K1-G2

Seq. No. 196862
Contig ID 26913_1.R1039
5'-most EST uC-gsflnu33B109g07b1
Method BLASTX
NCBI GI g129245
BLAST score 212
E value 2.0e-16
Match length 124
% identity 42
NCBI Description ORGAN SPECIFIC PROTEIN P4 >gi|72317|pir||KNPMP4 protein P4 - garden pea >gi|295829|emb|CAA35943| (X51594) P4 protein [Pisum sativum]

Seq. No. 196863
Contig ID 26913_2.R1039
5'-most EST LIB3147-023-Q1-K1-E12

Seq. No. 196864
Contig ID 26920_1.R1039

5'-most EST	uC-gsronu33B011e03b1
Method	BLASTX
NCBI GI	g2827634
BLAST score	157
E value	5.0e-10
Match length	153
% identity	37
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	196865
Contig ID	26924_2.R1039
5'-most EST	LIB3147-032-Q1-K1-D8
Method	BLASTX
NCBI GI	g1653702
BLAST score	668
E value	4.0e-70
Match length	215
% identity	61
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	196866
Contig ID	26930_1.R1039
5'-most EST	LIB3147-005-Q1-K1-A5

Seq. No.	196867
Contig ID	26933_1.R1039
5'-most EST	LIB3149-038-Q1-K1-E8

Seq. No.	196868
Contig ID	26947_1.R1039
5'-most EST	LIB3196-041-P1-M1-F10
Method	BLASTX
NCBI GI	g4455328
BLAST score	282
E value	3.0e-25
Match length	63
% identity	78
NCBI Description	(AL035525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196869
Contig ID	26957_1.R1039
5'-most EST	uC-gsflmaxxa026b08b1

Seq. No.	196870
Contig ID	26958_1.R1039
5'-most EST	LIB3166-034-P1-K1-C3
Method	BLASTX
NCBI GI	g4514716
BLAST score	254
E value	2.0e-21
Match length	137
% identity	36
NCBI Description	(AB017533) EPc [Nicotiana tabacum]

Seq. No.	196871
Contig ID	26965_1.R1039

5'-most EST	LIB3148-007-Q1-K1-H5
Method	BLASTN
NCBI GI	g166643
BLAST score	34
E value	2.0e-09
Match length	130
% identity	82
NCBI Description	Arabidopsis thaliana chlorophyll A/B-binding protein gene, complete cds

Seq. No.	196872
Contig ID	26976_1.R1039
5'-most EST	LIB3147-005-Q1-K1-F10
Method	BLASTX
NCBI GI	g4176531
BLAST score	258
E value	4.0e-22
Match length	138
% identity	43
NCBI Description	(AL035263) weak similarity to chick phosphatidylcholine-sterol acetyltransferase [Schizosaccharomyces pombe]

Seq. No.	196873
Contig ID	26989_1.R1039
5'-most EST	g5049598
Method	BLASTX
NCBI GI	g2827630
BLAST score	924
E value	1.0e-100
Match length	261
% identity	69
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	196874
Contig ID	26990_1.R1039
5'-most EST	uC-gsronu33B129d04b1
Method	BLASTX
NCBI GI	g1706329
BLAST score	1248
E value	1.0e-141
Match length	281
% identity	85
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi|2146788|pir||S65471 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC2) - Garden pea (fragment) >gi|1177605|emb|CAA91445| (Z66544) pyruvate decarboxylase [Pisum sativum]

Seq. No.	196875
Contig ID	26994_1.R1039
5'-most EST	LIB3147-005-Q1-K1-G8
Method	BLASTX
NCBI GI	g1407705
BLAST score	255
E value	6.0e-22
Match length	83
% identity	60

NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]
Seq. No.	196876
Contig ID	27014_1.R1039
5'-most EST	LIB3149-032-Q1-K1-C12
Method	BLASTX
NCBI GI	g3600047
BLAST score	441
E value	1.0e-46
Match length	148
% identity	69
NCBI Description	(AF080120) similar to elongation factor EF-Ts [Arabidopsis thaliana]
Seq. No.	196877
Contig ID	27016_1.R1039
5'-most EST	LIB3147-006-Q1-K1-A8
Method	BLASTX
NCBI GI	g2204077
BLAST score	190
E value	2.0e-14
Match length	83
% identity	48
NCBI Description	(D85623) extracellular insoluble cystatin [Daucus carota]
Seq. No.	196878
Contig ID	27038_1.R1039
5'-most EST	LIB3147-006-Q1-K1-D11
Seq. No.	196879
Contig ID	27053_1.R1039
5'-most EST	LIB3147-006-Q1-K1-F1
Method	BLASTX
NCBI GI	g4539350
BLAST score	178
E value	4.0e-20
Match length	98
% identity	52
NCBI Description	(AL035539) putative pectinesterase [Arabidopsis thaliana]
Seq. No.	196880
Contig ID	27059_1.R1039
5'-most EST	LIB3147-006-Q1-K1-F6
Method	BLASTX
NCBI GI	g2494076
BLAST score	612
E value	1.0e-63
Match length	130
% identity	88
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi|1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]
Seq. No.	196881

Contig ID	27075_1.R1039
5'-most EST	LIB3147-006-Q1-K1-H11
Method	BLASTX
NCBI GI	g2347189
BLAST score	328
E value	2.0e-30
Match length	93
% identity	72
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana] >gi|3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196882
Contig ID	27083_1.R1039
5'-most EST	uC-gsflmaxxa094e05b1

Seq. No.	196883
Contig ID	27089_1.R1039
5'-most EST	g5046995
Method	BLASTX
NCBI GI	g1008904
BLAST score	589
E value	6.0e-61
Match length	187
% identity	59
NCBI Description	(L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No.	196884
Contig ID	27102_1.R1039
5'-most EST	LIB3147-007-Q1-K1-C1
Method	BLASTX
NCBI GI	g4559346
BLAST score	414
E value	1.0e-40
Match length	131
% identity	56
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	196885
Contig ID	27103_1.R1039
5'-most EST	LIB3166-003-P1-K1-C10

Seq. No.	196886
Contig ID	27111_1.R1039
5'-most EST	LIB3189-035-P1-K1-E1

Seq. No.	196887
Contig ID	27115_1.R1039
5'-most EST	LIB3147-007-Q1-K1-D12
Method	BLASTX
NCBI GI	g3935187
BLAST score	386
E value	2.0e-37
Match length	119
% identity	66
NCBI Description	(AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No.	196888
Contig ID	27133_1.R1039
5'-most EST	LIB3147-007-Q1-K1-E9
Method	BLASTX
NCBI GI	g3395441
BLAST score	451
E value	6.0e-45
Match length	114
% identity	81
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	196889
Contig ID	27139_1.R1039
5'-most EST	LIB3147-007-Q1-K1-F3
Method	BLASTX
NCBI GI	g3135693
BLAST score	158
E value	1.0e-10
Match length	64
% identity	48
NCBI Description	(AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No.	196890
Contig ID	27146_1.R1039
5'-most EST	uC-gsflmaxxa048b03b1

Seq. No.	196891
Contig ID	27157_1.R1039
5'-most EST	LIB3165-044-Q1-K1-F4
Method	BLASTX
NCBI GI	g2651316
BLAST score	664
E value	2.0e-69
Match length	168
% identity	74
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	196892
Contig ID	27168_1.R1039
5'-most EST	LIB3147-008-Q1-K1-A12
Method	BLASTX
NCBI GI	g2498490
BLAST score	207
E value	3.0e-16
Match length	74
% identity	55
NCBI Description	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi|1854579 (L35556) Int-6 [Mus musculus] >gi|2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi|2351382 (U54562) eIF3-p48 [Homo sapiens] >gi|2688818 (U85947) Int-6 [Homo sapiens] >gi|2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi|4503521|ref|NP_001559.1|pEIF3S6| murine mammary tumor integration site 6 (oncogene homolog)

Seq. No.	196893
Contig ID	27181_1.R1039
5'-most EST	uC-gsflnu33B031a03b1

Method	BLASTX
NCBI GI	g2865416
BLAST score	411
E value	6.0e-40
Match length	147
% identity	57
NCBI Description	(AF039367) chromomethylase [Arabidopsis thaliana]

Seq. No.	196894
Contig ID	27201_1.R1039
5'-most EST	uC-gsronu33B157c02b1

Seq. No.	196895
Contig ID	27207_1.R1039
5'-most EST	uC-gsronu33B113c05b1
Method	BLASTX
NCBI GI	g1710530
BLAST score	725
E value	8.0e-77
Match length	146
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi|2129719|pir||S71256 ribosomal protein L27a - Arabidopsis thaliana >gi|1107487|emb|CAA63025| (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	196896
Contig ID	27216_1.R1039
5'-most EST	g5044398

Seq. No.	196897
Contig ID	27223_1.R1039
5'-most EST	uC-gsflnu33B144c05b1

Seq. No.	196898
Contig ID	27234_1.R1039
5'-most EST	LIB3166-039-P1-K1-H8
Method	BLASTX
NCBI GI	g1256771
BLAST score	656
E value	1.0e-68
Match length	187
% identity	67
NCBI Description	(U51270) COP9 [Spinacia oleracea]

Seq. No.	196899
Contig ID	27236_1.R1039
5'-most EST	LIB3197-031-Q1-M1-A5
Method	BLASTX
NCBI GI	g2132184
BLAST score	167
E value	1.0e-11
Match length	136
% identity	35
NCBI Description	hypothetical protein YPL093w - yeast (Saccharomyces cerevisiae) >gi|1151233 (U43281) Lpg15p [Saccharomyces cerevisiae]

Seq. No.	196900
Contig ID	27241_1.R1039
5'-most EST	uC-gsronu33B109b06b1
Method	BLASTX
NCBI GI	g3912920
BLAST score	144
E value	1.0e-08
Match length	120
% identity	33
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196901
Contig ID	27242_1.R1039
5'-most EST	LIB3272-004-P1-K1-A5
Method	BLASTX
NCBI GI	g1136741
BLAST score	448
E value	2.0e-44
Match length	138
% identity	63
NCBI Description	(D42052) predicted protein of 548 amino acids [Homo sapiens]

Seq. No.	196902
Contig ID	27246_1.R1039
5'-most EST	LIB3148-012-Q1-K1-C2
Method	BLASTX
NCBI GI	g2828291
BLAST score	382
E value	2.0e-64
Match length	276
% identity	42
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	196903
Contig ID	27268_1.R1039
5'-most EST	LIB3148-034-Q1-K1-C2

Seq. No.	196904
Contig ID	27272_1.R1039
5'-most EST	g5050170
Method	BLASTX
NCBI GI	g461736
BLAST score	622
E value	1.0e-64
Match length	196
% identity	64
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi|478786|pir||S29316 chaperonin 60 - cucurbit >gi|12546|emb|CAA50218| (X70868) chaperonin 60 [Cucurbita sp.]

Seq. No.	196905
Contig ID	27276_1.R1039
5'-most EST	LIB3189-039-P1-K1-B6
Method	BLASTX

NCBI GI	g3024017
BLAST score	533
E value	3.0e-54
Match length	115
% identity	92
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi|2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	196906
Contig ID	27276_2.R1039
5'-most EST	uC-gsflnu33B089f03b1
Method	BLASTX
NCBI GI	g3024017
BLAST score	507
E value	4.0e-51
Match length	99
% identity	97
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi|2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	196907
Contig ID	27277_1.R1039
5'-most EST	LIB3147-009-Q1-K1-C2
Method	BLASTX
NCBI GI	g3860257
BLAST score	401
E value	8.0e-39
Match length	137
% identity	58
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196908
Contig ID	27303_1.R1039
5'-most EST	LIB3148-056-Q1-K1-G8
Method	BLASTX
NCBI GI	g4567282
BLAST score	453
E value	6.0e-45
Match length	141
% identity	67
NCBI Description	(AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	196909
Contig ID	27310_1.R1039
5'-most EST	LIB3189-051-P1-K1-A10
Method	BLASTX
NCBI GI	g3033400
BLAST score	641
E value	6.0e-67
Match length	158
% identity	75
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 196910

Contig ID	27316_1.R1039
5'-most EST	LIB3166-044-P1-K1-G3
Method	BLASTX
NCBI GI	g1730771
BLAST score	162
E value	2.0e-12
Match length	172
% identity	19
NCBI Description	HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC REGION >gi|2132752|pir||S63064 probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae) >gi|1183950|emb|CAA93384| (Z69382) N1897 [Saccharomyces cerevisiae] >gi|1302054|emb|CAA96004| (Z71399) ORF YNL123w [Saccharomyces cerevisiae]

Seq. No.	196911
Contig ID	27339_1.R1039
5'-most EST	uC-gsronu33B145d07b1
Method	BLASTX
NCBI GI	g2245136
BLAST score	573
E value	2.0e-61
Match length	188
% identity	64
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	196912
Contig ID	27347_1.R1039
5'-most EST	LIB3166-050-P1-K1-G1
Method	BLASTX
NCBI GI	g2961375
BLAST score	159
E value	2.0e-10
Match length	51
% identity	55
NCBI Description	(AL022141) NAM like protein [Arabidopsis thaliana]

Seq. No.	196913
Contig ID	27355_1.R1039
5'-most EST	uC-gsflmaxxa011a04b1
Method	BLASTX
NCBI GI	g4432866
BLAST score	253
E value	2.0e-21
Match length	265
% identity	29
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	196914
Contig ID	27361_2.R1039
5'-most EST	LIB3166-044-P1-K1-G5
Method	BLASTX
NCBI GI	g4538913
BLAST score	415
E value	9.0e-41

Match length	100
% identity	79
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	196915
Contig ID	27365_1.R1039
5'-most EST	g5046579
Method	BLASTX
NCBI GI	g2789434
BLAST score	675
E value	6.0e-71
Match length	154
% identity	82
NCBI Description	(AB001389) CLB1 [Lycopersicon esculentum]

Seq. No.	196916
Contig ID	27372_1.R1039
5'-most EST	LIB3148-058-Q1-K1-D6

Seq. No.	196917
Contig ID	27376_1.R1039
5'-most EST	LIB3272-033-P1-K1-E9
Method	BLASTX
NCBI GI	g3522952
BLAST score	424
E value	8.0e-42
Match length	125
% identity	66
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	196918
Contig ID	27379_1.R1039
5'-most EST	LIB3189-050-P1-K1-C5

Seq. No.	196919
Contig ID	27384_1.R1039
5'-most EST	LIB3148-026-Q1-K1-C7

Seq. No.	196920
Contig ID	27389_1.R1039
5'-most EST	LIB3197-019-Q1-M1-H9
Method	BLASTX
NCBI GI	g3080405
BLAST score	209
E value	5.0e-21
Match length	100
% identity	52
NCBI Description	(AL022603) Lsd1 like protein [Arabidopsis thaliana] >gi|4455269|emb|CAB36805.1| (AL035527) Lsd1 like protein [Arabidopsis thaliana]

Seq. No.	196921
Contig ID	27393_1.R1039
5'-most EST	LIB3148-045-Q1-K1-B1
Method	BLASTN
NCBI GI	g3869075

BLAST score	35
E value	6.0e-10
Match length	155
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	196922
Contig ID	27399_1.R1039
5'-most EST	LIB3147-011-Q1-K1-A1
Method	BLASTX
NCBI GI	g3927830
BLAST score	217
E value	3.0e-17
Match length	57
% identity	38
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196923
Contig ID	27403_1.R1039
5'-most EST	uC-gsflmaxxa097a10b1
Method	BLASTX
NCBI GI	g4557062
BLAST score	570
E value	2.0e-58
Match length	201
% identity	58
NCBI Description	(AC007045) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196924
Contig ID	27404_1.R1039
5'-most EST	LIB3147-011-Q1-K1-A3
Method	BLASTX
NCBI GI	g3184280
BLAST score	690
E value	1.0e-72
Match length	197
% identity	66
NCBI Description	(AC004136) putative small multi-drug export protein [Arabidopsis thaliana]

Seq. No.	196925
Contig ID	27423_1.R1039
5'-most EST	LIB3147-011-Q1-K1-C2
Method	BLASTX
NCBI GI	g231736
BLAST score	370
E value	3.0e-35
Match length	91
% identity	70
NCBI Description	G2/MITOTIC-SPECIFIC CYCLIN 2 (B-LIKE CYCLIN) >gi|322706|pir||S29925 cyclin - alfalfa (fragment) >gi|322708|pir||PQ0490 cyclin 2 - alfalfa (fragment) >gi|19599|emb|CAA48675| (X68741) cyclin [Medicago sativa]

Seq. No.	196926
Contig ID	27426_1.R1039

5'-most EST	LIB3147-019-Q1-K1-E1
Seq. No.	196927
Contig ID	27429_1.R1039
5'-most EST	LIB3147-011-Q1-K1-D10
Seq. No.	196928
Contig ID	27448_1.R1039
5'-most EST	LIB3272-003-P1-K1-G5
Method	BLASTX
NCBI GI	g2245131
BLAST score	169
E value	7.0e-12
Match length	75
% identity	52
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196929
Contig ID	27462_1.R1039
5'-most EST	LIB3197-026-Q1-M1-C10
Method	BLASTX
NCBI GI	g4325345
BLAST score	958
E value	1.0e-104
Match length	253
% identity	31
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]
Seq. No.	196930
Contig ID	27467_1.R1039
5'-most EST	LIB3148-045-Q1-K1-F1
Method	BLASTX
NCBI GI	g1085384
BLAST score	318
E value	3.0e-29
Match length	74
% identity	74
NCBI Description	Sm protein F - human >gi|806564|emb|CAA59688| (X85372) Sm protein F [Homo sapiens] >gi|4507131|ref|NP_003086.1|pSNRPF| small nuclear ribonucleoprotein polypeptide F
Seq. No.	196931
Contig ID	27473_1.R1039
5'-most EST	LIB3149-013-Q1-K1-H5
Method	BLASTX
NCBI GI	g1706319
BLAST score	544
E value	2.0e-55
Match length	193
% identity	54
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi|481829|pir||S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi|416534|emb|CAA50719| (X71900)

histidine decarboxylase [Lycopersicon esculentum]

Seq. No.	196932
Contig ID	27477_1.R1039
5'-most EST	LIB3147-013-Q1-K1-A2
Method	BLASTX
NCBI GI	g2160166
BLAST score	225
E value	2.0e-27
Match length	190
% identity	39
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	196933
Contig ID	27481_1.R1039
5'-most EST	uC-gsflmaxxa067b10b1

Seq. No.	196934
Contig ID	27486_1.R1039
5'-most EST	LIB3147-013-Q1-K1-B12

Seq. No.	196935
Contig ID	27496_1.R1039
5'-most EST	LIB3147-013-Q1-K1-C11
Method	BLASTX
NCBI GI	g417488
BLAST score	337
E value	1.0e-31
Match length	69
% identity	88
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi|100452|pir||A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi|169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No.	196936
Contig ID	27499_1.R1039
5'-most EST	LIB3147-013-Q1-K1-C3
Method	BLASTX
NCBI GI	g1172995
BLAST score	287
E value	1.0e-25
Match length	117
% identity	55
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi|1083790|pir||S52084 ribosomal protein L22 - rat >gi|710295|emb|CAA55204| (X78444) ribosomal protein L22 [Rattus norvegicus] >gi|1093952|prf||2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	196937
Contig ID	27506_1.R1039
5'-most EST	uC-gsronu33B001f04b1

Seq. No.	196938
Contig ID	27507_1.R1039
5'-most EST	LIB3166-001-Q1-K1-H3

Method	BLASTX
NCBI GI	g285286
BLAST score	262
E value	2.0e-22
Match length	100
% identity	49
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	196939
Contig ID	27510_1.R1039
5'-most EST	LIB3148-055-Q1-K1-C4

Seq. No.	196940
Contig ID	27514_1.R1039
5'-most EST	LIB3147-013-Q1-K1-D8
Method	BLASTX
NCBI GI	g2104681
BLAST score	233
E value	3.0e-19
Match length	130
% identity	45
NCBI Description	(X97907) transcription factor [Vicia faba]

Seq. No.	196941
Contig ID	27531_1.R1039
5'-most EST	LIB3149-017-Q1-K1-C9

Seq. No.	196942
Contig ID	27534_1.R1039
5'-most EST	LIB3147-013-Q1-K1-F5
Method	BLASTX
NCBI GI	g2245066
BLAST score	199
E value	5.0e-33
Match length	133
% identity	53
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	196943
Contig ID	27536_1.R1039
5'-most EST	LIB3149-033-Q1-K1-H10

Seq. No.	196944
Contig ID	27537_1.R1039
5'-most EST	uC-gsronu33B036e08b1
Method	BLASTX
NCBI GI	g4415933
BLAST score	254
E value	1.0e-21
Match length	71
% identity	66
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi|4559390|gb|AAD23050.1|AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	196945
Contig ID	27540_1.R1039
5'-most EST	uC-gsflnu33B027g04b1
Method	BLASTX
NCBI GI	g3334299
BLAST score	946
E value	1.0e-102
Match length	197
% identity	93
NCBI Description	PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi|2315211|emb|CAA74725| (Y14339) proteasome alpha subunit [Lycopersicon esculentum]

Seq. No.	196946
Contig ID	27541_1.R1039
5'-most EST	g5050555
Method	BLASTX
NCBI GI	g4220532
BLAST score	220
E value	1.0e-17
Match length	106
% identity	52
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	196947
Contig ID	27544_1.R1039
5'-most EST	LIB3148-002-P1-K1-C12
Method	BLASTX
NCBI GI	g585963
BLAST score	263
E value	7.0e-23
Match length	69
% identity	78
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	196948
Contig ID	27544_2.R1039
5'-most EST	LIB3149-021-Q1-K1-A5
Method	BLASTX
NCBI GI	g585963
BLAST score	262
E value	8.0e-23
Match length	69
% identity	78
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	196949
Contig ID	27544_3.R1039
5'-most EST	LIB3149-018-Q1-K1-C7
Method	BLASTX
NCBI GI	g585963
BLAST score	264
E value	6.0e-23
Match length	69
% identity	78
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	196950
Contig ID	27544_4.R1039
5'-most EST	LIB3189-004-P1-K1-C1
Method	BLASTX
NCBI GI	g585963
BLAST score	255
E value	6.0e-22
Match length	69
% identity	77
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	196951
Contig ID	27546_1.R1039
5'-most EST	LIB3147-013-Q1-K1-H3

Seq. No.	196952
Contig ID	27569_1.R1039
5'-most EST	LIB3147-015-Q1-K1-B8
Method	BLASTX
NCBI GI	g2129564
BLAST score	146
E value	5.0e-09
Match length	148
% identity	38
NCBI Description	cryptochrome 2 apoprotein - Arabidopsis thaliana

Seq. No.	196953
Contig ID	27574_1.R1039
5'-most EST	LIB3147-015-Q1-K1-C2

Seq. No.	196954
Contig ID	27581_1.R1039
5'-most EST	LIB3147-015-Q1-K1-C9
Method	BLASTX
NCBI GI	g1754795
BLAST score	849
E value	2.0e-91
Match length	168
% identity	89
NCBI Description	(U59477) omega-3 fatty acid desaturase [Perilla frutescens]

Seq. No.	196955
Contig ID	27605_1.R1039
5'-most EST	LIB3166-017-P1-K1-H6
Method	BLASTX
NCBI GI	g2213884
BLAST score	676
E value	8.0e-71
Match length	181
% identity	70
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	196956
Contig ID	27607_1.R1039
5'-most EST	uC-gsflnu33B100a09b1

Seq. No.	196957
Contig ID	27610_1.R1039
5'-most EST	LIB3147-015-Q1-K1-F4

Seq. No.	196958
Contig ID	27649_1.R1039
5'-most EST	LIB3147-017-Q1-K1-B6
Method	BLASTX
NCBI GI	g2401257
BLAST score	325
E value	4.0e-30
Match length	138
% identity	48
NCBI Description	(D63951) TBZ17 [Nicotiana tabacum]

Seq. No.	196959
Contig ID	27655_1.R1039
5'-most EST	LIB3147-017-Q1-K1-C3

Seq. No.	196960
Contig ID	27661_1.R1039
5'-most EST	g5048023
Method	BLASTX
NCBI GI	g1079063
BLAST score	167
E value	3.0e-11
Match length	162
% identity	27
NCBI Description	deep orange protein - fruit fly (Drosophila melanogaster) >gi|798832|emb|CAA60382| (X86683) deep orange (dor) [Drosophila melanogaster]

Seq. No.	196961
Contig ID	27678_2.R1039
5'-most EST	g5045700
Method	BLASTX
NCBI GI	g4191783
BLAST score	201
E value	2.0e-15
Match length	51
% identity	73
NCBI Description	(AC005917) hypothetical protein [Arabidopsis thaliana]

Seq. No.	196962
Contig ID	27682_1.R1039
5'-most EST	LIB3166-030-P1-K1-G7
Method	BLASTX
NCBI GI	g4512653
BLAST score	1186
E value	1.0e-130
Match length	302
% identity	56
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	196963
Contig ID	27683_1.R1039
5'-most EST	LIB3147-023-Q1-K1-E4

Seq. No.	196964
Contig ID	27685_1.R1039
5'-most EST	uC-gsflmaxxa027g09b1
Method	BLASTX
NCBI GI	g1362091
BLAST score	355
E value	2.0e-33
Match length	76
% identity	86
NCBI Description	cellulase (EC 3.2.1.4) precursor - tomato >gi|924622 (U20590) endo-1,4-beta-glucanase precursor [Solanum lycopersicum]

Seq. No.	196965
Contig ID	27692_1.R1039
5'-most EST	LIB3147-017-Q1-K1-H10

Seq. No.	196966
Contig ID	27703_1.R1039
5'-most EST	LIB3147-018-Q1-K1-E10
Method	BLASTX
NCBI GI	g1708993
BLAST score	537
E value	5.0e-55
Match length	144
% identity	73
NCBI Description	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) >gi|2129567|pir||S61429 cystathionine beta-lyase (EC 4.4.1.8) - Arabidopsis thaliana >gi|704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana]

Seq. No.	196967
Contig ID	27707_1.R1039
5'-most EST	g5049420
Method	BLASTX
NCBI GI	g4008006
BLAST score	619
E value	2.0e-64
Match length	198
% identity	64
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	196968
Contig ID	27710_1.R1039
5'-most EST	LIB3147-039-Q1-K1-C7
Method	BLASTX
NCBI GI	g3935165
BLAST score	216
E value	2.0e-24
Match length	109
% identity	68
NCBI Description	(AC004557) F17L21.8 [Arabidopsis thaliana]

Seq. No.	196969

Contig ID	27727_1.R1039
5'-most EST	uC-gsflnu33B005h03b1
Seq. No.	196970
Contig ID	27728_1.R1039
5'-most EST	LIB3147-019-Q1-K1-A4
Seq. No.	196971
Contig ID	27732_1.R1039
5'-most EST	LIB3272-041-P1-K1-H11
Method	BLASTX
NCBI GI	g3860008
BLAST score	244
E value	2.0e-20
Match length	140
% identity	34
NCBI Description	(AF091085) unknown [Homo sapiens]
Seq. No.	196972
Contig ID	27738_1.R1039
5'-most EST	LIB3272-041-P1-K1-D8
Method	BLASTX
NCBI GI	g4105772
BLAST score	743
E value	6.0e-79
Match length	177
% identity	73
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]
Seq. No.	196973
Contig ID	27766_1.R1039
5'-most EST	uC-gsflmaxxa096e11b1
Method	BLASTX
NCBI GI	g4567249
BLAST score	1153
E value	1.0e-127
Match length	289
% identity	73
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196974
Contig ID	27768_1.R1039
5'-most EST	uC-gsflnu33B075h02b1
Method	BLASTX
NCBI GI	g130185
BLAST score	356
E value	1.0e-33
Match length	91
% identity	73
NCBI Description	PHYTOCHROME A >gi|65877|pir||FKPUZ phytochrome - zucchini >gi|167501 (M15265) phytochrome [Cucurbita pepo] >gi|225435|prf||1303260A phytochrome [Cucurbita pepo]
Seq. No.	196975
Contig ID	27770_1.R1039
5'-most EST	LIB3147-019-Q1-K1-E6
Method	BLASTX

NCBI GI	g2245001
BLAST score	487
E value	6.0e-49
Match length	102
% identity	89
NCBI Description	(Z97341) similarity to NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana]

Seq. No.	196976
Contig ID	27771_1.R1039
5'-most EST	uC-gsronu33B012f10b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	44
E value	2.0e-15
Match length	199
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	196977
Contig ID	27773_1.R1039
5'-most EST	LIB3147-019-Q1-K1-E9
Method	BLASTX
NCBI GI	g4454452
BLAST score	464
E value	3.0e-46
Match length	124
% identity	67
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	196978
Contig ID	27777_1.R1039
5'-most EST	LIB3147-019-Q1-K1-F2
Method	BLASTX
NCBI GI	g3334230
BLAST score	444
E value	5.0e-44
Match length	168
% identity	49
NCBI Description	D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi|2828803 (U84197) D-hydantoinase [Pseudomonas putida]

Seq. No.	196979
Contig ID	27793_1.R1039
5'-most EST	g5046913
Method	BLASTX
NCBI GI	g3549679
BLAST score	347
E value	2.0e-32
Match length	130
% identity	55
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	196980
Contig ID	27808_1.R1039
5'-most EST	LIB3149-025-Q1-K1-C3

Method	BLASTX
NCBI GI	g3660187
BLAST score	355
E value	1.0e-33
Match length	93
% identity	67
NCBI Description	Chain A, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi|3660188|pdb|1E2C|B Chain B, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi|3660189|pdb|1E2C|C Chain C, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi|4388942|pdb|2E2C| E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins

Seq. No.	196981
Contig ID	27813_1.R1039
5'-most EST	LIB3147-020-Q1-K1-B1
Method	BLASTX
NCBI GI	g2494034
BLAST score	651
E value	4.0e-82
Match length	178
% identity	88
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi|2129573|pir||S71467 diacylglycerol kinase - Arabidopsis thaliana >gi|1374772|dbj|BAA09856| (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	196982
Contig ID	27830_1.R1039
5'-most EST	g5047539
Method	BLASTX
NCBI GI	g107350
BLAST score	385
E value	7.0e-37
Match length	214
% identity	39
NCBI Description	Pm5 protein - human >gi|1335273|emb|CAA40655| (X57398) pm5 protein [Homo sapiens]

Seq. No.	196983
Contig ID	27832_1.R1039
5'-most EST	LIB3148-038-Q1-K1-A12
Method	BLASTX
NCBI GI	g4185133
BLAST score	138
E value	3.0e-15
Match length	76
% identity	61
NCBI Description	(AC005724) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	196984
Contig ID	27850_1.R1039
5'-most EST	uC-gsronu33B019b03b1

Seq. No.	196985
Contig ID	27851_1.R1039
5'-most EST	LIB3147-020-Q1-K1-E8
Method	BLASTX
NCBI GI	g1172558
BLAST score	225
E value	2.0e-18
Match length	72
% identity	60
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi|480122|pir||S36454 porin por1 - garden pea >gi|396819|emb|CAA80988| (Z25540) Porin [Pisum sativum]

Seq. No.	196986
Contig ID	27864_1.R1039
5'-most EST	LIB3147-020-Q1-K1-G1

Seq. No.	196987
Contig ID	27876_1.R1039
5'-most EST	LIB3147-020-Q1-K1-H8

Seq. No.	196988
Contig ID	27891_1.R1039
5'-most EST	LIB3147-021-Q1-K1-E11

Seq. No.	196989
Contig ID	27901_1.R1039
5'-most EST	LIB3196-058-P1-M1-A3
Method	BLASTX
NCBI GI	g1518540
BLAST score	1107
E value	1.0e-121
Match length	235
% identity	86
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	196990
Contig ID	27903_1.R1039
5'-most EST	LIB3147-022-Q1-K1-A3
Method	BLASTX
NCBI GI	g1911774
BLAST score	187
E value	1.0e-13
Match length	78
% identity	41
NCBI Description	(S83364) putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]

Seq. No.	196991
Contig ID	27904_1.R1039
5'-most EST	LIB3149-021-Q1-K1-D9
Method	BLASTX
NCBI GI	g2677830
BLAST score	755
E value	3.0e-80
Match length	164

% identity	90
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]
Seq. No.	196992
Contig ID	27915_1.R1039
5'-most EST	LIB3147-022-Q1-K1-B5
Seq. No.	196993
Contig ID	27921_1.R1039
5'-most EST	LIB3166-035-P1-K1-E7
Seq. No.	196994
Contig ID	27947_1.R1039
5'-most EST	g5047251
Method	BLASTX
NCBI GI	g731651
BLAST score	390
E value	1.0e-37
Match length	211
% identity	39
NCBI Description	HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN PUT2-SRB2 INTERGENIC REGION >gi|626608|pir||S46746 hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi|488180 (U00062) Yhr039cp [Saccharomyces cerevisiae]
Seq. No.	196995
Contig ID	27948_1.R1039
5'-most EST	uC-gsronu33B146e03b1
Method	BLASTX
NCBI GI	g2464914
BLAST score	302
E value	3.0e-27
Match length	126
% identity	50
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.	196996
Contig ID	27957_1.R1039
5'-most EST	uC-gsflmaxxa067c11b1
Seq. No.	196997
Contig ID	27974_1.R1039
5'-most EST	LIB3147-022-Q1-K1-H8
Method	BLASTX
NCBI GI	g3098571
BLAST score	271
E value	1.0e-23
Match length	126
% identity	42
NCBI Description	(AF049028) BURP domain containing protein [Brassica napus]
Seq. No.	196998
Contig ID	27990_1.R1039
5'-most EST	LIB3147-024-Q1-K1-C7
Method	BLASTX
NCBI GI	g2811278

BLAST score	746
E value	4.0e-79
Match length	176
% identity	79
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	196999
Contig ID	27999_1.R1039
5'-most EST	LIB3147-023-Q1-K1-C2

Seq. No.	197000
Contig ID	28000_1.R1039
5'-most EST	g5045471
Method	BLASTX
NCBI GI	g3142296
BLAST score	241
E value	4.0e-20
Match length	91
% identity	52
NCBI Description	(AC002411) Contains similarity to hypothetical mitochondrial import receptor subunit gb|Z98597 from S. pombe. ESTs gb|T45575 and gb|Z26435 and gb|AA394576 come from this gene. [Arabidopsis thaliana]

Seq. No.	197001
Contig ID	28001_1.R1039
5'-most EST	LIB3166-037-P1-K1-A9

Seq. No.	197002
Contig ID	28013_1.R1039
5'-most EST	LIB3148-022-Q1-K1-D3

Seq. No.	197003
Contig ID	28024_1.R1039
5'-most EST	g5044893

Seq. No.	197004
Contig ID	28028_1.R1039
5'-most EST	uC-gsflnu33B109g05b1
Method	BLASTX
NCBI GI	g4103635
BLAST score	303
E value	3.0e-27
Match length	115
% identity	47
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	197005
Contig ID	28031_1.R1039
5'-most EST	uC-gsronu33B062g12b1
Method	BLASTX
NCBI GI	g3924612
BLAST score	485
E value	1.0e-48
Match length	104
% identity	89
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis

thaliana] >gi|4263511|gb|AAD15337| (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	197006
Contig ID	28043_1.R1039
5'-most EST	LIB3272-050-P1-K1-C8
Method	BLASTX
NCBI GI	g3759184
BLAST score	313
E value	1.0e-28
Match length	103
% identity	59
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	197007
Contig ID	28047_1.R1039
5'-most EST	LIB3196-045-P1-M1-H1
Method	BLASTX
NCBI GI	g3776005
BLAST score	628
E value	2.0e-95
Match length	187
% identity	95
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	197008
Contig ID	28048_1.R1039
5'-most EST	uC-gsronu33B080d07b1

Seq. No.	197009
Contig ID	28060_1.R1039
5'-most EST	LIB3189-043-P1-K1-D10
Method	BLASTX
NCBI GI	g3202042
BLAST score	832
E value	2.0e-89
Match length	192
% identity	83
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	197010
Contig ID	28061_1.R1039
5'-most EST	uC-gsronu33B002f02b1
Method	BLASTN
NCBI GI	g2645198
BLAST score	42
E value	3.0e-14
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	197011
Contig ID	28069_1.R1039
5'-most EST	g5048094
Method	BLASTX

NCBI GI	g3157943
BLAST score	439
E value	4.0e-43
Match length	148
% identity	60
NCBI Description	(AC002131) Contains similarity to BAP31 protein gb|X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	197012
Contig ID	28080_1.R1039
5'-most EST	LIB3147-024-Q1-K1-E10
Method	BLASTN
NCBI GI	g170293
BLAST score	44
E value	2.0e-15
Match length	136
% identity	83
NCBI Description	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) mRNA, complete cds

Seq. No.	197013
Contig ID	28090_1.R1039
5'-most EST	LIB3147-024-Q1-K1-F1

Seq. No.	197014
Contig ID	28103_1.R1039
5'-most EST	LIB3148-022-Q1-K1-G7

Seq. No.	197015
Contig ID	28103_2.R1039
5'-most EST	LIB3147-024-Q1-K1-G2

Seq. No.	197016
Contig ID	28107_1.R1039
5'-most EST	LIB3166-052-P1-K1-B11
Method	BLASTX
NCBI GI	g2072626
BLAST score	447
E value	3.0e-44
Match length	136
% identity	66
NCBI Description	(Y12904) hypothetical protein [Arabidopsis thaliana] >gi|3281856|emb|CAA19751| (AL031004) Transcription factor II homolog [Arabidopsis thaliana]

Seq. No.	197017
Contig ID	28117_1.R1039
5'-most EST	uC-gsronu33B130e04b1

Seq. No.	197018
Contig ID	28122_1.R1039
5'-most EST	LIB3147-055-Q1-K1-E7
Method	BLASTX
NCBI GI	g1778145
BLAST score	640
E value	9.0e-67
Match length	178

% identity	72
NCBI Description	(U66402) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum]

Seq. No.	197019
Contig ID	28124_1.R1039
5'-most EST	LIB3147-026-Q1-K1-B1
Method	BLASTX
NCBI GI	g2529662
BLAST score	314
E value	3.0e-37
Match length	107
% identity	81
NCBI Description	(AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi|3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

Seq. No.	197020
Contig ID	28138_1.R1039
5'-most EST	g5048900
Method	BLASTX
NCBI GI	g2865623
BLAST score	862
E value	9.0e-93
Match length	193
% identity	85
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	197021
Contig ID	28145_1.R1039
5'-most EST	LIB3147-026-Q1-K1-D1
Method	BLASTX
NCBI GI	g3135611
BLAST score	240
E value	5.0e-20
Match length	55
% identity	80
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	197022
Contig ID	28155_1.R1039
5'-most EST	g5049759
Method	BLASTX
NCBI GI	g2493495
BLAST score	382
E value	5.0e-61
Match length	154
% identity	77
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi|2129878|pir||S72370 carboxypeptidase - garden pea (fragment) >gi|1089904|emb|CAA92216| (Z68130) carboxypeptidase [Pisum sativum] >gi|1587217|prf||2206338A Ser carboxypeptidase [Pisum sativum]

Seq. No.	197023
Contig ID	28175_1.R1039
5'-most EST	LIB3196-043-P1-M1-F9
Method	BLASTX
NCBI GI	g2213610
BLAST score	227
E value	1.0e-18
Match length	108
% identity	44
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	197024
Contig ID	28176_1.R1039
5'-most EST	LIB3147-026-Q1-K1-G9
Method	BLASTX
NCBI GI	g72307
BLAST score	146
E value	2.0e-21
Match length	142
% identity	49
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi|168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No.	197025
Contig ID	28192_1.R1039
5'-most EST	g5048121
Method	BLASTX
NCBI GI	g2262100
BLAST score	641
E value	6.0e-67
Match length	156
% identity	77
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	197026
Contig ID	28194_1.R1039
5'-most EST	LIB3147-027-Q1-K1-A12

Seq. No.	197027
Contig ID	28198_1.R1039
5'-most EST	g5044337
Method	BLASTX
NCBI GI	g322752
BLAST score	293
E value	4.0e-26
Match length	161
% identity	40
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi|559921|emb|CAA56570| (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	197028
Contig ID	28216_1.R1039
5'-most EST	LIB3166-029-P1-K1-A9
Method	BLASTX
NCBI GI	g3873408
BLAST score	151
E value	1.0e-09

Match length	119
% identity	38
NCBI Description	(L76926) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	197029
Contig ID	28216_2.R1039
5'-most EST	g5050392
Method	BLASTX
NCBI GI	g2244955
BLAST score	283
E value	6.0e-26
Match length	202
% identity	38
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197030
Contig ID	28217_1.R1039
5'-most EST	uC-gsronu33B116f07b1

Seq. No.	197031
Contig ID	28224_1.R1039
5'-most EST	LIB3147-027-Q1-K1-E3
Method	BLASTX
NCBI GI	g1731146
BLAST score	203
E value	6.0e-16
Match length	85
% identity	47
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi|3881615|emb|CAA87435| (Z47358) similar to YJU2 protein [Caenorhabditis elegans]

Seq. No.	197032
Contig ID	28234_1.R1039
5'-most EST	LIB3147-027-Q1-K1-F5

Seq. No.	197033
Contig ID	28239_1.R1039
5'-most EST	uC-gsflnu33B136h06b1

Seq. No.	197034
Contig ID	28239_2.R1039
5'-most EST	LIB3272-039-P1-K1-G2

Seq. No.	197035
Contig ID	28249_1.R1039
5'-most EST	LIB3147-027-Q1-K1-H7
Method	BLASTX
NCBI GI	g1432056
BLAST score	194
E value	1.0e-14
Match length	110
% identity	45
NCBI Description	(U56834) WRKY3 [Petroselinum crispum]

Seq. No.	197036

Contig ID	28251_1.R1039
5'-most EST	LIB3197-051-Q1-M1-F12
Method	BLASTX
NCBI GI	g4580389
BLAST score	514
E value	2.0e-52
Match length	134
% identity	72
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	197037
Contig ID	28262_1.R1039
5'-most EST	LIB3147-028-Q1-K1-D11

Seq. No.	197038
Contig ID	28263_1.R1039
5'-most EST	LIB3147-028-Q1-K1-D5

Seq. No.	197039
Contig ID	28269_1.R1039
5'-most EST	LIB3147-028-Q1-K1-E12
Method	BLASTX
NCBI GI	g1172635
BLAST score	1012
E value	1.0e-113
Match length	250
% identity	89
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi|556558|dbj|BAA04615| (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	197040
Contig ID	28284_1.R1039
5'-most EST	uC-gsronu33B098e11b1
Method	BLASTX
NCBI GI	g2746335
BLAST score	160
E value	9.0e-11
Match length	72
% identity	44
NCBI Description	(AF037205) RING zinc finger protein [Mus musculus]

Seq. No.	197041
Contig ID	28289_1.R1039
5'-most EST	LIB3147-046-Q1-K1-E9
Method	BLASTX
NCBI GI	g2642158
BLAST score	300
E value	6.0e-27
Match length	107
% identity	54
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197042
Contig ID	28290_1.R1039
5'-most EST	LIB3189-003-P1-K1-H7

Seq. No.	197043
Contig ID	28299_1.R1039
5'-most EST	uC-gsronu33B154a07b2
Method	BLASTX
NCBI GI	g3367593
BLAST score	720
E value	2.0e-76
Match length	175
% identity	75
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi|3805841|emb|CAA21461| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	197044
Contig ID	28303_1.R1039
5'-most EST	g5047238
Method	BLASTX
NCBI GI	g445612
BLAST score	582
E value	5.0e-60
Match length	122
% identity	92
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	197045
Contig ID	28303_2.R1039
5'-most EST	g3326358
Method	BLASTX
NCBI GI	g445612
BLAST score	600
E value	3.0e-62
Match length	122
% identity	96
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	197046
Contig ID	28303_3.R1039
5'-most EST	uC-gsflmaxxa026b02b1
Method	BLASTX
NCBI GI	g445612
BLAST score	596
E value	1.0e-61
Match length	122
% identity	95
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	197047
Contig ID	28332_1.R1039
5'-most EST	LIB3147-029-Q1-K1-E3

Seq. No.	197048
Contig ID	28334_1.R1039
5'-most EST	LIB3147-029-Q1-K1-E5

Seq. No.	197049
Contig ID	28339_1.R1039
5'-most EST	LIB3147-029-Q1-K1-F1

Seq. No.	197050
Contig ID	28341_1.R1039
5'-most EST	g5050324
Method	BLASTX
NCBI GI	g3877595
BLAST score	409
E value	1.0e-39
Match length	166
% identity	52
NCBI Description	(Z79696) predicted using Genefinder; Similarity to Human HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from this gene; cDNA EST yk281b1.3 comes from this gene [Caenorhabditis elegans] >gi|3879853|emb|CAB04734| (Z81592) predicted using Genefinder; Similarity to Human HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from this gene; cDNA EST yk281b1.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	197051
Contig ID	28341_3.R1039
5'-most EST	LIB3149-060-Q1-K1-H2
Method	BLASTX
NCBI GI	g4544409
BLAST score	266
E value	6.0e-23
Match length	85
% identity	62
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No.	197052
Contig ID	28342_1.R1039
5'-most EST	uC-gsflmaxxa057f03b1

Seq. No.	197053
Contig ID	28355_1.R1039
5'-most EST	LIB3147-029-Q1-K1-G4
Method	BLASTX
NCBI GI	g4206122
BLAST score	551
E value	2.0e-56
Match length	132
% identity	78
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	197054
Contig ID	28366_1.R1039
5'-most EST	LIB3147-029-Q1-K1-H6
Method	BLASTN
NCBI GI	g3449313
BLAST score	34
E value	1.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	197055
Contig ID	28373_1.R1039
5'-most EST	LIB3147-031-Q1-K1-A7

Seq. No.	197056
Contig ID	28379_2.R1039
5'-most EST	LIB3147-031-Q1-K1-B3

Seq. No.	197057
Contig ID	28389_1.R1039
5'-most EST	LIB3147-031-Q1-K1-C5

Seq. No.	197058
Contig ID	28396_1.R1039
5'-most EST	g5046070
Method	BLASTX
NCBI GI	g399046
BLAST score	716
E value	1.0e-75
Match length	170
% identity	82
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi|99657|pir||S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi|16164|emb|CAA41497| (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	197059
Contig ID	28397_1.R1039
5'-most EST	g5047816
Method	BLASTX
NCBI GI	g3414809
BLAST score	195
E value	2.0e-14
Match length	217
% identity	3
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	197060
Contig ID	28404_1.R1039
5'-most EST	g5044870
Method	BLASTX
NCBI GI	g3329368
BLAST score	876
E value	2.0e-94
Match length	272
% identity	62
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	197061
Contig ID	28404_2.R1039
5'-most EST	LIB3147-031-Q1-K1-E1
Method	BLASTX

NCBI GI	g3329368
BLAST score	583
E value	3.0e-60
Match length	162
% identity	69
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	197062
Contig ID	28413_1.R1039
5'-most EST	LIB3147-031-Q1-K1-E8
Method	BLASTX
NCBI GI	g2501102
BLAST score	506
E value	2.0e-51
Match length	147
% identity	70
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi|1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi|1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi|3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi|1587182|prf||2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	197063
Contig ID	28427_1.R1039
5'-most EST	LIB3147-031-Q1-K1-G11
Method	BLASTX
NCBI GI	g4455274
BLAST score	492
E value	2.0e-49
Match length	127
% identity	76
NCBI Description	(AL035527) spliceosome associated protein-like [Arabidopsis thaliana]

Seq. No.	197064
Contig ID	28437_1.R1039
5'-most EST	uC-gsronu33B129a05b1
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi|70771|pir||HSZM4 histone H4 - maize >gi|81642|pir||S06904 histone H4 - Arabidopsis thaliana >gi|2119028|pir||S60475 histone H4 - garden pea >gi|21795|emb|CAA24924| (X00043) histone H4 [Triticum aestivum] >gi|166740 (M17132) histone H4 [Arabidopsis thaliana] >gi|166742 (M17133) histone H4 [Arabidopsis thaliana] >gi|168499 (M36659) histone H4 (H4C13) [Zea mays] >gi|168501 (M13370) histone H4 [Zea mays] >gi|168503 (M13377) histone H4 [Zea mays] >gi|498898 (U10042) histone H4 homolog [Pisum sativum] >gi|1806285|emb|CAB01914| (Z79638) histone H4 homologue [Sesbania rostrata] >gi|3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi|4580385|gb|AAD24364.1|AC007184_4 (AC007184) histone H4

[Arabidopsis thaliana] >gi|225838|prf||1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	197065
Contig ID	28455_1.R1039
5'-most EST	LIB3165-042-Q1-K1-G11
Method	BLASTX
NCBI GI	g4262181
BLAST score	212
E value	2.0e-16
Match length	191
% identity	37
NCBI Description	(AC005508) 37496 [Arabidopsis thaliana]

Seq. No.	197066
Contig ID	28465_1.R1039
5'-most EST	LIB3166-029-P1-K1-A6
Method	BLASTX
NCBI GI	g485514
BLAST score	314
E value	7.0e-29
Match length	68
% identity	88
NCBI Description	ADR11-2 protein - soybean (fragment) >gi|296443|emb|CAA49341| (X69640) auxin down regulated [Glycine max]

Seq. No.	197067
Contig ID	28483_1.R1039
5'-most EST	LIB3165-049-Q1-K1-E12
Method	BLASTX
NCBI GI	g2281633
BLAST score	468
E value	6.0e-51
Match length	182
% identity	64
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	197068
Contig ID	28492_1.R1039
5'-most EST	LIB3147-032-Q1-K1-E12
Method	BLASTX
NCBI GI	g322641
BLAST score	467
E value	1.0e-46
Match length	141
% identity	55
NCBI Description	beta-1,3-glucanase homolog (clone A6) - rape (fragment) >gi|17738|emb|CAA49513| (X69887) beta-1,3-glucanase homologue [Brassica napus]

Seq. No.	197069
Contig ID	28505_1.R1039
5'-most EST	LIB3149-063-Q1-K1-C9
Method	BLASTX
NCBI GI	g2244970

BLAST score	418
E value	5.0e-41
Match length	127
% identity	59
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi|2326365|emb|CAA74765| (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	197070
Contig ID	28507_1.R1039
5'-most EST	g5046183
Method	BLASTX
NCBI GI	g2062172
BLAST score	594
E value	5.0e-63
Match length	180
% identity	68
NCBI Description	(AC001645) unknown protein [Arabidopsis thaliana]

Seq. No.	197071
Contig ID	28513_1.R1039
5'-most EST	LIB3166-017-P1-K1-H12
Method	BLASTX
NCBI GI	g2129517
BLAST score	1641
E value	0.0e+00
Match length	355
% identity	85
NCBI Description	24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No.	197072
Contig ID	28522_1.R1039
5'-most EST	LIB3166-019-P1-K1-B3
Method	BLASTX
NCBI GI	g4406780
BLAST score	873
E value	3.0e-94
Match length	203
% identity	82
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	197073
Contig ID	28536_1.R1039
5'-most EST	LIB3147-033-Q1-K1-B1

Seq. No.	197074
Contig ID	28551_1.R1039
5'-most EST	LIB3272-018-P1-K1-B6

Seq. No.	197075
Contig ID	28561_1.R1039
5'-most EST	LIB3166-042-P1-K1-G5
Method	BLASTX
NCBI GI	g4006924
BLAST score	1372

E value	1.0e-152
Match length	313
% identity	80
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	197076
Contig ID	28562_1.R1039
5'-most EST	LIB3165-016-P1-K1-E6
Method	BLASTX
NCBI GI	g4544427
BLAST score	649
E value	7.0e-68
Match length	145
% identity	85
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	197077
Contig ID	28564_1.R1039
5'-most EST	uC-gsronu33B145g02b1
Method	BLASTX
NCBI GI	g549732
BLAST score	215
E value	4.0e-17
Match length	67
% identity	55
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi|481110|pir||S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi|407488|emb|CAA81494| (Z26877) unknown [Saccharomyces cerevisiae] >gi|486279|emb|CAA82002| (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi|1582545|prf||2118404F ORF [Saccharomyces cerevisiae]

Seq. No.	197078
Contig ID	28565_1.R1039
5'-most EST	uC-gsronu33B141c02b1
Method	BLASTX
NCBI GI	g3522952
BLAST score	617
E value	5.0e-64
Match length	247
% identity	51
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	197079
Contig ID	28567_1.R1039
5'-most EST	g5044840
Method	BLASTX
NCBI GI	g2827554
BLAST score	124
E value	1.0e-08
Match length	156
% identity	31
NCBI Description	(AL021635) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No.	197080
Contig ID	28570_1.R1039
5'-most EST	LIB3147-033-Q1-K1-E12
Method	BLASTX
NCBI GI	g2244832
BLAST score	166
E value	2.0e-11
Match length	63
% identity	56
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197081
Contig ID	28572_1.R1039
5'-most EST	LIB3197-059-Q1-M1-G5
Method	BLASTX
NCBI GI	g3063710
BLAST score	766
E value	1.0e-81
Match length	213
% identity	69
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	197082
Contig ID	28576_1.R1039
5'-most EST	LIB3147-033-Q1-K1-F10

Seq. No.	197083
Contig ID	28578_1.R1039
5'-most EST	LIB3147-033-Q1-K1-F12
Method	BLASTX
NCBI GI	g3786011
BLAST score	665
E value	5.0e-70
Match length	146
% identity	85
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	197084
Contig ID	28580_1.R1039
5'-most EST	LIB3147-033-Q1-K1-F4
Method	BLASTX
NCBI GI	g543868
BLAST score	334
E value	3.0e-31
Match length	70
% identity	86
NCBI Description	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi|1076683|pir||B47493 H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - sweet potato >gi|303625|dbj|BAA03527| (D14700) F1-ATPase epsilon-subunit [Ipomoea batatas]

Seq. No.	197085
Contig ID	28596_1.R1039

5'-most EST	LIB3147-034-Q1-K1-A1
Method	BLASTX
NCBI GI	g3341679
BLAST score	1215
E value	1.0e-134
Match length	348
% identity	67
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	197086
Contig ID	28598_1.R1039
5'-most EST	g5047504
Method	BLASTX
NCBI GI	g134584
BLAST score	442
E value	1.0e-43
Match length	182
% identity	51
NCBI Description	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1 >gi|479804|pir||S35457 SNF2 protein homolog - human >gi|292496 (M88163) transcription activator [Homo sapiens] >gi|4507067|ref|NP_003060.1|pSMARCA1| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member

Seq. No.	197087
Contig ID	28615_1.R1039
5'-most EST	LIB3148-010-Q1-K1-G6

Seq. No.	197088
Contig ID	28624_1.R1039
5'-most EST	g5046180
Method	BLASTX
NCBI GI	g3258570
BLAST score	662
E value	2.0e-69
Match length	185
% identity	68
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	197089
Contig ID	28647_1.R1039
5'-most EST	LIB3147-034-Q1-K1-E9
Method	BLASTX
NCBI GI	g3236258
BLAST score	322
E value	3.0e-29
Match length	175
% identity	39
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	197090
Contig ID	28662_1.R1039
5'-most EST	LIB3148-022-Q1-K1-E5

Seq. No.	197091
Contig ID	28666_1.R1039
5'-most EST	uC-gsflnu33B085c11b1
Method	BLASTX
NCBI GI	g1841355
BLAST score	413
E value	5.0e-40
Match length	150
% identity	61
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	197092
Contig ID	28666_2.R1039
5'-most EST	g5048213
Method	BLASTX
NCBI GI	g1841355
BLAST score	465
E value	4.0e-46
Match length	166
% identity	58
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	197093
Contig ID	28666_3.R1039
5'-most EST	g5045996
Method	BLASTX
NCBI GI	g1841355
BLAST score	406
E value	3.0e-39
Match length	153
% identity	55
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	197094
Contig ID	28682_1.R1039
5'-most EST	LIB3147-035-Q1-K1-B12

Seq. No.	197095
Contig ID	28684_1.R1039
5'-most EST	LIB3147-035-Q1-K1-B4

Seq. No.	197096
Contig ID	28685_1.R1039
5'-most EST	LIB3147-035-Q1-K1-B6
Method	BLASTX
NCBI GI	g3860251
BLAST score	509
E value	9.0e-52
Match length	119
% identity	80
NCBI Description	(AC005824) putative permease [Arabidopsis thaliana]

Seq. No.	197097
Contig ID	28704_1.R1039

09605-0704-0960

5'-most EST	LIB3147-035-Q1-K1-D3
Method	BLASTX
NCBI GI	g1709923
BLAST score	260
E value	2.0e-22
Match length	102
% identity	57
NCBI Description	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE PRECURSOR (GART) (GAR TRANSFORMYLASE) (5'-PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) >gi|984818 (U30875) glycinamide ribonucleotide transformylase (GART) [Vigna unguiculata]

Seq. No.	197098
Contig ID	28710_1.R1039
5'-most EST	LIB3147-035-Q1-K1-E1
Method	BLASTX
NCBI GI	g4185515
BLAST score	468
E value	6.0e-47
Match length	111
% identity	77
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	197099
Contig ID	28712_1.R1039
5'-most EST	LIB3147-035-Q1-K1-E2
Method	BLASTX
NCBI GI	g4263048
BLAST score	179
E value	1.0e-12
Match length	52
% identity	58
NCBI Description	(AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No.	197100
Contig ID	28733_1.R1039
5'-most EST	LIB3147-035-Q1-K1-G4

Seq. No.	197101
Contig ID	28743_1.R1039
5'-most EST	g3326250

Seq. No.	197102
Contig ID	28752_1.R1039
5'-most EST	LIB3147-036-Q1-K1-A3
Method	BLASTX
NCBI GI	g100673
BLAST score	454
E value	5.0e-45
Match length	135
% identity	70
NCBI Description	DNA-binding protein GT-2 - rice (fragment)

Seq. No.	197103
Contig ID	28757_1.R1039
5'-most EST	LIB3148-004-Q1-K1-A12

Method	BLASTX
NCBI GI	g82035
BLAST score	475
E value	1.0e-47
Match length	188
% identity	36
NCBI Description	ricin E - castor bean (fragment) >gi|169715 (M17631) ricin E beta chain [Ricinus communis] >gi|225896|prf||1402359A ricin E [Ricinus communis]

Seq. No.	197104
Contig ID	28771_1.R1039
5'-most EST	g3325588
Method	BLASTX
NCBI GI	g4539399
BLAST score	349
E value	1.0e-32
Match length	73
% identity	95
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	197105
Contig ID	28771_2.R1039
5'-most EST	g5049961
Method	BLASTX
NCBI GI	g4539399
BLAST score	978
E value	1.0e-106
Match length	218
% identity	89
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	197106
Contig ID	28787_1.R1039
5'-most EST	uC-gsronu33B116a12b1
Method	BLASTX
NCBI GI	g1172977
BLAST score	841
E value	3.0e-90
Match length	187
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi|606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	197107
Contig ID	28800_1.R1039
5'-most EST	LIB3149-034-Q1-K1-B4
Method	BLASTN
NCBI GI	g3021347
BLAST score	62
E value	6.0e-26
Match length	194
% identity	85
NCBI Description	Cicer arietinum mRNA for cytoplasmic ribosomal protein L18

Seq. No.	197108
Contig ID	28803_1.R1039
5'-most EST	uC-gsflnu33B137c01b1
Seq. No.	197109
Contig ID	28824_1.R1039
5'-most EST	LIB3166-047-P1-K1-B2
Method	BLASTX
NCBI GI	g3892057
BLAST score	871
E value	6.0e-94
Match length	216
% identity	43
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.	197110
Contig ID	28828_1.R1039
5'-most EST	LIB3148-004-Q1-K1-C11
Seq. No.	197111
Contig ID	28829_1.R1039
5'-most EST	LIB3147-037-Q1-K1-A10
Seq. No.	197112
Contig ID	28831_1.R1039
5'-most EST	LIB3147-037-Q1-K2-A2
Method	BLASTX
NCBI GI	g3386546
BLAST score	148
E value	2.0e-09
Match length	55
% identity	58
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]
Seq. No.	197113
Contig ID	28832_1.R1039
5'-most EST	LIB3147-037-Q1-K2-A3
Seq. No.	197114
Contig ID	28835_1.R1039
5'-most EST	LIB3147-037-Q1-K2-A6
Seq. No.	197115
Contig ID	28839_1.R1039
5'-most EST	LIB3147-037-Q1-K2-B1
Seq. No.	197116
Contig ID	28843_1.R1039
5'-most EST	LIB3147-037-Q1-K2-B2
Seq. No.	197117
Contig ID	28845_1.R1039
5'-most EST	LIB3147-037-Q1-K1-B5
Method	BLASTN
NCBI GI	g1143321
BLAST score	37

E value	3.0e-11
Match length	77
% identity	87
NCBI Description	Glycine max alfa-carboxyltransferase (accA-2) precursor mRNA, complete cds

Seq. No.	197118
Contig ID	28850_1.R1039
5'-most EST	LIB3147-037-Q1-K1-C1
Method	BLASTX
NCBI GI	g4056480
BLAST score	160
E value	8.0e-11
Match length	61
% identity	49
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	197119
Contig ID	28851_1.R1039
5'-most EST	LIB3166-022-P1-K1-B1
Method	BLASTX
NCBI GI	g2811029
BLAST score	1110
E value	1.0e-122
Match length	270
% identity	78
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi|1944511|emb|CAA69936| (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	197120
Contig ID	28852_1.R1039
5'-most EST	uC-gsflnu33B015a01b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	261
E value	3.0e-22
Match length	160
% identity	40
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	197121
Contig ID	28852_2.R1039
5'-most EST	uC-gsronu33B036h12b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	172
E value	4.0e-15
Match length	103
% identity	49
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	197122
Contig ID	28853_1.R1039

5'-most EST	LIB3147-037-Q1-K1-C12
Method	BLASTX
NCBI GI	g1916290
BLAST score	230
E value	5.0e-19
Match length	135
% identity	41
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	197123
Contig ID	28855_1.R1039
5'-most EST	LIB3147-037-Q1-K1-C3

Seq. No.	197124
Contig ID	28859_1.R1039
5'-most EST	uC-gsronu33B111h10b1
Method	BLASTX
NCBI GI	g1778051
BLAST score	253
E value	2.0e-21
Match length	149
% identity	36
NCBI Description	(U62583) Prt1 homolog [Homo sapiens] >gi|4503527|ref|NP_003742.1|pEIF3S9| UNKNOWN

Seq. No.	197125
Contig ID	28861_1.R1039
5'-most EST	LIB3147-037-Q1-K1-D11
Method	BLASTX
NCBI GI	g3832528
BLAST score	180
E value	3.0e-13
Match length	114
% identity	39
NCBI Description	(AF100167) unknown [Glycine max]

Seq. No.	197126
Contig ID	28862_1.R1039
5'-most EST	LIB3147-037-Q1-K1-D12

Seq. No.	197127
Contig ID	28863_1.R1039
5'-most EST	LIB3147-037-Q1-K1-D3
Method	BLASTX
NCBI GI	g3355490
BLAST score	144
E value	5.0e-09
Match length	31
% identity	87
NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	197128
Contig ID	28865_1.R1039
5'-most EST	LIB3149-032-Q1-K1-C9
Method	BLASTX
NCBI GI	g4204761

BLAST score	782
E value	1.0e-107
Match length	308
% identity	66
NCBI Description	(U51192) peroxidase precursor [Glycine max]

Seq. No.	197129
Contig ID	28867_1.R1039
5'-most EST	LIB3147-037-Q1-K2-D7

Seq. No.	197130
Contig ID	28871_1.R1039
5'-most EST	uC-gsflnu33B145g10b1
Method	BLASTN
NCBI GI	g2832639
BLAST score	34
E value	2.0e-09
Match length	122
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	197131
Contig ID	28872_1.R1039
5'-most EST	LIB3147-057-Q1-K1-C2
Method	BLASTX
NCBI GI	g2961346
BLAST score	649
E value	6.0e-68
Match length	157
% identity	75
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	197132
Contig ID	28876_1.R1039
5'-most EST	LIB3147-037-Q1-K1-E5
Method	BLASTN
NCBI GI	g3046856
BLAST score	33
E value	6.0e-09
Match length	203
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	197133
Contig ID	28882_1.R1039
5'-most EST	LIB3147-037-Q1-K1-F10
Method	BLASTX
NCBI GI	g3878119
BLAST score	296
E value	9.0e-27
Match length	126
% identity	44
NCBI Description	(Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709

comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353

Seq. No.	197134
Contig ID	28883_1.R1039
5'-most EST	LIB3147-037-Q1-K2-F12

Seq. No.	197135
Contig ID	28885_1.R1039
5'-most EST	LIB3197-021-Q1-M1-F12
Method	BLASTX
NCBI GI	g3269289
BLAST score	315
E value	7.0e-29
Match length	89
% identity	70
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	197136
Contig ID	28886_1.R1039
5'-most EST	LIB3147-037-Q1-K1-F4

Seq. No.	197137
Contig ID	28889_1.R1039
5'-most EST	LIB3165-031-P1-K1-D2

Seq. No.	197138
Contig ID	28892_1.R1039
5'-most EST	LIB3147-037-Q1-K2-G11
Method	BLASTX
NCBI GI	g3738285
BLAST score	650
E value	7.0e-68
Match length	155
% identity	78
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	197139
Contig ID	28907_1.R1039
5'-most EST	LIB3147-037-Q1-K1-H6
Method	BLASTX
NCBI GI	g1922937
BLAST score	310
E value	2.0e-28
Match length	109
% identity	56
NCBI Description	(AC000106) Similar to Glycine SRC2 (gb|AB000130). ESTs gb|H76869,gb|T21700,gb|ATTS5089 come from this gene. [Arabidopsis thaliana]

Seq. No.	197140
Contig ID	28982_1.R1039
5'-most EST	LIB3166-020-P1-K1-F12
Method	BLASTX
NCBI GI	g2065013
BLAST score	371

E value	1.0e-35
Match length	121
% identity	65
NCBI Description	(Y11650) cyclic phosphodiesterase [Arabidopsis thaliana] >gi|2832621|emb|CAA16750| (AL021711) cyclic phosphodiesterase [Arabidopsis thaliana]

Seq. No.	197141
Contig ID	28987_1.R1039
5'-most EST	uC-gsronu33B055e03b1

Seq. No.	197142
Contig ID	28989_1.R1039
5'-most EST	LIB3147-038-Q1-K2-A11
Method	BLASTX
NCBI GI	g4467153
BLAST score	392
E value	2.0e-39
Match length	121
% identity	66
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	197143
Contig ID	28996_1.R1039
5'-most EST	LIB3196-039-P1-M1-B8

Seq. No.	197144
Contig ID	29000_1.R1039
5'-most EST	LIB3147-058-Q1-K1-B3
Method	BLASTX
NCBI GI	g4406787
BLAST score	392
E value	1.0e-37
Match length	102
% identity	78
NCBI Description	(AC006532) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	197145
Contig ID	29022_1.R1039
5'-most EST	LIB3147-038-Q1-K2-D11
Method	BLASTX
NCBI GI	g541979
BLAST score	494
E value	1.0e-49
Match length	121
% identity	79
NCBI Description	guanine nucleotide regulatory protein - fava bean >gi|303744|dbj|BAA02113| (D12545) GTP-binding protein [Pisum sativum] >gi|452361|emb|CAA82709| (Z29592) guanine nucleotide regulatory protein [Vicia faba] >gi|738937|prf||2001457E GTP-binding protein [Pisum sativum] >gi|1098295|prf||2115367C small GTP-binding protein [Vicia faba]

Seq. No.	197146
Contig ID	29053_1.R1039

5'-most EST	uC-gsflmaxxa038f05b1
Method	BLASTX
NCBI GI	g419789
BLAST score	718
E value	6.0e-76
Match length	192
% identity	73
NCBI Description	hypothetical protein - potato

Seq. No.	197147
Contig ID	29072_1.R1039
5'-most EST	LIB3147-038-Q1-K2-H5

Seq. No.	197148
Contig ID	29078_1.R1039
5'-most EST	LIB3147-039-Q1-K1-A10

Seq. No.	197149
Contig ID	29092_1.R1039
5'-most EST	uC-gsronu33B017e11b1
Method	BLASTX
NCBI GI	g2642215
BLAST score	317
E value	3.0e-29
Match length	75
% identity	80
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	197150
Contig ID	29112_1.R1039
5'-most EST	g5046930
Method	BLASTX
NCBI GI	g4220529
BLAST score	626
E value	3.0e-65
Match length	170
% identity	72
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	197151
Contig ID	29123_1.R1039
5'-most EST	LIB3147-039-Q1-K1-E12
Method	BLASTX
NCBI GI	g1922251
BLAST score	608
E value	3.0e-63
Match length	125
% identity	93
NCBI Description	(Y12072) farnesyl pyrophosphate synthase [Gossypium arboreum]

Seq. No.	197152
Contig ID	29132_2.R1039
5'-most EST	uC-gsflnu33B064g05b1
Method	BLASTX
NCBI GI	g2117168
BLAST score	670

E value	3.0e-70
Match length	135
% identity	93
NCBI Description	(Z73961) RAC1 [Lotus japonicus]

Seq. No.	197153
Contig ID	29140_1.R1039
5'-most EST	g5050750
Method	BLASTX
NCBI GI	g3421413
BLAST score	1081
E value	1.0e-118
Match length	229
% identity	87
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi|3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	197154
Contig ID	29146_1.R1039
5'-most EST	uC-gsronu33B011a05b1
Method	BLASTX
NCBI GI	g3913633
BLAST score	570
E value	2.0e-58
Match length	162
% identity	72
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi|2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	197155
Contig ID	29150_1.R1039
5'-most EST	uC-gsflnu33B134a12b1
Method	BLASTX
NCBI GI	g3337356
BLAST score	896
E value	1.0e-96
Match length	189
% identity	93
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	197156
Contig ID	29164_1.R1039
5'-most EST	LIB3147-040-Q1-K1-A12
Method	BLASTX
NCBI GI	g2244846
BLAST score	458
E value	1.0e-45
Match length	135
% identity	66
NCBI Description	(Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No.	197157
Contig ID	29167_1.R1039
5'-most EST	g5044594

Seq. No.	197158
Contig ID	29171_1.R1039
5'-most EST	LIB3147-040-Q1-K1-A9
Method	BLASTX
NCBI GI	g4572671
BLAST score	533
E value	3.0e-57
Match length	240
% identity	51
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	197159
Contig ID	29177_1.R1039
5'-most EST	LIB3147-040-Q1-K1-B3

Seq. No.	197160
Contig ID	29195_1.R1039
5'-most EST	uC-gsflnu33B136c08b1

Seq. No.	197161
Contig ID	29200_1.R1039
5'-most EST	g5044732
Method	BLASTX
NCBI GI	g3747026
BLAST score	218
E value	2.0e-17
Match length	79
% identity	44
NCBI Description	(AF093244) import protein Tim9p [Saccharomyces cerevisiae]

Seq. No.	197162
Contig ID	29220_1.R1039
5'-most EST	g5046041
Method	BLASTX
NCBI GI	g4240305
BLAST score	207
E value	6.0e-16
Match length	182
% identity	35
NCBI Description	(AB020715) KIAA0908 protein [Homo sapiens]

Seq. No.	197163
Contig ID	29242_1.R1039
5'-most EST	LIB3147-040-Q1-K1-H6
Method	BLASTX
NCBI GI	g294668
BLAST score	716
E value	6.0e-76
Match length	147
% identity	94
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	197164
Contig ID	29255_1.R1039
5'-most EST	g5049546
Method	BLASTX

NCBI GI	g1762945
BLAST score	287
E value	1.0e-52
Match length	156
% identity	67
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	197165
Contig ID	29255_2.R1039
5'-most EST	uC-gsronu33B160a09b1

Seq. No.	197166
Contig ID	29263_1.R1039
5'-most EST	LIB3272-004-P1-K1-E3
Method	BLASTX
NCBI GI	g2352492
BLAST score	618
E value	2.0e-64
Match length	142
% identity	81
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi|2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	197167
Contig ID	29269_1.R1039
5'-most EST	uC-gsflnu33B035a09b1

Seq. No.	197168
Contig ID	29273_1.R1039
5'-most EST	g5047476
Method	BLASTX
NCBI GI	g4325354
BLAST score	363
E value	2.0e-34
Match length	143
% identity	46
NCBI Description	(AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No.	197169
Contig ID	29284_1.R1039
5'-most EST	LIB3147-041-Q1-K1-F7

Seq. No.	197170
Contig ID	29292_1.R1039
5'-most EST	g5048532
Method	BLASTX
NCBI GI	g2463569
BLAST score	1287
E value	1.0e-142
Match length	323
% identity	76
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	197171
Contig ID	29293_1.R1039
5'-most EST	uC-gsronu33B155c10b2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	197172
Contig ID	29311_1.R1039
5'-most EST	LIB3197-015-P1-M1-D10

Seq. No.	197173
Contig ID	29312_1.R1039
5'-most EST	LIB3147-042-Q1-K1-B10
Method	BLASTX
NCBI GI	g2501056
BLAST score	198
E value	4.0e-15
Match length	55
% identity	71
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi|2129737|pir||S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi|1359497|emb|CAA94388| (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	197174
Contig ID	29315_1.R1039
5'-most EST	LIB3189-033-P1-K1-F7
Method	BLASTX
NCBI GI	g133939
BLAST score	455
E value	2.0e-45
Match length	101
% identity	85
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi|70865|pir||R3NT3 ribosomal protein S3 - common tobacco chloroplast >gi|11865|emb|CAA77381| (Z00044) ribosomal protein S3 [Nicotiana tabacum] >gi|225235|prf||1211235BT ribosomal protein S3 [Nicotiana tabacum]

Seq. No.	197175
Contig ID	29316_1.R1039
5'-most EST	LIB3147-042-Q1-K1-B3
Method	BLASTX
NCBI GI	g2270994
BLAST score	362
E value	2.0e-34
Match length	131
% identity	52
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	197176
Contig ID	29328_1.R1039

5'-most EST	LIB3166-016-P1-K1-G4
Method	BLASTX
NCBI GI	g2736186
BLAST score	476
E value	6.0e-48
Match length	128
% identity	69
NCBI Description	(AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.	197177
Contig ID	29344_1.R1039
5'-most EST	LIB3166-046-P1-K1-G1
Method	BLASTX
NCBI GI	g4263711
BLAST score	524
E value	4.0e-53
Match length	186
% identity	55
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	197178
Contig ID	29347_1.R1039
5'-most EST	LIB3147-042-Q1-K1-E4
Method	BLASTX
NCBI GI	g3861188
BLAST score	256
E value	7.0e-22
Match length	103
% identity	51
NCBI Description	(AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia prowazekii]

Seq. No.	197179
Contig ID	29364_1.R1039
5'-most EST	LIB3147-042-Q1-K1-G11

Seq. No.	197180
Contig ID	29368_1.R1039
5'-most EST	LIB3148-030-Q1-K1-B12

Seq. No.	197181
Contig ID	29387_1.R1039
5'-most EST	g5048598
Method	BLASTX
NCBI GI	g2951777
BLAST score	288
E value	2.0e-25
Match length	194
% identity	37
NCBI Description	(AB011823) translation initiation factor 3 [Schizosaccharomyces pombe]

Seq. No.	197182
Contig ID	29389_1.R1039
5'-most EST	LIB3272-055-P1-K1-G6

Seq. No.	197183
Contig ID	29393_1.R1039
5'-most EST	LIB3147-043-Q1-K1-A9

Seq. No.	197184
Contig ID	29422_1.R1039
5'-most EST	LIB3147-043-Q1-K1-D2
Method	BLASTX
NCBI GI	g1724114
BLAST score	305
E value	8.0e-28
Match length	68
% identity	85
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	197185
Contig ID	29433_1.R1039
5'-most EST	LIB3189-005-P1-K1-C12
Method	BLASTX
NCBI GI	g4263704
BLAST score	292
E value	5.0e-26
Match length	134
% identity	45
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	197186
Contig ID	29438_1.R1039
5'-most EST	LIB3147-043-Q1-K1-E7
Method	BLASTX
NCBI GI	g82308
BLAST score	752
E value	5.0e-80
Match length	180
% identity	79
NCBI Description	myb protein 308 - garden snapdragon

Seq. No.	197187
Contig ID	29445_1.R1039
5'-most EST	LIB3197-001-P1-M1-F4

Seq. No.	197188
Contig ID	29451_1.R1039
5'-most EST	LIB3147-043-Q1-K1-F9

Seq. No.	197189
Contig ID	29465_1.R1039
5'-most EST	LIB3149-042-Q1-K1-A9
Method	BLASTX
NCBI GI	g508545
BLAST score	187
E value	2.0e-20
Match length	96
% identity	62
NCBI Description	(L34340) zein [Zea mays]

Seq. No.	197190
Contig ID	29493_1.R1039
5'-most EST	LIB3147-044-Q1-K1-C1

Seq. No.	197191
Contig ID	29504_1.R1039
5'-most EST	LIB3147-044-Q1-K1-D1
Method	BLASTX
NCBI GI	g3834307
BLAST score	352
E value	2.0e-33
Match length	125
% identity	62
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi|2832679 putative protein from Arabidopsis thaliana BAC gb|AL021712. ESTs gb|N65887 and gb|N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	197192
Contig ID	29509_1.R1039
5'-most EST	LIB3148-041-Q1-K1-D12
Method	BLASTX
NCBI GI	g1350720
BLAST score	455
E value	4.0e-45
Match length	111
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	197193
Contig ID	29516_1.R1039
5'-most EST	uC-gsronu33B040c11b1
Method	BLASTX
NCBI GI	g3522938
BLAST score	231
E value	2.0e-19
Match length	97
% identity	51
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	197194
Contig ID	29533_1.R1039
5'-most EST	LIB3147-044-Q1-K1-F5
Method	BLASTX
NCBI GI	g3776013
BLAST score	276
E value	3.0e-24
Match length	86
% identity	64
NCBI Description	(AJ010470) RNA helicase [Arabidopsis thaliana]

Seq. No.	197195
Contig ID	29542_1.R1039
5'-most EST	LIB3147-044-Q1-K1-G2

Seq. No.	197196
Contig ID	29543_1.R1039

5'-most EST	LIB3147-044-Q1-K1-G3
Method	BLASTX
NCBI GI	g3913648
BLAST score	779
E value	4.0e-83
Match length	180
% identity	82
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)

Seq. No.	197197
Contig ID	29544_1.R1039
5'-most EST	uC-gsflmaxxa027e07b1

Seq. No.	197198
Contig ID	29559_1.R1039
5'-most EST	LIB3272-029-P1-K1-F3

Seq. No.	197199
Contig ID	29567_1.R1039
5'-most EST	LIB3147-056-Q1-K1-B10
Method	BLASTX
NCBI GI	g3157922
BLAST score	382
E value	9.0e-37
Match length	111
% identity	69
NCBI Description	(AC002131) Contains similarity to proline-rich protein, gb|S68113 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	197200
Contig ID	29576_1.R1039
5'-most EST	uC-gsflmaxxa048g09b1

Seq. No.	197201
Contig ID	29588_1.R1039
5'-most EST	uC-gsronu33B098d04b1
Method	BLASTX
NCBI GI	g2583108
BLAST score	1264
E value	1.0e-140
Match length	340
% identity	75
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	197202
Contig ID	29593_1.R1039
5'-most EST	uC-gsronu33B021d09b1
Method	BLASTX
NCBI GI	g2583133
BLAST score	268
E value	1.0e-42
Match length	110
% identity	85
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	197203
Contig ID	29602_1.R1039

5'-most EST	LIB3147-045-Q1-K1-E11
Seq. No.	197204
Contig ID	29606_1.R1039
5'-most EST	LIB3147-045-Q1-K1-E4
Seq. No.	197205
Contig ID	29607_1.R1039
5'-most EST	LIB3147-045-Q1-K1-E5
Method	BLASTX
NCBI GI	g4567203
BLAST score	672
E value	2.0e-70
Match length	144
% identity	88
NCBI Description	(AC007168) putative beta-hydroxyacyl-ACP dehydratase [Arabidopsis thaliana]
Seq. No.	197206
Contig ID	29615_1.R1039
5'-most EST	LIB3197-035-Q1-M1-H3
Method	BLASTX
NCBI GI	g2500341
BLAST score	166
E value	2.0e-11
Match length	38
% identity	76
NCBI Description	50S RIBOSOMAL PROTEIN L36 >gi|1652406|dbj|BAA17328| (D90905) 50S ribosomal protein L36 [Synechocystis sp.]
Seq. No.	197207
Contig ID	29640_1.R1039
5'-most EST	uC-gsronu33B127d10b1
Seq. No.	197208
Contig ID	29643_1.R1039
5'-most EST	LIB3147-046-Q1-K1-A7
Method	BLASTX
NCBI GI	g1169839
BLAST score	162
E value	5.0e-11
Match length	79
% identity	39
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 1 PRECURSOR >gi|2129588|pir||S71441 GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana >gi|887939 (U11766) GAST1 protein homolog [Arabidopsis thaliana]
Seq. No.	197209
Contig ID	29648_1.R1039
5'-most EST	uC-gsflmaxxa060c08b1
Method	BLASTX
NCBI GI	g1351834
BLAST score	306
E value	6.0e-28
Match length	94
% identity	62

NCBI Description	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi|1016162 (U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No.	197210
Contig ID	29656_1.R1039
5'-most EST	LIB3166-011-P1-K1-D6
Method	BLASTX
NCBI GI	g2500378
BLAST score	419
E value	5.0e-41
Match length	83
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	197211
Contig ID	29657_1.R1039
5'-most EST	LIB3147-046-Q1-K1-C10
Method	BLASTX
NCBI GI	g3287270
BLAST score	619
E value	1.0e-64
Match length	138
% identity	85
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	197212
Contig ID	29658_1.R1039
5'-most EST	g5049424
Method	BLASTX
NCBI GI	g4321399
BLAST score	977
E value	1.0e-106
Match length	238
% identity	71
NCBI Description	(AF047039) omega-3 fatty acid desaturase [Perilla frutescens]

Seq. No.	197213
Contig ID	29659_1.R1039
5'-most EST	uC-gsronu33B167e10b1

Seq. No.	197214
Contig ID	29678_1.R1039
5'-most EST	uC-gsflmaxxa045a05b1
Method	BLASTX
NCBI GI	g4508078
BLAST score	465
E value	1.0e-46
Match length	96
% identity	86
NCBI Description	(AC005882) 64134 [Arabidopsis thaliana]

Seq. No.	197215
Contig ID	29679_1.R1039
5'-most EST	LIB3165-043-Q1-K1-F4

Seq. No.	197216

Contig ID	29681_1.R1039
5'-most EST	LIB3149-043-Q1-K1-G10
Seq. No.	197217
Contig ID	29681_2.R1039
5'-most EST	LIB3196-023-P1-M1-H10
Seq. No.	197218
Contig ID	29683_1.R1039
5'-most EST	LIB3148-013-Q1-K1-B3
Seq. No.	197219
Contig ID	29694_1.R1039
5'-most EST	LIB3147-046-Q1-K1-G10
Seq. No.	197220
Contig ID	29696_1.R1039
5'-most EST	LIB3147-046-Q1-K1-G12
Method	BLASTX
NCBI GI	g4126403
BLAST score	506
E value	2.0e-51
Match length	144
% identity	64
NCBI Description	(AB011796) flavonol synthase [Citrus unshiu]
Seq. No.	197221
Contig ID	29711_1.R1039
5'-most EST	LIB3147-047-Q1-K1-A7
Method	BLASTX
NCBI GI	g2129605
BLAST score	784
E value	7.0e-84
Match length	158
% identity	94
NCBI Description	GTP-binding protein 2 - Arabidopsis thaliana >gi|2129702|pir||S71585 Rab2 homolog GTP-binding protein ATGB2 - Arabidopsis thaliana >gi|1184983 (U46925) ATGB2 [Arabidopsis thaliana] >gi|3805852|emb|CAA21472| (AL031986) GTP-binding protein GB2 [Arabidopsis thaliana]
Seq. No.	197222
Contig ID	29716_1.R1039
5'-most EST	LIB3147-047-Q1-K1-B7
Method	BLASTX
NCBI GI	g2854070
BLAST score	157
E value	2.0e-10
Match length	43
% identity	74
NCBI Description	(AF044914) putative histone deacetylase [Arabidopsis thaliana]
Seq. No.	197223
Contig ID	29719_1.R1039
5'-most EST	LIB3148-049-Q1-K1-B5
Method	BLASTX

NCBI GI g4454480
BLAST score 234
E value 2.0e-19
Match length 98
% identity 45
NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No. 197224
Contig ID 29720_1.R1039
5'-most EST LIB3147-047-Q1-K1-C8
Method BLASTX
NCBI GI g4337201
BLAST score 179
E value 5.0e-13
Match length 69
% identity 51
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 197225
Contig ID 29750_1.R1039
5'-most EST LIB3165-025-P1-K1-G10
Method BLASTX
NCBI GI g2623295
BLAST score 369
E value 5.0e-35
Match length 144
% identity 51
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 197226
Contig ID 29753_1.R1039
5'-most EST uC-gsronu33B138e05b1
Method BLASTX
NCBI GI g2982331
BLAST score 316
E value 4.0e-29
Match length 64
% identity 98
NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 197227
Contig ID 29768_1.R1039
5'-most EST uC-gsflnu33B084c06b1

Seq. No. 197228
Contig ID 29775_1.R1039
5'-most EST LIB3166-052-P1-K1-F3
Method BLASTX
NCBI GI g3341685
BLAST score 451
E value 9.0e-45
Match length 135
% identity 70
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 197229

Contig ID	29777_1.R1039
5'-most EST	uC-gsronu33B160e10b1
Method	BLASTX
NCBI GI	g2660673
BLAST score	337
E value	3.0e-31
Match length	258
% identity	15
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	197230
Contig ID	29779_1.R1039
5'-most EST	LIB3149-056-Q1-K1-F9
Method	BLASTX
NCBI GI	g2739366
BLAST score	243
E value	1.0e-20
Match length	126
% identity	37
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	197231
Contig ID	29780_1.R1039
5'-most EST	uC-gsflnu33B111a09b1
Method	BLASTX
NCBI GI	g3024516
BLAST score	843
E value	1.0e-90
Match length	178
% identity	94
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi|2160157 (AC000132) Strong similarity to A. thaliana ara-2 (gb|ATHARA2). ESTs gb|ATTS2483,gb|ATTS2484,gb|AA042159 come from this gene. [Arabidopsis thaliana] >gi|2231303 (U74669) ras-related small GTPase [Arabidopsis thaliana]

Seq. No.	197232
Contig ID	29783_1.R1039
5'-most EST	LIB3147-050-Q1-K1-A1
Method	BLASTX
NCBI GI	g461929
BLAST score	917
E value	3.0e-99
Match length	216
% identity	82
NCBI Description	PROBABLE TONOPLAST INTRINSIC PROTEIN DIP >gi|1076688|pir||S51781 integral membrane protein - garden snapdragon >gi|414088|emb|CAA49854| (X70417) integral membrane protein [Antirrhinum majus]

Seq. No.	197233
Contig ID	29785_1.R1039
5'-most EST	uC-gsflnu33B059h03b1
Method	BLASTN
NCBI GI	g1794146
BLAST score	104
E value	4.0e-51

Match length	466
% identity	84
NCBI Description	Carrot mRNA for root specific gene, complete cds

Seq. No.	197234
Contig ID	29794_1.R1039
5'-most EST	LIB3147-049-Q1-K1-F3
Method	BLASTX
NCBI GI	g4567279
BLAST score	390
E value	9.0e-38
Match length	118
% identity	66
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	197235
Contig ID	29798_1.R1039
5'-most EST	uC-gsronu33B061e11b1
Method	BLASTX
NCBI GI	g2323410
BLAST score	616
E value	4.0e-64
Match length	189
% identity	65
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	197236
Contig ID	29799_1.R1039
5'-most EST	g5045302

Seq. No.	197237
Contig ID	29807_1.R1039
5'-most EST	LIB3147-049-Q1-K1-G8

Seq. No.	197238
Contig ID	29808_1.R1039
5'-most EST	LIB3166-054-P1-K1-A2

Seq. No.	197239
Contig ID	29824_1.R1039
5'-most EST	LIB3165-060-Q1-K1-D6
Method	BLASTX
NCBI GI	g1946368
BLAST score	674
E value	7.0e-71
Match length	189
% identity	74
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	197240
Contig ID	29828_1.R1039
5'-most EST	uC-gsronu33B114d12b1

Seq. No.	197241
Contig ID	29828_2.R1039
5'-most EST	LIB3166-011-P1-K1-H5

Method	BLASTN
NCBI GI	g3201608
BLAST score	33
E value	6.0e-09
Match length	89
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	197242
Contig ID	29832_1.R1039
5'-most EST	LIB3149-019-Q1-K1-B8
Method	BLASTX
NCBI GI	g4522012
BLAST score	479
E value	5.0e-48
Match length	131
% identity	66
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197243
Contig ID	29835_1.R1039
5'-most EST	LIB3196-010-P1-M1-F9

Seq. No.	197244
Contig ID	29838_1.R1039
5'-most EST	LIB3147-050-Q1-K1-C7
Method	BLASTX
NCBI GI	g416662
BLAST score	406
E value	1.0e-47
Match length	136
% identity	70
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi|99954|pir||S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860| (X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No.	197245
Contig ID	29848_1.R1039
5'-most EST	uC-gsflnu33B011f04b1
Method	BLASTX
NCBI GI	g2129575
BLAST score	354
E value	2.0e-33
Match length	119
% identity	60
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No.	197246
Contig ID	29858_1.R1039
5'-most EST	LIB3166-017-P1-K1-C10
Method	BLASTX
NCBI GI	g3123264
BLAST score	553
E value	1.0e-56
Match length	135
% identity	77

NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi|2244857|emb|CAB10279| (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	197247
Contig ID	29865_1.R1039
5'-most EST	LIB3147-050-Q1-K1-G3
Seq. No.	197248
Contig ID	29872_1.R1039
5'-most EST	LIB3147-050-Q1-K1-H1
Seq. No.	197249
Contig ID	29874_1.R1039
5'-most EST	LIB3147-050-Q1-K1-H11
Method	BLASTX
NCBI GI	g2980770
BLAST score	961
E value	1.0e-104
Match length	201
% identity	89
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.	197250
Contig ID	29878_1.R1039
5'-most EST	LIB3272-038-P1-K1-D1
Seq. No.	197251
Contig ID	29884_1.R1039
5'-most EST	LIB3147-051-Q1-K1-A2
Method	BLASTX
NCBI GI	g3540181
BLAST score	199
E value	3.0e-15
Match length	71
% identity	48
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.	197252
Contig ID	29896_1.R1039
5'-most EST	uC-gsflnu33B029e09b1
Method	BLASTX
NCBI GI	g2827709
BLAST score	1189
E value	1.0e-131
Match length	276
% identity	83
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	197253
Contig ID	29899_1.R1039
5'-most EST	LIB3147-051-Q1-K1-D8
Method	BLASTX
NCBI GI	g3860321
BLAST score	330
E value	1.0e-30
Match length	75
% identity	73

NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]
Seq. No.	197254
Contig ID	29903_1.R1039
5'-most EST	uC-gsflnu33B001b02b1
Seq. No.	197255
Contig ID	29918_1.R1039
5'-most EST	uC-gsronu33B149f06b1
Seq. No.	197256
Contig ID	29922_1.R1039
5'-most EST	LIB3197-002-P1-M1-G8
Seq. No.	197257
Contig ID	29924_1.R1039
5'-most EST	LIB3196-058-P1-M1-C12
Method	BLASTN
NCBI GI	g415924
BLAST score	40
E value	3.0e-13
Match length	68
% identity	90
NCBI Description	B.napus mRNA for plastid chaperonin-60 alpha subunit
Seq. No.	197258
Contig ID	29935_1.R1039
5'-most EST	uC-gsflnu33B127e07b1
Method	BLASTX
NCBI GI	g3510252
BLAST score	376
E value	1.0e-35
Match length	168
% identity	48
NCBI Description	(AC005310) putative RNA-binding protein [Arabidopsis thaliana]
Seq. No.	197259
Contig ID	29952_1.R1039
5'-most EST	g5046634
Method	BLASTN
NCBI GI	g3510247
BLAST score	34
E value	4.0e-09
Match length	90
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	197260
Contig ID	29969_1.R1039
5'-most EST	uC-gsronu33B021f08b1
Seq. No.	197261
Contig ID	29971_1.R1039
5'-most EST	LIB3148-030-Q1-K1-F5
Method	BLASTX

NCBI GI	g2879867
BLAST score	411
E value	5.0e-40
Match length	115
% identity	68
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	197262
Contig ID	29982_1.R1039
5'-most EST	LIB3165-034-P1-K6-A1
Method	BLASTN
NCBI GI	g2618605
BLAST score	92
E value	6.0e-44
Match length	244
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	197263
Contig ID	29985_1.R1039
5'-most EST	LIB3189-036-P1-K1-D2

Seq. No.	197264
Contig ID	29994_1.R1039
5'-most EST	uC-gsflnu33B029b06b1
Method	BLASTX
NCBI GI	g3386608
BLAST score	149
E value	2.0e-09
Match length	81
% identity	46
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197265
Contig ID	30005_1.R1039
5'-most EST	LIB3147-052-Q1-K1-F12
Method	BLASTX
NCBI GI	g1420887
BLAST score	213
E value	6.0e-17
Match length	89
% identity	45
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	197266
Contig ID	30034_1.R1039
5'-most EST	g5049267
Method	BLASTX
NCBI GI	g322577
BLAST score	699
E value	1.0e-73
Match length	150
% identity	87
NCBI Description	Raf protein kinase homolog CTR1 - Arabidopsis thaliana

Seq. No. 197267
Contig ID 30047_1.R1039
5'-most EST LIB3147-054-Q1-K1-B12
Method BLASTX
NCBI GI g2398829
BLAST score 522
E value 2.0e-76
Match length 161
% identity 67
NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No. 197268
Contig ID 30049_1.R1039
5'-most EST LIB3147-054-Q1-K1-B3

Seq. No. 197269
Contig ID 30054_1.R1039
5'-most EST LIB3147-054-Q1-K1-B9
Method BLASTX
NCBI GI g2960069
BLAST score 640
E value 9.0e-67
Match length 231
% identity 52
NCBI Description (Y12777) acyl-CoA synthetase-like protein [Homo sapiens]

Seq. No. 197270
Contig ID 30056_1.R1039
5'-most EST LIB3147-054-Q1-K1-C10
Method BLASTX
NCBI GI g1483218
BLAST score 126
E value 3.0e-16
Match length 180
% identity 37
NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 197271
Contig ID 30060_1.R1039
5'-most EST uC-gsflnu33B085g10b1

Seq. No. 197272
Contig ID 30071_1.R1039
5'-most EST LIB3147-054-Q1-K1-D4

Seq. No. 197273
Contig ID 30071_2.R1039
5'-most EST LIB3166-023-P1-K1-B8

Seq. No. 197274
Contig ID 30073_1.R1039
5'-most EST uC-gsflnu33B131c09b1
Method BLASTX
NCBI GI g2244939

BLAST score 496
E value 4.0e-50
Match length 163
% identity 63
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 197275
Contig ID 30081_1.R1039
5'-most EST uC-gsflmaxxa043g03b1

Seq. No. 197276
Contig ID 30097_1.R1039
5'-most EST uC-gsflmaxxa004e03b1
Method BLASTX
NCBI GI g3451078
BLAST score 299
E value 9.0e-27
Match length 219
% identity 36
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 197277
Contig ID 30100_1.R1039
5'-most EST LIB3147-054-Q1-K1-G6
Method BLASTX
NCBI GI g4558659
BLAST score 490
E value 2.0e-49
Match length 140
% identity 67
NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]

Seq. No. 197278
Contig ID 30105_1.R1039
5'-most EST uC-gsronu33b023f11b1
Method BLASTX
NCBI GI g2623311
BLAST score 475
E value 2.0e-47
Match length 158
% identity 61
NCBI Description (AC002409) unknown protein [Arabidopsis thaliana] >gi|3402720 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 197279
Contig ID 30114_1.R1039
5'-most EST uC-gsronu33B082b09b1

Seq. No. 197280
Contig ID 30117_1.R1039
5'-most EST uC-gsflnu33B026f03b1
Method BLASTX
NCBI GI g3287693
BLAST score 434
E value 8.0e-43
Match length 90

% identity	89
NCBI Description	(AC003979) Similar to LIM17 gene product gb|1653769 from the genome of Synechocystis sp. gb|D90916. [Arabidopsis thaliana]

Seq. No.	197281
Contig ID	30122_1.R1039
5'-most EST	uC-gsronu33B110f12b1

Seq. No.	197282
Contig ID	30133_1.R1039
5'-most EST	LIB3147-055-Q1-K1-B4
Method	BLASTX
NCBI GI	g4206122
BLAST score	994
E value	1.0e-108
Match length	222
% identity	83
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	197283
Contig ID	30138_1.R1039
5'-most EST	LIB3147-055-Q1-K1-C10

Seq. No.	197284
Contig ID	30154_1.R1039
5'-most EST	LIB3147-055-Q1-K1-D8

Seq. No.	197285
Contig ID	30155_1.R1039
5'-most EST	uC-gsronu33B076e11b1
Method	BLASTN
NCBI GI	g4519263
BLAST score	48
E value	7.0e-18
Match length	100
% identity	88
NCBI Description	Citrus unshiu mRNA for vacuolar H+-ATPase B subunit, complete cds

Seq. No.	197286
Contig ID	30160_1.R1039
5'-most EST	LIB3147-055-Q1-K1-E4
Method	BLASTX
NCBI GI	g3080395
BLAST score	294
E value	2.0e-26
Match length	103
% identity	56
NCBI Description	(AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197287
Contig ID	30175_1.R1039
5'-most EST	LIB3147-055-Q1-K1-G11

Seq. No.	197288

Contig ID 30196_1.R1039
5'-most EST LIB3147-056-Q1-K1-A2
Method BLASTX
NCBI GI g1708191
BLAST score 644
E value 2.0e-67
Match length 171
% identity 68
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi|467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No. 197289
Contig ID 30198_1.R1039
5'-most EST LIB3148-035-Q1-K1-D2
Method BLASTX
NCBI GI g4539350
BLAST score 371
E value 1.0e-35
Match length 80
% identity 81
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 197290
Contig ID 30200_1.R1039
5'-most EST LIB3196-006-P1-M1-D11

Seq. No. 197291
Contig ID 30206_1.R1039
5'-most EST LIB3147-056-Q1-K1-B12
Method BLASTX
NCBI GI g730463
BLAST score 322
E value 1.0e-29
Match length 105
% identity 59
NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi|630323|pir||S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi|484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi|1420537|emb|CAA99454| (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No. 197292
Contig ID 30221_1.R1039
5'-most EST LIB3196-039-P1-M1-F11
Method BLASTX
NCBI GI g3947719
BLAST score 249
E value 4.0e-21
Match length 53
% identity 92
NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica] >gi|3947721|emb|CAA10102| (AJ012654) ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103| (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No. 197293

Contig ID	30225_2.R1039
5'-most EST	uC-gsronu33B147d02b1
Method	BLASTX
NCBI GI	g140201
BLAST score	386
E value	4.0e-37
Match length	156
% identity	50
NCBI Description	PROTEIN KINASE YAK1 >gi|101423|pir||A32582 protein kinase YAK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) >gi|4796|emb|CAA34192| (X16056) Yak1 kinase (AA 1 - 807) [Saccharomyces cerevisiae] >gi|854556|emb|CAA60814| (X87371) protein kinase [Saccharomyces cerevisiae] >gi|1015551|emb|CAA89437| (Z49417) ORF YJL141c [Saccharomyces cerevisiae]

Seq. No.	197294
Contig ID	30240_1.R1039
5'-most EST	g5046523
Method	BLASTN
NCBI GI	g2735255
BLAST score	64
E value	3.0e-27
Match length	168
% identity	85
NCBI Description	Lycopersicon esculentum protein kinase (LePK6) gene, partial cds

Seq. No.	197295
Contig ID	30260_1.R1039
5'-most EST	g5050539
Method	BLASTX
NCBI GI	g3924596
BLAST score	470
E value	7.0e-47
Match length	97
% identity	92
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	197296
Contig ID	30262_1.R1039
5'-most EST	g5047036
Method	BLASTX
NCBI GI	g1946329
BLAST score	720
E value	3.0e-76
Match length	200
% identity	71
NCBI Description	(U69154) prohibitin [Nicotiana tabacum]

Seq. No.	197297
Contig ID	30271_1.R1039
5'-most EST	g5044630
Method	BLASTX
NCBI GI	g2494416
BLAST score	639

E value	8.0e-67
Match length	134
% identity	89
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi|166956 (M80597) fructose-1,6-bisphosphatase [Beta vulgaris] >gi|444324|prf||1906373A cytosolic fructose bisphosphatase [Beta vulgaris]

Seq. No.	197298
Contig ID	30273_1.R1039
5'-most EST	LIB3147-057-Q1-K1-A5

Seq. No.	197299
Contig ID	30276_1.R1039
5'-most EST	LIB3165-019-P1-K1-A5
Method	BLASTX
NCBI GI	g1711606
BLAST score	149
E value	1.0e-21
Match length	108
% identity	52
NCBI Description	SULFITE OXIDASE PRECURSOR >gi|1362942|pir||S55874 sulfite oxidase (EC 1.8.3.1) precursor, mitochondrial - human >gi|508502 (L31573) sulfite oxidase [Homo sapiens] >gi|1098062|prf||2115221A sulfide oxidase [Homo sapiens] >gi|4557867|ref|NP_000447.1|pSUOX| sulfite oxidase

Seq. No.	197300
Contig ID	30292_1.R1039
5'-most EST	uC-gsflmaxxa048d04b1
Method	BLASTX
NCBI GI	g2244841
BLAST score	288
E value	2.0e-25
Match length	129
% identity	48
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197301
Contig ID	30319_1.R1039
5'-most EST	LIB3148-002-P1-K1-A3

Seq. No.	197302
Contig ID	30335_1.R1039
5'-most EST	LIB3147-058-Q1-K1-D3
Method	BLASTX
NCBI GI	g1653033
BLAST score	263
E value	7.0e-23
Match length	66
% identity	74
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	197303
Contig ID	30339_1.R1039
5'-most EST	uC-gsronu33B148d05b1

Method	BLASTX
NCBI GI	g2146797
BLAST score	715
E value	1.0e-75
Match length	223
% identity	45
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi|1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi|1587210|prf||2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	197304
Contig ID	30344_1.R1039
5'-most EST	g5050176
Method	BLASTX
NCBI GI	g2245120
BLAST score	681
E value	2.0e-71
Match length	172
% identity	72
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197305
Contig ID	30350_1.R1039
5'-most EST	uC-gsflmaxxa047c11b1
Method	BLASTX
NCBI GI	g4204285
BLAST score	810
E value	1.0e-86
Match length	238
% identity	65
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	197306
Contig ID	30351_1.R1039
5'-most EST	uC-gsronu33B155e09b2
Method	BLASTX
NCBI GI	g2811014
BLAST score	173
E value	3.0e-12
Match length	75
% identity	52
NCBI Description	DYNEIN LIGHT CHAIN LC6, FLAGELLAR OUTER ARM >gi|2208914|dbj|BAA20525| (AB004830) outer arm dynein LC6 [Anthocidaris crassispina]

Seq. No.	197307
Contig ID	30352_1.R1039
5'-most EST	LIB3147-058-Q1-K1-G10

Seq. No.	197308
Contig ID	30357_1.R1039
5'-most EST	LIB3147-058-Q1-K1-F2

Seq. No.	197309
Contig ID	30360_1.R1039

5'-most EST	g5048553
Method	BLASTX
NCBI GI	g4455192
BLAST score	531
E value	6.0e-54
Match length	206
% identity	51
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	197310
Contig ID	30379_1.R1039
5'-most EST	LIB3147-058-Q1-K1-H3
Method	BLASTX
NCBI GI	g2529665
BLAST score	180
E value	4.0e-13
Match length	50
% identity	70
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	197311
Contig ID	30383_1.R1039
5'-most EST	LIB3147-058-Q1-K1-H8
Method	BLASTX
NCBI GI	g2105430
BLAST score	521
E value	3.0e-53
Match length	128
% identity	74
NCBI Description	(U97079) U5-116kD [Mus musculus]

Seq. No.	197312
Contig ID	30386_1.R1039
5'-most EST	uC-gsflnu33B023d10b1
Method	BLASTX
NCBI GI	g729842
BLAST score	789
E value	3.0e-84
Match length	205
% identity	77
NCBI Description	CHLOROPLAST MEMBRANE-ASSOCIATED 30 KD PROTEIN PRECURSOR (M30) >gi|1076532|pir||S47966 probable lipid transfer protein M30 precursor - garden pea >gi|169107 (M73744) IM30 [Pisum sativum]

Seq. No.	197313
Contig ID	30393_1.R1039
5'-most EST	uC-gsflnu33B146e03b1

Seq. No.	197314
Contig ID	30402_1.R1039
5'-most EST	LIB3197-011-P1-M1-F1
Method	BLASTX
NCBI GI	g2462825
BLAST score	274
E value	3.0e-24

Match length	91
% identity	59
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	197315
Contig ID	30404_1.R1039
5'-most EST	g5048164
Method	BLASTX
NCBI GI	g3142301
BLAST score	451
E value	1.0e-44
Match length	236
% identity	43
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb|M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb|Q05946. ESTs gb|N65081 gb|Z30910, gb|Z34190, gb|Z34611, gb|R30101, gb|H3630

Seq. No.	197316
Contig ID	30412_1.R1039
5'-most EST	LIB3148-044-Q1-K1-H3

Seq. No.	197317
Contig ID	30413_1.R1039
5'-most EST	LIB3147-059-Q1-K1-C6
Method	BLASTN
NCBI GI	g4512110
BLAST score	43
E value	8.0e-15
Match length	79
% identity	89
NCBI Description	Phalaenopsis sp. 'KCbutterfly' putative profilin mRNA, complete cds

Seq. No.	197318
Contig ID	30419_1.R1039
5'-most EST	LIB3197-052-Q1-M1-B12
Method	BLASTX
NCBI GI	g2104681
BLAST score	388
E value	3.0e-37
Match length	164
% identity	54
NCBI Description	(X97907) transcription factor [Vicia faba]

Seq. No.	197319
Contig ID	30424_1.R1039
5'-most EST	LIB3147-059-Q1-K1-E10
Method	BLASTX
NCBI GI	g2493046
BLAST score	234
E value	1.0e-19
Match length	77
% identity	60
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi|82297|pir||A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato
>gi|217938|dbj|BAA01511| (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	197320
Contig ID	30430_1.R1039
5'-most EST	g5046726
Method	BLASTX
NCBI GI	g3820614
BLAST score	503
E value	9.0e-51
Match length	233
% identity	48
NCBI Description	(AF094516) E1-like protein [Homo sapiens]

Seq. No.	197321
Contig ID	30432_1.R1039
5'-most EST	LIB3149-001-P1-K1-H10
Method	BLASTX
NCBI GI	g2911071
BLAST score	243
E value	2.0e-20
Match length	79
% identity	58
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197322
Contig ID	30433_1.R1039
5'-most EST	uC-gsronu33B109a05b1
Method	BLASTX
NCBI GI	g3822223
BLAST score	372
E value	2.0e-35
Match length	143
% identity	57
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	197323
Contig ID	30472_1.R1039
5'-most EST	LIB3148-012-Q1-K1-E1

Seq. No.	197324
Contig ID	30479_1.R1039
5'-most EST	uC-gsflmaxxa057a12b1
Method	BLASTX
NCBI GI	g2811026
BLAST score	381
E value	1.0e-36
Match length	80
% identity	90
NCBI Description	TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi|1946375 (U93215) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi|2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]

Seq. No.	197325
Contig ID	30488_1.R1039
5'-most EST	uC-gsronu33B109e04b1
Method	BLASTX
NCBI GI	g2982311
BLAST score	729
E value	2.0e-77
Match length	165
% identity	79
NCBI Description	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No.	197326
Contig ID	30502_1.R1039
5'-most EST	LIB3147-060-Q1-K1-E8
Method	BLASTX
NCBI GI	g3080415
BLAST score	523
E value	3.0e-53
Match length	130
% identity	78
NCBI Description	(AL022604) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	197327
Contig ID	30512_1.R1039
5'-most EST	LIB3147-060-Q1-K1-F8

Seq. No.	197328
Contig ID	30528_1.R1039
5'-most EST	LIB3147-060-Q1-K1-H8
Method	BLASTX
NCBI GI	g4105772
BLAST score	386
E value	3.0e-37
Match length	80
% identity	46
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	197329
Contig ID	30533_1.R1039
5'-most EST	LIB3148-046-Q1-K1-A2
Method	BLASTX
NCBI GI	g2829204
BLAST score	363
E value	2.0e-34
Match length	96
% identity	66
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	197330
Contig ID	30540_1.R1039
5'-most EST	uC-gsronu33B027e01b1

Seq. No.	197331
Contig ID	30541_1.R1039

5'-most EST	g5047186
Method	BLASTX
NCBI GI	g1706326
BLAST score	642
E value	1.0e-124
Match length	262
% identity	81
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi|2146786|pir||S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi|1177603|emb|CAA91444| (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.	197332
Contig ID	30565_1.R1039
5'-most EST	uC-gsflmaxxa028a06b1
Method	BLASTX
NCBI GI	g4309732
BLAST score	209
E value	2.0e-16
Match length	56
% identity	68
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197333
Contig ID	30567_1.R1039
5'-most EST	uC-gsronu33B078g08b1

Seq. No.	197334
Contig ID	30577_1.R1039
5'-most EST	LIB3166-011-P1-K1-E9

Seq. No.	197335
Contig ID	30590_1.R1039
5'-most EST	LIB3148-002-P1-K1-C5

Seq. No.	197336
Contig ID	30592_1.R1039
5'-most EST	uC-gsflnu33B027f08b1

Seq. No.	197337
Contig ID	30593_1.R1039
5'-most EST	LIB3148-002-P1-K1-C8
Method	BLASTX
NCBI GI	g4191789
BLAST score	176
E value	1.0e-12
Match length	64
% identity	64
NCBI Description	(AC005917) putative transmembrane transport protein [Arabidopsis thaliana]

Seq. No.	197338
Contig ID	30595_1.R1039
5'-most EST	uC-gsflnu33B112h12b1
Method	BLASTX
NCBI GI	g130718
BLAST score	314

E value	1.0e-28
Match length	120
% identity	43
NCBI Description	ACID PHOSPHATASE PRECURSOR 1 >gi|170370 (M83211) acid phosphatase type 1 [Lycopersicon esculentum] >gi|170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi|445121|prf||1908427A acid phosphatase 1 [Lycopersicon esculentum]

Seq. No.	197339
Contig ID	30599_1.R1039
5'-most EST	LIB3148-002-P1-K1-D7

Seq. No.	197340
Contig ID	30608_1.R1039
5'-most EST	LIB3148-002-P1-K1-E8

Seq. No.	197341
Contig ID	30610_1.R1039
5'-most EST	g5047550
Method	BLASTX
NCBI GI	g1483218
BLAST score	552
E value	2.0e-56
Match length	230
% identity	51
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	197342
Contig ID	30613_1.R1039
5'-most EST	LIB3148-002-P1-K1-F4

Seq. No.	197343
Contig ID	30621_1.R1039
5'-most EST	uC-gsflnu33B083b05b1
Method	BLASTX
NCBI GI	g1814401
BLAST score	696
E value	2.0e-73
Match length	209
% identity	62
NCBI Description	(U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq. No.	197344
Contig ID	30636_1.R1039
5'-most EST	LIB3197-060-Q1-M1-H9

Seq. No.	197345
Contig ID	30638_1.R1039
5'-most EST	LIB3148-034-Q1-K1-F12
Method	BLASTX
NCBI GI	g1364059
BLAST score	322
E value	1.0e-29
Match length	158
% identity	41

NCBI Description	dioscorin class A precursor - Dioscorea cayenensis >gi|433463|emb|CAA53781| (X76187) storage protein [Dioscorea cayenensis]
Seq. No.	197346
Contig ID	30647_1.R1039
5'-most EST	LIB3272-002-P1-K1-C3
Method	BLASTX
NCBI GI	g3879145
BLAST score	184
E value	3.0e-13
Match length	79
% identity	41
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]
Seq. No.	197347
Contig ID	30662_1.R1039
5'-most EST	LIB3148-003-P1-K1-D3
Method	BLASTX
NCBI GI	g1172002
BLAST score	1601
E value	1.0e-179
Match length	355
% identity	86
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi|556424 (L36822) phenylalanine ammonia lyase [Stylosanthes humilis]
Seq. No.	197348
Contig ID	30683_1.R1039
5'-most EST	LIB3272-033-P1-K1-H10
Seq. No.	197349
Contig ID	30702_1.R1039
5'-most EST	LIB3272-044-P1-K1-B1
Method	BLASTN
NCBI GI	g499025
BLAST score	133
E value	3.0e-68
Match length	725
% identity	81
NCBI Description	V.vinifera PAL mRNA for phenylalanine ammonia lyase
Seq. No.	197350
Contig ID	30706_1.R1039
5'-most EST	uC-gsronu33B117e01b1
Method	BLASTX
NCBI GI	g2832658
BLAST score	221
E value	1.0e-17
Match length	73
% identity	52
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]
Seq. No.	197351
Contig ID	30720_1.R1039

5'-most EST	LIB3149-044-Q1-K1-G9
Seq. No.	197352
Contig ID	30722_1.R1039
5'-most EST	LIB3149-027-Q1-K1-B3
Method	BLASTX
NCBI GI	g3850821
BLAST score	332
E value	9.0e-35
Match length	139
% identity	54
NCBI Description	(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]
Seq. No.	197353
Contig ID	30730_1.R1039
5'-most EST	LIB3148-031-Q1-K1-C4
Method	BLASTX
NCBI GI	g4567225
BLAST score	284
E value	5.0e-25
Match length	71
% identity	72
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.	197354
Contig ID	30732_1.R1039
5'-most EST	LIB3148-036-Q1-K1-H11
Method	BLASTX
NCBI GI	g3080393
BLAST score	258
E value	3.0e-22
Match length	51
% identity	90
NCBI Description	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]
Seq. No.	197355
Contig ID	30734_1.R1039
5'-most EST	LIB3166-004-P1-K1-C7
Seq. No.	197356
Contig ID	30739_1.R1039
5'-most EST	LIB3148-004-Q1-K1-E9
Method	BLASTX
NCBI GI	g1705463
BLAST score	143
E value	1.0e-08
Match length	39
% identity	69
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi|2129547|pir||S71201 biotin sythase - Arabidopsis thaliana >gi|1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi|1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi|1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi|2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi|1589016|prf||2209438A biotin synthase [Arabidopsis

thaliana]

Seq. No.	197357
Contig ID	30749_1.R1039
5'-most EST	LIB3148-004-Q1-K1-G2

Seq. No.	197358
Contig ID	30759_1.R1039
5'-most EST	LIB3189-024-P1-K1-B5
Method	BLASTX
NCBI GI	g2827559
BLAST score	417
E value	1.0e-40
Match length	169
% identity	49
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi|3292808|emb|CAA19798| (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	197359
Contig ID	30762_2.R1039
5'-most EST	LIB3148-014-Q1-K1-H11
Method	BLASTX
NCBI GI	g3831441
BLAST score	104
E value	6.0e-09
Match length	43
% identity	81
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197360
Contig ID	30765_1.R1039
5'-most EST	LIB3165-032-P1-K1-E2
Method	BLASTX
NCBI GI	g2493694
BLAST score	333
E value	6.0e-31
Match length	135
% identity	50
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi|1076268|pir||S53025 photosystem II protein - spinach >gi|728716|emb|CAA59409| (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	197361
Contig ID	30776_1.R1039
5'-most EST	LIB3148-005-Q1-K1-B11
Method	BLASTX
NCBI GI	g4263711
BLAST score	240
E value	4.0e-20
Match length	88
% identity	51
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No. 197362

Contig ID 30786_1.R1039
5'-most EST uC-gsflnu33B079g09b1

Seq. No. 197363
Contig ID 30788_1.R1039
5'-most EST LIB3149-003-P1-K1-F5

Seq. No. 197364
Contig ID 30792_1.R1039
5'-most EST LIB3148-005-Q1-K1-C8
Method BLASTX
NCBI GI g3928090
BLAST score 215
E value 5.0e-28
Match length 138
% identity 46
NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 197365
Contig ID 30794_1.R1039
5'-most EST LIB3197-055-Q1-M1-G10
Method BLASTX
NCBI GI g4558665
BLAST score 180
E value 2.0e-13
Match length 38
% identity 79
NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]

Seq. No. 197366
Contig ID 30795_1.R1039
5'-most EST LIB3148-005-Q1-K1-D11

Seq. No. 197367
Contig ID 30800_1.R1039
5'-most EST LIB3197-046-Q1-M1-E7

Seq. No. 197368
Contig ID 30806_1.R1039
5'-most EST LIB3196-028-P1-M1-H3

Seq. No. 197369
Contig ID 30822_1.R1039
5'-most EST uC-gsronu33B145g04b1
Method BLASTX
NCBI GI g4263712
BLAST score 481
E value 3.0e-48
Match length 122
% identity 70
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 197370
Contig ID 30822_2.R1039
5'-most EST LIB3149-006-Q1-K1-A9
Method BLASTX

NCBI GI	g4263712
BLAST score	312
E value	7.0e-42
Match length	120
% identity	70
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	197371
Contig ID	30834_1.R1039
5'-most EST	LIB3148-005-Q1-K1-H4
Method	BLASTX
NCBI GI	g3098571
BLAST score	188
E value	4.0e-14
Match length	64
% identity	55
NCBI Description	(AF049028) BURP domain containing protein [Brassica napus]

Seq. No.	197372
Contig ID	30839_1.R1039
5'-most EST	uC-gsflmaxxa060d10b1

Seq. No.	197373
Contig ID	30866_1.R1039
5'-most EST	LIB3148-006-Q1-K1-D3

Seq. No.	197374
Contig ID	30872_1.R1039
5'-most EST	g5049738
Method	BLASTX
NCBI GI	g2673910
BLAST score	145
E value	7.0e-09
Match length	82
% identity	44
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197375
Contig ID	30881_1.R1039
5'-most EST	LIB3148-008-Q1-K1-E12
Method	BLASTX
NCBI GI	g4572668
BLAST score	227
E value	8.0e-19
Match length	100
% identity	44
NCBI Description	(AC006954) putative retrotransposon polyprotein [Arabidopsis thaliana]

Seq. No.	197376
Contig ID	30898_1.R1039
5'-most EST	LIB3148-006-Q1-K1-H11

Seq. No.	197377
Contig ID	30911_1.R1039
5'-most EST	LIB3148-007-Q1-K1-A5

Seq. No.	197378
Contig ID	30916_1.R1039
5'-most EST	LIB3148-007-Q1-K1-B7

Seq. No.	197379
Contig ID	30922_1.R1039
5'-most EST	LIB3148-007-Q1-K1-C5
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	45
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	197380
Contig ID	30924_1.R1039
5'-most EST	LIB3148-007-Q1-K1-C1

Seq. No.	197381
Contig ID	30940_1.R1039
5'-most EST	uC-gsflnu33B085g12b1
Method	BLASTX
NCBI GI	g2346972
BLAST score	282
E value	5.0e-25
Match length	127
% identity	36
NCBI Description	(AB006598) ZPT2-11 [Petunia x hybrida]

Seq. No.	197382
Contig ID	30941_1.R1039
5'-most EST	LIB3148-007-Q1-K1-E7

Seq. No.	197383
Contig ID	30945_1.R1039
5'-most EST	LIB3148-007-Q1-K1-F11
Method	BLASTX
NCBI GI	g2804280
BLAST score	624
E value	4.0e-65
Match length	143
% identity	76
NCBI Description	(AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi|3929918|dbj|BAA34711| (AB017331) 6-4 photolyase [Arabidopsis thaliana]

Seq. No.	197384
Contig ID	30957_1.R1039
5'-most EST	LIB3148-007-Q1-K1-G8

Seq. No.	197385
Contig ID	30974_1.R1039
5'-most EST	LIB3148-008-Q1-K1-A5
Method	BLASTX
NCBI GI	g4102727

BLAST score	159
E value	1.0e-10
Match length	100
% identity	40
NCBI Description	(AF015782) blight-associated protein p12 precursor [Citrus jambhiri]

Seq. No.	197386
Contig ID	30976_1.R1039
5'-most EST	uC-gsronu33B047c08b1
Method	BLASTX
NCBI GI	g3287687
BLAST score	353
E value	2.0e-58
Match length	228
% identity	53
NCBI Description	(AC003979) Match to sucrose-proton symporter (SUC2) gene gb|X75382 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	197387
Contig ID	30994_1.R1039
5'-most EST	uC-gsflmaxxa061g07b1

Seq. No.	197388
Contig ID	30997_1.R1039
5'-most EST	LIB3148-044-Q1-K1-G1

Seq. No.	197389
Contig ID	31000_1.R1039
5'-most EST	LIB3148-008-Q1-K1-D4

Seq. No.	197390
Contig ID	31006_1.R1039
5'-most EST	uC-gsronu33B154c02b2

Seq. No.	197391
Contig ID	31035_1.R1039
5'-most EST	g5049845
Method	BLASTX
NCBI GI	g4204315
BLAST score	782
E value	2.0e-83
Match length	241
% identity	58
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	197392
Contig ID	31036_1.R1039
5'-most EST	LIB3149-016-Q1-K1-E12
Method	BLASTX
NCBI GI	g4567309
BLAST score	153
E value	5.0e-10
Match length	70
% identity	46
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197393
Contig ID	31046_1.R1039
5'-most EST	LIB3196-059-P1-M1-C7
Method	BLASTX
NCBI GI	g3242753
BLAST score	238
E value	1.0e-19
Match length	166
% identity	33
NCBI Description	(AC005162) probable carboxypeptidase precursor; 64% similar to P42660 (PID:g1718107) [Homo sapiens]

Seq. No.	197394
Contig ID	31054_1.R1039
5'-most EST	LIB3148-019-Q1-K1-G8

Seq. No.	197395
Contig ID	31062_1.R1039
5'-most EST	g3326569
Method	BLASTX
NCBI GI	g1041704
BLAST score	510
E value	3.0e-96
Match length	219
% identity	75
NCBI Description	(U30478) expansin At-EXP5 [Arabidopsis thaliana]

Seq. No.	197396
Contig ID	31067_1.R1039
5'-most EST	LIB3148-009-Q1-K1-C11
Method	BLASTX
NCBI GI	g3885343
BLAST score	263
E value	1.0e-22
Match length	121
% identity	42
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197397
Contig ID	31070_1.R1039
5'-most EST	LIB3148-009-Q1-K1-C3
Method	BLASTX
NCBI GI	g1079393
BLAST score	168
E value	6.0e-12
Match length	121
% identity	42
NCBI Description	chromokinesin - chicken >gi|603761 (U18309) chromokinesin [Gallus gallus]

Seq. No.	197398
Contig ID	31071_1.R1039
5'-most EST	LIB3189-044-P1-K1-H8
Method	BLASTX
NCBI GI	g3646340
BLAST score	726
E value	4.0e-77

Match length 156
% identity 91
NCBI Description (AJ000763) MADS-box protein [Malus domestica]

Seq. No. 197399
Contig ID 31073_1.R1039
5'-most EST LIB3148-009-Q1-K1-C7

Seq. No. 197400
Contig ID 31077_1.R1039
5'-most EST LIB3148-055-Q1-K1-G1

Seq. No. 197401
Contig ID 31089_1.R1039
5'-most EST LIB3148-009-Q1-K1-E6

Seq. No. 197402
Contig ID 31107_1.R1039
5'-most EST LIB3148-009-Q1-K1-G8
Method BLASTX
NCBI GI g4468813
BLAST score 233
E value 2.0e-24
Match length 104
% identity 55
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 197403
Contig ID 31109_1.R1039
5'-most EST LIB3148-009-Q1-K1-H10
Method BLASTX
NCBI GI g2213871
BLAST score 295
E value 2.0e-26
Match length 90
% identity 72
NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No. 197404
Contig ID 31112_1.R1039
5'-most EST LIB3148-009-Q1-K1-H2
Method BLASTX
NCBI GI g231503
BLAST score 705
E value 2.0e-74
Match length 142
% identity 94
NCBI Description ACTIN 97 >gi|100417|pir||S20098 actin - potato >gi|21544|emb|CAA39280| (X55751) actin [Solanum tuberosum]

Seq. No. 197405
Contig ID 31125_1.R1039
5'-most EST LIB3148-010-Q1-K1-A8
Method BLASTX
NCBI GI g3805956
BLAST score 188

E value	4.0e-14
Match length	52
% identity	94
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	197406
Contig ID	31127_1.R1039
5'-most EST	LIB3148-010-Q1-K1-B7
Method	BLASTX
NCBI GI	g2245131
BLAST score	146
E value	3.0e-09
Match length	81
% identity	40
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197407
Contig ID	31137_1.R1039
5'-most EST	uC-gsflnu33B089c01b1
Method	BLASTX
NCBI GI	g4262140
BLAST score	360
E value	4.0e-34
Match length	117
% identity	63
NCBI Description	(AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No.	197408
Contig ID	31138_1.R1039
5'-most EST	LIB3165-021-P1-K1-F2
Method	BLASTX
NCBI GI	g1237082
BLAST score	1414
E value	1.0e-157
Match length	289
% identity	93
NCBI Description	(X96765) ADP-glucose pyrophosphorylase [Pisum sativum]

Seq. No.	197409
Contig ID	31139_1.R1039
5'-most EST	uC-gsflnu33B004f08b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	197410
Contig ID	31146_1.R1039
5'-most EST	uC-gsronu33B019e03b1

Seq. No.	197411
Contig ID	31156_1.R1039
5'-most EST	LIB3148-010-Q1-K1-E11
Method	BLASTX

NCBI GI	g4455177
BLAST score	265
E value	4.0e-23
Match length	102
% identity	52
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	197412
Contig ID	31157_1.R1039
5'-most EST	LIB3272-007-P1-K1-D2

Seq. No.	197413
Contig ID	31162_1.R1039
5'-most EST	LIB3148-010-Q1-K1-E7

Seq. No.	197414
Contig ID	31166_1.R1039
5'-most EST	LIB3148-010-Q1-K1-F10

Seq. No.	197415
Contig ID	31175_1.R1039
5'-most EST	LIB3148-010-Q1-K1-G11
Method	BLASTX
NCBI GI	g4455210
BLAST score	537
E value	4.0e-55
Match length	127
% identity	80
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	197416
Contig ID	31187_1.R1039
5'-most EST	LIB3148-010-Q1-K1-H5
Method	BLASTX
NCBI GI	g533256
BLAST score	544
E value	1.0e-55
Match length	187
% identity	56
NCBI Description	(L27101) pectinesterase [Petunia inflata]

Seq. No.	197417
Contig ID	31208_1.R1039
5'-most EST	LIB3148-011-Q1-K1-B8
Method	BLASTX
NCBI GI	g3122572
BLAST score	649
E value	6.0e-68
Match length	156
% identity	78
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi|1084434|pir||S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi|758340|emb|CAA59818| (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No. 197418
Contig ID 31212_1.R1039
5'-most EST LIB3149-024-Q1-K1-F6
Method BLASTX
NCBI GI g4376815
BLAST score 481
E value 4.0e-48
Match length 231
% identity 42
NCBI Description (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia pneumoniae]

Seq. No. 197419
Contig ID 31218_1.R1039
5'-most EST uC-gsflnu33B085f10b1

Seq. No. 197420
Contig ID 31236_1.R1039
5'-most EST uC-gsronu33B079d08b1
Method BLASTX
NCBI GI g1255954
BLAST score 534
E value 1.0e-54
Match length 118
% identity 83
NCBI Description (Z70677) thioredoxin [Ricinus communis]

Seq. No. 197421
Contig ID 31236_2.R1039
5'-most EST uC-gsflnu33B062f08b1
Method BLASTX
NCBI GI g2129752
BLAST score 346
E value 1.0e-32
Match length 114
% identity 52
NCBI Description thioredoxin - Arabidopsis thaliana >gi|992964|emb|CAA84612| (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No. 197422
Contig ID 31238_1.R1039
5'-most EST LIB3196-031-P1-M1-G6
Method BLASTX
NCBI GI g4567303
BLAST score 355
E value 2.0e-33
Match length 68
% identity 88
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 197423
Contig ID 31249_1.R1039
5'-most EST LIB3148-017-Q1-K1-H1

Seq. No. 197424
Contig ID 31253_1.R1039

5'-most EST	LIB3149-019-Q1-K1-E5
Method	BLASTX
NCBI GI	g2500376
BLAST score	378
E value	5.0e-38
Match length	94
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi|4262177|gb|AAD14494| (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	197425
Contig ID	31265_1.R1039
5'-most EST	LIB3272-058-P1-K1-H4
Method	BLASTX
NCBI GI	g1730843
BLAST score	213
E value	6.0e-17
Match length	149
% identity	14
NCBI Description	HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION >gi|2131945|pir||S63228 hypothetical protein YNL255c - yeast (Saccharomyces cerevisiae) >gi|1255963|emb|CAA65489| (X96722) ORF N0852 [Saccharomyces cerevisiae] >gi|1302303|emb|CAA96162| (Z71531) ORF YNL255c [Saccharomyces cerevisiae]

Seq. No.	197426
Contig ID	31274_1.R1039
5'-most EST	LIB3196-037-P1-M1-D8
Method	BLASTX
NCBI GI	g2944446
BLAST score	1125
E value	1.0e-123
Match length	247
% identity	83
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No.	197427
Contig ID	31283_1.R1039
5'-most EST	LIB3149-021-Q1-K1-H12

Seq. No.	197428
Contig ID	31292_1.R1039
5'-most EST	LIB3148-012-Q1-K1-D5

Seq. No.	197429
Contig ID	31305_1.R1039
5'-most EST	LIB3272-014-P1-K1-B9
Method	BLASTX
NCBI GI	g3492806
BLAST score	1099
E value	1.0e-120
Match length	291
% identity	73
NCBI Description	(AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No.	197430
Contig ID	31342_2.R1039
5'-most EST	uC-gsflmaxxa089f05b1

Seq. No.	197431
Contig ID	31354_1.R1039
5'-most EST	LIB3148-023-Q1-K1-A7
Method	BLASTN
NCBI GI	g1871173
BLAST score	49
E value	3.0e-18
Match length	237
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	197432
Contig ID	31366_1.R1039
5'-most EST	g5047303
Method	BLASTX
NCBI GI	g1871196
BLAST score	729
E value	3.0e-77
Match length	164
% identity	85
NCBI Description	(U90439) GMP kinase isolog [Arabidopsis thaliana] >gi|2335091 (AC002339) putative GMP kinase [Arabidopsis thaliana]

Seq. No.	197433
Contig ID	31370_1.R1039
5'-most EST	LIB3148-013-Q1-K1-D4
Method	BLASTX
NCBI GI	g2245030
BLAST score	426
E value	1.0e-41
Match length	172
% identity	56
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	197434
Contig ID	31373_2.R1039
5'-most EST	uC-gsflnu33B091d01b1

Seq. No.	197435
Contig ID	31377_1.R1039
5'-most EST	LIB3166-005-P1-K1-C4

Seq. No.	197436
Contig ID	31378_1.R1039
5'-most EST	LIB3148-044-Q1-K1-C7
Method	BLASTX
NCBI GI	g231509
BLAST score	342
E value	4.0e-45

Match length	114
% identity	72
NCBI Description	ACTIN DEPOLYMERIZING FACTOR (ADF) >gi|419809|pir||S30935 actin-depolymerizing factor - trumpet lily >gi|22748|emb|CAA78483| (Z14110) actin depolymerizing factor [Lilium longiflorum]

Seq. No.	197437
Contig ID	31381_1.R1039
5'-most EST	LIB3197-015-P1-M1-G2
Method	BLASTX
NCBI GI	g3914386
BLAST score	178
E value	8.0e-13
Match length	77
% identity	48
NCBI Description	ALLERGEN MF1 >gi|3445490|dbj|BAA32435| (AB011804) MF1 [Malassezia furfur]

Seq. No.	197438
Contig ID	31385_1.R1039
5'-most EST	uC-gsflnu33B015b02b1

Seq. No.	197439
Contig ID	31405_1.R1039
5'-most EST	LIB3189-051-P1-K1-B8
Method	BLASTX
NCBI GI	g3790359
BLAST score	196
E value	7.0e-15
Match length	67
% identity	55
NCBI Description	(AB013359) DPM2 [Rattus norvegicus]

Seq. No.	197440
Contig ID	31406_1.R1039
5'-most EST	LIB3148-013-Q1-K1-H10

Seq. No.	197441
Contig ID	31413_1.R1039
5'-most EST	LIB3148-013-Q1-K1-H6
Method	BLASTX
NCBI GI	g3548801
BLAST score	143
E value	7.0e-09
Match length	66
% identity	39
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi|4335768|gb|AAD17445| (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	197442
Contig ID	31442_1.R1039
5'-most EST	LIB3189-051-P1-K1-E2
Method	BLASTN
NCBI GI	g167346
BLAST score	51

E value	2.0e-19
Match length	202
% identity	85
NCBI Description	Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds

Seq. No.	197443
Contig ID	31463_1.R1039
5'-most EST	LIB3148-014-Q1-K1-F6
Method	BLASTX
NCBI GI	g477280
BLAST score	230
E value	8.0e-19
Match length	57
% identity	70
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi|410633|bbs|136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	197444
Contig ID	31481_1.R1039
5'-most EST	LIB3166-025-P1-K1-F3

Seq. No.	197445
Contig ID	31487_1.R1039
5'-most EST	LIB3148-015-Q1-K1-A8

Seq. No.	197446
Contig ID	31488_1.R1039
5'-most EST	LIB3165-060-Q1-K1-C12

Seq. No.	197447
Contig ID	31517_1.R1039
5'-most EST	LIB3148-015-Q1-K1-E10

Seq. No.	197448
Contig ID	31525_1.R1039
5'-most EST	LIB3148-015-Q1-K1-E8
Method	BLASTX
NCBI GI	g130600
BLAST score	466
E value	4.0e-65
Match length	201
% identity	62
NCBI Description	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi|76782|pir||S01283 hypothetical protein 5 - figwort mosaic virus >gi|58813|emb|CAA29527| (X06166) ORF V (AA 1-666) [Figwort mosaic virus]

Seq. No.	197449
Contig ID	31527_1.R1039
5'-most EST	LIB3148-015-Q1-K1-F1

Seq. No.	197450

Contig ID 31539_1.R1039
5'-most EST uC-gsflnu33B143f09b1

Seq. No. 197451
Contig ID 31545_1.R1039
5'-most EST LIB3148-015-Q1-K1-H11

Seq. No. 197452
Contig ID 31553_1.R1039
5'-most EST uC-gsronu33B016d06b1

Seq. No. 197453
Contig ID 31562_1.R1039
5'-most EST uC-gsronu33B082e08b1

Seq. No. 197454
Contig ID 31570_1.R1039
5'-most EST g5047296
Method BLASTX
NCBI GI g4056480
BLAST score 640
E value 2.0e-66
Match length 210
% identity 61
NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 197455
Contig ID 31570_2.R1039
5'-most EST g5050876
Method BLASTX
NCBI GI g4056480
BLAST score 293
E value 2.0e-26
Match length 77
% identity 70
NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 197456
Contig ID 31576_1.R1039
5'-most EST uC-gsflmaxxa048d07b1
Method BLASTX
NCBI GI g730217
BLAST score 270
E value 3.0e-24
Match length 101
% identity 57
NCBI Description ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID AMINOTRANSFERASE) >gi|550311|emb|CAA57398| (X81802) ornithine< aminotransferase [Bacillus subtilis] >gi|1064807|dbj|BAA11293| (D78193) orthinine aminotransferase [Bacillus subtilis] >gi|2636581|emb|CAB16071| (Z99124) ornithine aminotransferase [Bacillus subtilis]

Seq. No. 197457
Contig ID 31595_1.R1039
5'-most EST uC-gsronu33B110h09b1

Method	BLASTX
NCBI GI	g4455276
BLAST score	474
E value	2.0e-47
Match length	122
% identity	72
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	197458
Contig ID	31599_1.R1039
5'-most EST	g5048186
Method	BLASTX
NCBI GI	g4406820
BLAST score	590
E value	7.0e-61
Match length	173
% identity	71
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No.	197459
Contig ID	31652_1.R1039
5'-most EST	LIB3148-017-Q1-K1-C1
Method	BLASTX
NCBI GI	g3879792
BLAST score	166
E value	2.0e-11
Match length	83
% identity	47
NCBI Description	(Z81120) similar to Ank repeat; cDNA EST yk400c12.5 comes from this gene; cDNA EST EMBL:D75223 comes from this gene; cDNA EST yk400c12.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	197460
Contig ID	31657_1.R1039
5'-most EST	uC-gsflmaxxa001d01b1
Method	BLASTX
NCBI GI	g4056432
BLAST score	1574
E value	1.0e-176
Match length	424
% identity	67
NCBI Description	(AC005990) Similar to gi|2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb|Z97341. ESTs gb|T20778 and gb|AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	197461
Contig ID	31667_1.R1039
5'-most EST	LIB3148-017-Q1-K1-D8
Method	BLASTX
NCBI GI	g1076511
BLAST score	801
E value	8.0e-86
Match length	188

% identity	80
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi|758250|emb|CAA59799| (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	197462
Contig ID	31677_1.R1039
5'-most EST	LIB3148-017-Q1-K1-G4
Method	BLASTX
NCBI GI	g2392025
BLAST score	812
E value	6.0e-87
Match length	167
% identity	88
NCBI Description	(D88420) stromal ascorbate peroxidase [Cucurbita sp.]

Seq. No.	197463
Contig ID	31701_1.R1039
5'-most EST	uC-gsronu33B011f10b1

Seq. No.	197464
Contig ID	31710_1.R1039
5'-most EST	LIB3148-058-Q1-K1-G2
Method	BLASTX
NCBI GI	g3924613
BLAST score	313
E value	2.0e-28
Match length	128
% identity	48
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana] >gi|4263512|gb|AAD15338| (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197465
Contig ID	31714_1.R1039
5'-most EST	LIB3149-049-Q1-K1-G5
Method	BLASTN
NCBI GI	g2760168
BLAST score	34
E value	2.0e-09
Match length	87
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	197466
Contig ID	31729_1.R1039
5'-most EST	uC-gsflnu33B111b08b1
Method	BLASTX
NCBI GI	g585337
BLAST score	604
E value	1.0e-62
Match length	159
% identity	75
NCBI Description	ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE) >gi|391877|dbj|BAA01180| (D10334) adenylate kinase-a [Oryza sativa]

Seq. No.	197467
Contig ID	31750_1.R1039
5'-most EST	g5047790
Method	BLASTX
NCBI GI	g3540181
BLAST score	513
E value	9.0e-52
Match length	240
% identity	47
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	197468
Contig ID	31766_1.R1039
5'-most EST	g5047276
Method	BLASTX
NCBI GI	g3128194
BLAST score	734
E value	8.0e-78
Match length	223
% identity	66
NCBI Description	(AC004521) putative heme A:farnesyltransferase [Arabidopsis thaliana]

Seq. No.	197469
Contig ID	31772_1.R1039
5'-most EST	LIB3189-047-P1-K1-C3

Seq. No.	197470
Contig ID	31791_1.R1039
5'-most EST	LIB3148-019-Q1-K1-D10
Method	BLASTX
NCBI GI	g4510389
BLAST score	763
E value	3.0e-81
Match length	225
% identity	67
NCBI Description	(AC007017) putative solute carrier protein [Arabidopsis thaliana]

Seq. No.	197471
Contig ID	31792_1.R1039
5'-most EST	uC-gsflmaxxa042h09b1
Method	BLASTX
NCBI GI	g3482910
BLAST score	272
E value	6.0e-37
Match length	103
% identity	63
NCBI Description	(AC003970) Similar to rice water stress induced protein gi|537404 [Arabidopsis thaliana]

Seq. No.	197472
Contig ID	31809_1.R1039
5'-most EST	LIB3148-019-Q1-K1-F12
Method	BLASTX
NCBI GI	g4388834

BLAST score 169
E value 7.0e-12
Match length 134
% identity 11
NCBI Description (AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]

Seq. No. 197473
Contig ID 31824_1.R1039
5'-most EST LIB3148-023-Q1-K1-B1

Seq. No. 197474
Contig ID 31831_1.R1039
5'-most EST LIB3196-041-P1-M1-G6
Method BLASTX
NCBI GI g2765244
BLAST score 433
E value 1.0e-42
Match length 170
% identity 51
NCBI Description (Y12807) invertase inhibitor homolog [Arabidopsis thaliana]

Seq. No. 197475
Contig ID 31839_1.R1039
5'-most EST g5048372

Seq. No. 197476
Contig ID 31840_1.R1039
5'-most EST LIB3148-020-Q1-K1-A7
Method BLASTX
NCBI GI g2463509
BLAST score 216
E value 2.0e-17
Match length 87
% identity 51
NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 197477
Contig ID 31843_1.R1039
5'-most EST LIB3148-034-Q1-K1-A5
Method BLASTN
NCBI GI g3449312
BLAST score 36
E value 1.0e-10
Match length 72
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No. 197478
Contig ID 31846_1.R1039
5'-most EST LIB3148-020-Q1-K1-B12
Method BLASTX
NCBI GI g3915845
BLAST score 309
E value 5.0e-28
Match length 124

% identity	52
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S9 >gi|3603065|gb|AAC35726| (AF041468) ribosomal protein S9 [Guillardia theta]

Seq. No.	197479
Contig ID	31848_1.R1039
5'-most EST	LIB3148-020-Q1-K1-B4

Seq. No.	197480
Contig ID	31850_1.R1039
5'-most EST	LIB3166-032-P1-K1-F3
Method	BLASTX
NCBI GI	g3702339
BLAST score	215
E value	2.0e-17
Match length	89
% identity	48
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	197481
Contig ID	31855_1.R1039
5'-most EST	uC-gsronu33B050e03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	5.0e-10
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	197482
Contig ID	31869_1.R1039
5'-most EST	LIB3197-002-P1-M1-H2
Method	BLASTX
NCBI GI	g3088333
BLAST score	187
E value	2.0e-13
Match length	196
% identity	31
NCBI Description	(D86951) CYP3A31 [Mesocricetus auratus]

Seq. No.	197483
Contig ID	31871_1.R1039
5'-most EST	uC-gsronu33B028b04b1
Method	BLASTX
NCBI GI	g2288981
BLAST score	482
E value	3.0e-48
Match length	166
% identity	60
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi|3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	197484
Contig ID	31879_1.R1039

5'-most EST	LIB3272-050-P1-K1-D11
Seq. No.	197485
Contig ID	31890_1.R1039
5'-most EST	LIB3196-050-P1-M1-B9
Method	BLASTX
NCBI GI	g2739383
BLAST score	1012
E value	1.0e-110
Match length	297
% identity	69
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.	197486
Contig ID	31895_1.R1039
5'-most EST	LIB3197-043-Q1-M1-G1
Method	BLASTX
NCBI GI	g4432830
BLAST score	712
E value	3.0e-75
Match length	240
% identity	61
NCBI Description	(AC006283) similar to pheromone receptor deficient mutant [Arabidopsis thaliana]
Seq. No.	197487
Contig ID	31900_2.R1039
5'-most EST	LIB3149-049-Q1-K1-H6
Seq. No.	197488
Contig ID	31905_1.R1039
5'-most EST	uC-gsflmaxxa011b12b1
Seq. No.	197489
Contig ID	31909_1.R1039
5'-most EST	uC-gsronu33B126a09b1
Method	BLASTX
NCBI GI	g4544412
BLAST score	241
E value	5.0e-20
Match length	116
% identity	39
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	197490
Contig ID	31911_1.R1039
5'-most EST	LIB3148-021-Q1-K1-A7
Seq. No.	197491
Contig ID	31912_1.R1039
5'-most EST	LIB3166-051-P1-K1-H7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	6.0e-11
Match length	36
% identity	100

NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	197492
Contig ID	31916_1.R1039
5'-most EST	LIB3148-021-Q1-K1-B11
Seq. No.	197493
Contig ID	31923_1.R1039
5'-most EST	uC-gsflmaxxa028a05b1
Method	BLASTX
NCBI GI	g1040877
BLAST score	377
E value	3.0e-36
Match length	96
% identity	73
NCBI Description	(U30460) expansin S2 precursor [Cucumis sativus]
Seq. No.	197494
Contig ID	31934_1.R1039
5'-most EST	LIB3148-021-Q1-K1-D10
Method	BLASTX
NCBI GI	g3335353
BLAST score	186
E value	4.0e-14
Match length	93
% identity	43
NCBI Description	(AC004512) Similar to cytochrome P450 gb|X90458 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	197495
Contig ID	31946_1.R1039
5'-most EST	uC-gsflnu33B056h10b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	350
E value	8.0e-33
Match length	150
% identity	55
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.	197496
Contig ID	31951_1.R1039
5'-most EST	uC-gsflnu33B057f12b1
Method	BLASTX
NCBI GI	g2914701
BLAST score	306
E value	1.0e-27
Match length	119
% identity	49
NCBI Description	(AC003974) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.	197497
Contig ID	31956_2.R1039
5'-most EST	uC-gsflmaxxa046h03b1
Seq. No.	197498
Contig ID	31966_1.R1039

5'-most EST	LIB3148-021-Q1-K1-G2
Method	BLASTX
NCBI GI	g1743009
BLAST score	1322
E value	1.0e-146
Match length	289
% identity	87
NCBI Description	(Y10036) SNF1-related protein kinase [Cucumis sativus]

Seq. No.	197499
Contig ID	31975_1.R1039
5'-most EST	LIB3148-021-Q1-K1-H3

Seq. No.	197500
Contig ID	31978_1.R1039
5'-most EST	uC-gsronu33b112e01b1
Method	BLASTX
NCBI GI	g3033397
BLAST score	557
E value	3.0e-57
Match length	116
% identity	89
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	197501
Contig ID	31997_1.R1039
5'-most EST	LIB3189-041-P1-K1-C4

Seq. No.	197502
Contig ID	31997_2.R1039
5'-most EST	LIB3272-058-P1-K1-F1
Method	BLASTX
NCBI GI	g2950478
BLAST score	311
E value	2.0e-28
Match length	128
% identity	49
NCBI Description	(AL022070) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	197503
Contig ID	32005_1.R1039
5'-most EST	g5047470
Method	BLASTN
NCBI GI	g1432057
BLAST score	53
E value	1.0e-20
Match length	199
% identity	85
NCBI Description	Petroselinum crispum DNA-binding protein WRKY2 mRNA, partial cds

Seq. No.	197504
Contig ID	32006_1.R1039
5'-most EST	LIB3148-022-Q1-K1-C7

Seq. No.	197505
Contig ID	32009_1.R1039

5'-most EST	LIB3148-047-Q1-K1-G7
Seq. No.	197506
Contig ID	32014_1.R1039
5'-most EST	LIB3148-022-Q1-K1-E10
Method	BLASTX
NCBI GI	g1781299
BLAST score	222
E value	4.0e-18
Match length	66
% identity	62
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]
Seq. No.	197507
Contig ID	32024_1.R1039
5'-most EST	uC-gsronu33B111g11b1
Method	BLASTX
NCBI GI	g1435021
BLAST score	146
E value	5.0e-17
Match length	122
% identity	55
NCBI Description	(D26575) DNA-binding protein [Daucus carota]
Seq. No.	197508
Contig ID	32048_1.R1039
5'-most EST	uC-gsronu33B050e01b1
Seq. No.	197509
Contig ID	32077_1.R1039
5'-most EST	g5045045
Method	BLASTX
NCBI GI	g481384
BLAST score	166
E value	2.0e-11
Match length	124
% identity	36
NCBI Description	outer envelope protein omp24, chloroplast - spinach >gi|1076265|pir||S46542 chloroplast outer envelope 24 kD protein - spinach >gi|414200|emb|CAA53243| (X75563) chloroplast outer envelope 24 kD protein (omp24) [Spinacia oleracea]
Seq. No.	197510
Contig ID	32078_1.R1039
5'-most EST	uC-gsronu33B103g11b1
Seq. No.	197511
Contig ID	32081_1.R1039
5'-most EST	LIB3149-021-Q1-K1-G4
Seq. No.	197512
Contig ID	32089_1.R1039
5'-most EST	g5048491
Method	BLASTX
NCBI GI	g4204297

BLAST score	370
E value	5.0e-35
Match length	296
% identity	33
NCBI Description	(AC003027) ADK1 [Arabidopsis thaliana]

Seq. No.	197513
Contig ID	32104_1.R1039
5'-most EST	g5044882
Method	BLASTX
NCBI GI	g3046693
BLAST score	727
E value	5.0e-77
Match length	140
% identity	91
NCBI Description	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No.	197514
Contig ID	32133_1.R1039
5'-most EST	LIB3197-005-P1-M1-H12

Seq. No.	197515
Contig ID	32137_1.R1039
5'-most EST	g5044801
Method	BLASTX
NCBI GI	g3915186
BLAST score	331
E value	1.0e-30
Match length	147
% identity	46
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi|3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]

Seq. No.	197516
Contig ID	32154_1.R1039
5'-most EST	LIB3148-032-Q1-K1-F8

Seq. No.	197517
Contig ID	32167_1.R1039
5'-most EST	LIB3148-024-Q1-K1-F1
Method	BLASTX
NCBI GI	g4455323
BLAST score	483
E value	2.0e-48
Match length	152
% identity	63
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	197518
Contig ID	32168_1.R1039
5'-most EST	LIB3148-024-Q1-K1-F10

Seq. No. 197519

Contig ID	32170_1.R1039
5'-most EST	LIB3148-024-Q1-K1-F12

Seq. No.	197520
Contig ID	32177_1.R1039
5'-most EST	LIB3148-024-Q1-K1-G11
Method	BLASTX
NCBI GI	g3046700
BLAST score	644
E value	3.0e-67
Match length	233
% identity	60
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi|3093276|emb|CAA06671| (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi|4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	197521
Contig ID	32183_1.R1039
5'-most EST	uC-gsronu33B157e05b1

Seq. No.	197522
Contig ID	32185_1.R1039
5'-most EST	uC-gsflnu33B143h08b1
Method	BLASTX
NCBI GI	g1346766
BLAST score	379
E value	5.0e-36
Match length	257
% identity	36
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi|1362741|pir||S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi|1037164|dbj|BAA07237| (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi|3702282 (AC005789) PP31_HUMAN [Homo sapiens] >gi|4506233|ref|NP_002803.1|pPSMD8| proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No.	197523
Contig ID	32197_1.R1039
5'-most EST	uC-gsflnu33B050b03b1

Seq. No.	197524
Contig ID	32200_1.R1039
5'-most EST	LIB3166-017-P1-K1-B1
Method	BLASTX
NCBI GI	g2194124
BLAST score	588
E value	6.0e-61
Match length	153
% identity	73
NCBI Description	(AC002062) Similar to Glycine metalloendoproteinase (gb|U63725). [Arabidopsis thaliana]

Seq. No.	197525
Contig ID	32207_1.R1039
5'-most EST	uC-gsflnu33B140d08b1

Method	BLASTN
NCBI GI	g485808
BLAST score	32
E value	1.0e-08
Match length	56
% identity	89
NCBI Description	Populus kitakamiensis gene for phenylalanine ammonia-lyase, complete cds, clone palg1

Seq. No.	197526
Contig ID	32222_1.R1039
5'-most EST	uC-gsflnu33B093h07b1
Method	BLASTX
NCBI GI	g1707480
BLAST score	339
E value	2.0e-31
Match length	184
% identity	40
NCBI Description	(Y08614) CRM1 [Homo sapiens]

Seq. No.	197527
Contig ID	32224_1.R1039
5'-most EST	LIB3148-025-Q1-K1-D8
Method	BLASTX
NCBI GI	g3549670
BLAST score	257
E value	4.0e-22
Match length	66
% identity	70
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	197528
Contig ID	32249_1.R1039
5'-most EST	LIB3148-025-Q1-K1-G3

Seq. No.	197529
Contig ID	32250_1.R1039
5'-most EST	LIB3189-043-P1-K1-H2
Method	BLASTX
NCBI GI	g3068704
BLAST score	619
E value	1.0e-64
Match length	149
% identity	79
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	197530
Contig ID	32259_1.R1039
5'-most EST	LIB3148-045-Q1-K1-D3
Method	BLASTX
NCBI GI	g303732
BLAST score	166
E value	1.0e-11
Match length	34
% identity	88
NCBI Description	(D12549) GTP-binding protein [Pisum sativum] >gi|738941|prf||2001457J GTP-binding protein [Pisum

sativum]

Seq. No.	197531
Contig ID	32263_1.R1039
5'-most EST	uC-gsflmaxxa048e07b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	225
E value	1.0e-18
Match length	60
% identity	72
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	197532
Contig ID	32265_1.R1039
5'-most EST	LIB3149-017-Q1-K1-H7
Method	BLASTX
NCBI GI	g3201541
BLAST score	524
E value	2.0e-53
Match length	113
% identity	85
NCBI Description	(AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No.	197533
Contig ID	32275_1.R1039
5'-most EST	LIB3148-026-Q1-K1-B2
Method	BLASTX
NCBI GI	g1363487
BLAST score	471
E value	4.0e-47
Match length	98
% identity	91
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi|972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	197534
Contig ID	32280_1.R1039
5'-most EST	LIB3148-026-Q1-K1-C4

Seq. No.	197535
Contig ID	32281_1.R1039
5'-most EST	g5045366
Method	BLASTX
NCBI GI	g3559805
BLAST score	240
E value	5.0e-20
Match length	51
% identity	80
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	197536
Contig ID	32294_1.R1039
5'-most EST	LIB3148-026-Q1-K1-D3
Method	BLASTX
NCBI GI	g1483150

BLAST score	949
E value	1.0e-103
Match length	216
% identity	80
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	197537
Contig ID	32305_1.R1039
5'-most EST	LIB3148-026-Q1-K1-F10
Method	BLASTX
NCBI GI	g3540181
BLAST score	209
E value	2.0e-16
Match length	116
% identity	43
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	197538
Contig ID	32309_1.R1039
5'-most EST	LIB3148-057-Q1-K1-B1
Method	BLASTX
NCBI GI	g3522933
BLAST score	704
E value	3.0e-74
Match length	193
% identity	68
NCBI Description	(AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	197539
Contig ID	32335_1.R1039
5'-most EST	LIB3189-046-P1-K1-B12
Method	BLASTX
NCBI GI	g4567285
BLAST score	375
E value	2.0e-61
Match length	171
% identity	77
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197540
Contig ID	32346_1.R1039
5'-most EST	uC-gsronu33B044e11b1

Seq. No.	197541
Contig ID	32351_1.R1039
5'-most EST	uC-gsronu33B079c06b1
Method	BLASTX
NCBI GI	g4115377
BLAST score	557
E value	4.0e-57
Match length	154
% identity	68
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	197542

Contig ID 32354_1.R1039
5'-most EST uC-gsronu33B087e09b1

Seq. No. 197543
Contig ID 32364_1.R1039
5'-most EST LIB3148-027-Q1-K1-E12
Method BLASTX
NCBI GI g2832683
BLAST score 542
E value 3.0e-55
Match length 148
% identity 68
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 197544
Contig ID 32365_1.R1039
5'-most EST uC-gsflnu33B100b03b1

Seq. No. 197545
Contig ID 32371_1.R1039
5'-most EST LIB3166-022-P1-K1-B12

Seq. No. 197546
Contig ID 32390_1.R1039
5'-most EST LIB3148-044-Q1-K1-D5

Seq. No. 197547
Contig ID 32400_1.R1039
5'-most EST LIB3148-028-Q1-K1-A11
Method BLASTX
NCBI GI g2462759
BLAST score 360
E value 4.0e-34
Match length 74
% identity 85
NCBI Description (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana]

Seq. No. 197548
Contig ID 32403_1.R1039
5'-most EST uC-gsronu33B058f04b1

Seq. No. 197549
Contig ID 32410_1.R1039
5'-most EST g5047001

Seq. No. 197550
Contig ID 32439_1.R1039
5'-most EST LIB3272-015-P1-K1-G11

Seq. No. 197551
Contig ID 32446_1.R1039
5'-most EST LIB3196-034-P1-M1-C7

Seq. No. 197552
Contig ID 32451_1.R1039
5'-most EST g5048080
Method BLASTX

NCBI GI	g3402672
BLAST score	1041
E value	1.0e-114
Match length	279
% identity	73
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]

Seq. No.	197553
Contig ID	32453_1.R1039
5'-most EST	LIB3148-028-Q1-K1-F11
Method	BLASTX
NCBI GI	g4558678
BLAST score	213
E value	6.0e-17
Match length	67
% identity	55
NCBI Description	(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No.	197554
Contig ID	32461_1.R1039
5'-most EST	LIB3148-028-Q1-K1-G1
Method	BLASTX
NCBI GI	g1781330
BLAST score	204
E value	4.0e-16
Match length	64
% identity	58
NCBI Description	(Y10466) peroxidase [Spinacia oleracea]

Seq. No.	197555
Contig ID	32464_1.R1039
5'-most EST	LIB3148-028-Q1-K1-G4
Method	BLASTX
NCBI GI	g4185146
BLAST score	297
E value	3.0e-54
Match length	140
% identity	74
NCBI Description	(AC005724) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	197556
Contig ID	32509_1.R1039
5'-most EST	LIB3148-029-Q1-K1-C9
Method	BLASTX
NCBI GI	g2244835
BLAST score	559
E value	1.0e-57
Match length	118
% identity	80
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	197557
Contig ID	32522_2.R1039
5'-most EST	LIB3189-036-P1-K1-D5

Seq. No.	197558

Contig ID	32536_1.R1039
5'-most EST	uC-gsronu33B146b10b1

Seq. No.	197559
Contig ID	32537_1.R1039
5'-most EST	g5044726
Method	BLASTX
NCBI GI	g1669655
BLAST score	692
E value	1.0e-72
Match length	211
% identity	63
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	197560
Contig ID	32537_2.R1039
5'-most EST	uC-gsflnu33B022h05b1
Method	BLASTX
NCBI GI	g1669655
BLAST score	159
E value	2.0e-10
Match length	38
% identity	87
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	197561
Contig ID	32541_1.R1039
5'-most EST	LIB3165-014-P1-K1-F5
Method	BLASTX
NCBI GI	g1563719
BLAST score	771
E value	4.0e-82
Match length	171
% identity	83
NCBI Description	(Y08320) cyclophylin [Digitalis lanata]

Seq. No.	197562
Contig ID	32551_1.R1039
5'-most EST	LIB3149-002-P1-K2-E3

Seq. No.	197563
Contig ID	32553_1.R1039
5'-most EST	LIB3148-029-Q1-K1-G9
Method	BLASTX
NCBI GI	g3152606
BLAST score	391
E value	1.0e-37
Match length	168
% identity	52
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	197564
Contig ID	32576_1.R1039
5'-most EST	LIB3189-006-P1-K1-D12
Method	BLASTX
NCBI GI	g4406781

BLAST score	197
E value	4.0e-15
Match length	132
% identity	45
NCBI Description	(AC006532) putative Na+/H+ antiporter [Arabidopsis thaliana]

Seq. No.	197565
Contig ID	32579_1.R1039
5'-most EST	LIB3166-043-P1-K1-E8
Method	BLASTX
NCBI GI	g2654868
BLAST score	154
E value	1.0e-12
Match length	52
% identity	77
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	197566
Contig ID	32602_1.R1039
5'-most EST	LIB3148-030-Q1-K1-D9
Method	BLASTX
NCBI GI	g1916290
BLAST score	186
E value	9.0e-14
Match length	55
% identity	62
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	197567
Contig ID	32605_1.R1039
5'-most EST	LIB3149-022-Q1-K1-H6

Seq. No.	197568
Contig ID	32609_1.R1039
5'-most EST	LIB3166-058-P1-K1-F9

Seq. No.	197569
Contig ID	32613_1.R1039
5'-most EST	uC-gsronu33B136b10b1

Seq. No.	197570
Contig ID	32615_1.R1039
5'-most EST	LIB3148-030-Q1-K1-F2
Method	BLASTX
NCBI GI	g3786008
BLAST score	486
E value	1.0e-48
Match length	187
% identity	54
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	197571
Contig ID	32644_1.R1039
5'-most EST	LIB3148-031-Q1-K1-A6
Method	BLASTX
NCBI GI	g4539305

BLAST score	284
E value	1.0e-44
Match length	148
% identity	61
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	197572
Contig ID	32666_1.R1039
5'-most EST	uC-gsflnu33B126d10b1

Seq. No.	197573
Contig ID	32680_1.R1039
5'-most EST	g5045090
Method	BLASTX
NCBI GI	g2633727
BLAST score	188
E value	7.0e-14
Match length	128
% identity	32
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	197574
Contig ID	32683_1.R1039
5'-most EST	LIB3148-031-Q1-K1-E5
Method	BLASTX
NCBI GI	g1169837
BLAST score	181
E value	2.0e-13
Match length	61
% identity	51
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 3 PRECURSOR >gi|2129590|pir||S60231 GAST1 protein homolog (clone GASA3) - Arabidopsis thaliana >gi|887935 (U11764) GAST1 protein homolog [Arabidopsis thaliana]

Seq. No.	197575
Contig ID	32698_1.R1039
5'-most EST	uC-gsflnu33B115a07b1

Seq. No.	197576
Contig ID	32707_1.R1039
5'-most EST	LIB3189-015-P1-K1-G8
Method	BLASTN
NCBI GI	g4337024
BLAST score	37
E value	6.0e-11
Match length	228
% identity	82
NCBI Description	Arabidopsis thaliana AIM1 protein (AIM1) gene, complete cds

Seq. No.	197577
Contig ID	32720_1.R1039
5'-most EST	LIB3197-059-Q1-M1-A3
Method	BLASTX
NCBI GI	g2133786
BLAST score	145
E value	7.0e-11

Match length	447
% identity	7
NCBI Description	NF-180 - sea lamprey >gi|632549 (U19361) NF-180 [Petromyzon marinus]

Seq. No.	197578
Contig ID	32726_1.R1039
5'-most EST	uC-gsflnu33B100g10b1
Method	BLASTX
NCBI GI	g464981
BLAST score	750
E value	1.0e-79
Match length	147
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	197579
Contig ID	32734_1.R1039
5'-most EST	LIB3197-004-P1-M1-B5
Method	BLASTX
NCBI GI	g3046700
BLAST score	661
E value	3.0e-69
Match length	222
% identity	61
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi|3093276|emb|CAA06671| (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi|4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	197580
Contig ID	32749_1.R1039
5'-most EST	LIB3148-032-Q1-K1-D11

Seq. No.	197581
Contig ID	32785_1.R1039
5'-most EST	LIB3189-007-P1-K1-H4

Seq. No.	197582
Contig ID	32806_1.R1039
5'-most EST	uC-gsflnu33B064f06b1
Method	BLASTX
NCBI GI	g3080389
BLAST score	736
E value	7.0e-78
Match length	184
% identity	79
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	197583
Contig ID	32819_1.R1039
5'-most EST	LIB3166-031-P1-K1-B4
Method	BLASTX
NCBI GI	g2262159

BLAST score	393
E value	4.0e-38
Match length	129
% identity	59
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]

Seq. No.	197584
Contig ID	32822_1.R1039
5'-most EST	LIB3149-049-Q1-K1-B2
Method	BLASTX
NCBI GI	g2583128
BLAST score	916
E value	5.0e-99
Match length	221
% identity	77
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197585
Contig ID	32823_1.R1039
5'-most EST	uC-gsflmaxxa047b03b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	342
E value	8.0e-32
Match length	107
% identity	34
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	197586
Contig ID	32824_1.R1039
5'-most EST	uC-gsronu33B137e03b1

Seq. No.	197587
Contig ID	32857_1.R1039
5'-most EST	uC-gsronu33B155b02b2
Method	BLASTX
NCBI GI	g4185140
BLAST score	406
E value	2.0e-39
Match length	88
% identity	91
NCBI Description	(AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]

Seq. No.	197588
Contig ID	32859_1.R1039
5'-most EST	LIB3197-031-Q1-M1-B11
Method	BLASTX
NCBI GI	g4165018
BLAST score	407
E value	1.0e-39
Match length	152
% identity	51
NCBI Description	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]

Seq. No.	197589
Contig ID	32875_1.R1039
5'-most EST	LIB3148-033-Q1-K1-H2
Method	BLASTX
NCBI GI	g2632252
BLAST score	258
E value	2.0e-22
Match length	124
% identity	40
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	197590
Contig ID	32892_1.R1039
5'-most EST	LIB3165-007-P1-K1-B7
Method	BLASTX
NCBI GI	g3021357
BLAST score	261
E value	1.0e-22
Match length	55
% identity	85
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	197591
Contig ID	32899_1.R1039
5'-most EST	uC-gsronu33B108a12b1
Method	BLASTX
NCBI GI	g4558552
BLAST score	1066
E value	1.0e-122
Match length	343
% identity	34
NCBI Description	(AC007138) putative P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No.	197592
Contig ID	32913_1.R1039
5'-most EST	LIB3148-034-Q1-K1-D8

Seq. No.	197593
Contig ID	32929_1.R1039
5'-most EST	LIB3148-034-Q1-K1-F7
Method	BLASTX
NCBI GI	g2880049
BLAST score	314
E value	7.0e-29
Match length	127
% identity	54
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197594
Contig ID	32931_1.R1039
5'-most EST	uC-gsronu33B012d05b1

Seq. No.	197595
Contig ID	32944_1.R1039
5'-most EST	LIB3197-034-Q1-M1-D6

Method	BLASTX
NCBI GI	g2688830
BLAST score	574
E value	2.0e-59
Match length	150
% identity	76
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	197596
Contig ID	32971_1.R1039
5'-most EST	LIB3148-035-Q1-K1-C1

Seq. No.	197597
Contig ID	32976_1.R1039
5'-most EST	LIB3148-035-Q1-K1-C3

Seq. No.	197598
Contig ID	32985_1.R1039
5'-most EST	LIB3148-035-Q1-K1-D3

Seq. No.	197599
Contig ID	32988_1.R1039
5'-most EST	g5045782
Method	BLASTX
NCBI GI	g3785989
BLAST score	677
E value	2.0e-81
Match length	318
% identity	54
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	197600
Contig ID	33002_1.R1039
5'-most EST	uC-gsf1maxxa055c06b1
Method	BLASTX
NCBI GI	g1617206
BLAST score	354
E value	1.0e-33
Match length	77
% identity	82
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	197601
Contig ID	33055_1.R1039
5'-most EST	g5048452
Method	BLASTX
NCBI GI	g3790567
BLAST score	243
E value	2.0e-20
Match length	150
% identity	37
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	197602
Contig ID	33066_1.R1039
5'-most EST	LIB3148-036-Q1-K1-F12

Method	BLASTN
NCBI GI	g2160155
BLAST score	38
E value	9.0e-12
Match length	74
% identity	88
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	197603
Contig ID	33090_1.R1039
5'-most EST	LIB3272-052-P1-K1-A2
Method	BLASTX
NCBI GI	g2801536
BLAST score	377
E value	2.0e-36
Match length	118
% identity	60
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	197604
Contig ID	33094_1.R1039
5'-most EST	LIB3148-037-Q1-K1-A10

Seq. No.	197605
Contig ID	33103_1.R1039
5'-most EST	g5048794
Method	BLASTX
NCBI GI	g3150415
BLAST score	1433
E value	1.0e-159
Match length	301
% identity	86
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi|3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	197606
Contig ID	33166_1.R1039
5'-most EST	g5049507
Method	BLASTX
NCBI GI	g2921340
BLAST score	702
E value	4.0e-74
Match length	195
% identity	70
NCBI Description	(AF034134) MYB-like DNA-binding domain protein [Gossypium hirsutum]

Seq. No.	197607
Contig ID	33168_1.R1039
5'-most EST	uC-gsflmaxxa107d02b1

Seq. No.	197608
Contig ID	33179_1.R1039
5'-most EST	LIB3148-038-Q1-K1-A5

Seq. No.	197609
Contig ID	33184_1.R1039
5'-most EST	LIB3148-038-Q1-K1-B6

Seq. No.	197610
Contig ID	33194_1.R1039
5'-most EST	LIB3148-038-Q1-K1-C11
Method	BLASTX
NCBI GI	g1778374
BLAST score	392
E value	9.0e-38
Match length	114
% identity	72
NCBI Description	(U81287) glycine-rich RNA-binding protein PsGRBP [Pisum sativum]

Seq. No.	197611
Contig ID	33203_1.R1039
5'-most EST	LIB3148-038-Q1-K1-D1
Method	BLASTX
NCBI GI	g4455246
BLAST score	543
E value	9.0e-56
Match length	135
% identity	75
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	197612
Contig ID	33209_1.R1039
5'-most EST	uC-gsflnu33B055g07b1
Method	BLASTX
NCBI GI	g2499489
BLAST score	1308
E value	1.0e-145
Match length	272
% identity	92
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi|483536|emb|CAA83683| (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]

Seq. No.	197613
Contig ID	33211_1.R1039
5'-most EST	LIB3148-038-Q1-K1-D9

Seq. No.	197614
Contig ID	33218_1.R1039
5'-most EST	uC-gsflnu33B141e10b1
Method	BLASTX
NCBI GI	g3036796
BLAST score	247
E value	5.0e-21
Match length	53
% identity	85
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

>gi|3805858|emb|CAA21478| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	197615
Contig ID	33233_1.R1039
5'-most EST	uC-gsflmaxxa026c07b1

Seq. No.	197616
Contig ID	33238_1.R1039
5'-most EST	uC-gsronu33B077b05b1
Method	BLASTX
NCBI GI	g2497540
BLAST score	247
E value	6.0e-21
Match length	70
% identity	69
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No.	197617
Contig ID	33248_1.R1039
5'-most EST	LIB3148-038-Q1-K1-H5
Method	BLASTX
NCBI GI	g1245372
BLAST score	147
E value	6.0e-09
Match length	81
% identity	43
NCBI Description	(U50383) NN8-4AG [Homo sapiens]

Seq. No.	197618
Contig ID	33259_1.R1039
5'-most EST	LIB3196-009-P1-M1-D12

Seq. No.	197619
Contig ID	33281_1.R1039
5'-most EST	g5046410

Seq. No.	197620
Contig ID	33288_1.R1039
5'-most EST	LIB3166-014-P1-K1-F9
Method	BLASTX
NCBI GI	g3236251
BLAST score	587
E value	2.0e-61
Match length	165
% identity	75
NCBI Description	(AC004684) putative phosphoribosylaminoimidazole carboxylase [Arabidopsis thaliana]

Seq. No.	197621
Contig ID	33293_1.R1039
5'-most EST	LIB3148-039-Q1-K1-E8

Seq. No.	197622
Contig ID	33295_1.R1039
5'-most EST	LIB3148-039-Q1-K1-E4
Method	BLASTX

NCBI GI	g486757
BLAST score	148
E value	3.0e-09
Match length	79
% identity	54
NCBI Description	anther-specific protein (clone Bgp1) - field mustard >gi|311938|emb|CAA48292| (X68210) bgp1 [Brassica rapa] >gi|448272|prf||1916399A Bgp1 gene [Brassica rapa]

Seq. No.	197623
Contig ID	33304_1.R1039
5'-most EST	uC-gsflmaxxa088a03b1

Seq. No.	197624
Contig ID	33311_1.R1039
5'-most EST	LIB3197-060-Q1-M1-A9

Seq. No.	197625
Contig ID	33332_1.R1039
5'-most EST	LIB3148-043-Q1-K1-E6
Method	BLASTX
NCBI GI	g4263771
BLAST score	166
E value	2.0e-11
Match length	162
% identity	28
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	197626
Contig ID	33369_1.R1039
5'-most EST	uC-gsflnu33B064d07b1
Method	BLASTX
NCBI GI	g4539369
BLAST score	563
E value	8.0e-58
Match length	167
% identity	63
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	197627
Contig ID	33371_1.R1039
5'-most EST	LIB3148-040-Q1-K1-F4
Method	BLASTX
NCBI GI	g2149640
BLAST score	700
E value	4.0e-74
Match length	137
% identity	94
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	197628
Contig ID	33378_1.R1039
5'-most EST	LIB3196-045-P1-M1-E7
Method	BLASTX
NCBI GI	g2914700
BLAST score	349

E value	8.0e-33
Match length	126
% identity	58
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	197629
Contig ID	33386_1.R1039
5'-most EST	uC-gsflmaxxa054c12b1
Method	BLASTX
NCBI GI	g2677826
BLAST score	400
E value	1.0e-38
Match length	163
% identity	48
NCBI Description	(U93165) major allergen protein homolog [Prunus armeniaca]

Seq. No.	197630
Contig ID	33395_1.R1039
5'-most EST	LIB3149-029-Q1-K1-D10
Method	BLASTN
NCBI GI	g1732362
BLAST score	41
E value	1.0e-13
Match length	130
% identity	90
NCBI Description	Malus domestica pAFD103 mRNA, partial cds

Seq. No.	197631
Contig ID	33439_1.R1039
5'-most EST	uC-gsflnu33B145e12b1

Seq. No.	197632
Contig ID	33447_1.R1039
5'-most EST	LIB3148-041-Q1-K1-H2
Method	BLASTX
NCBI GI	g4455223
BLAST score	528
E value	8.0e-54
Match length	190
% identity	33
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	197633
Contig ID	33472_1.R1039
5'-most EST	LIB3149-051-Q1-K1-F12

Seq. No.	197634
Contig ID	33476_1.R1039
5'-most EST	LIB3148-042-Q1-K1-C4
Method	BLASTX
NCBI GI	g2196878
BLAST score	557
E value	2.0e-57
Match length	113
% identity	90

NCBI Description	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	197635
Contig ID	33477_1.R1039
5'-most EST	g2604002
Method	BLASTX
NCBI GI	g3894178
BLAST score	203
E value	1.0e-15
Match length	49
% identity	78
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	197636
Contig ID	33484_1.R1039
5'-most EST	LIB3148-049-Q1-K1-B4
Method	BLASTX
NCBI GI	g730290
BLAST score	363
E value	1.0e-34
Match length	119
% identity	55
NCBI Description	PECTATE LYASE PRECURSOR >gi|322883|pir||S29612 pectate lyase - trumpet lily >gi|19451|emb|CAA78976| (Z17328) pectate lyase [Lilium longiflorum] >gi|308902 (L18911) pectate lyase [Lilium longiflorum]

Seq. No.	197637
Contig ID	33499_1.R1039
5'-most EST	LIB3148-042-Q1-K1-F11
Method	BLASTX
NCBI GI	g2529683
BLAST score	722
E value	1.0e-76
Match length	164
% identity	79
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	197638
Contig ID	33525_1.R1039
5'-most EST	uC-gsflmaxxa004d05b1

Seq. No.	197639
Contig ID	33528_1.R1039
5'-most EST	uC-gsflmaxxa049g08b1

Seq. No.	197640
Contig ID	33531_1.R1039
5'-most EST	LIB3148-043-Q1-K1-A9

Seq. No.	197641
Contig ID	33544_1.R1039
5'-most EST	LIB3148-043-Q1-K1-C1
Method	BLASTX
NCBI GI	g4138912

BLAST score 336
E value 2.0e-31
Match length 69
% identity 84
NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No. 197642
Contig ID 33551_1.R1039
5'-most EST LIB3148-043-Q1-K1-D10
Method BLASTX
NCBI GI g3021355
BLAST score 277
E value 4.0e-24
Match length 51
% identity 90
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 197643
Contig ID 33573_1.R1039
5'-most EST LIB3148-043-Q1-K1-F5

Seq. No. 197644
Contig ID 33594_1.R1039
5'-most EST uC-gsronu33B032b01b1
Method BLASTX
NCBI GI g401621
BLAST score 269
E value 4.0e-23
Match length 184
% identity 37
NCBI Description HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION >gi|290561 (L10328) o188 [Escherichia coli] >gi|1790149 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No. 197645
Contig ID 33595_1.R1039
5'-most EST LIB3148-050-Q1-K1-E11
Method BLASTX
NCBI GI g113512
BLAST score 178
E value 6.0e-13
Match length 49
% identity 69
NCBI Description FLORAL HOMEOTIC PROTEIN AGL2 >gi|81610|pir||B39534 floral homeotic protein AGL2 - Arabidopsis thaliana >gi|166591 (M55551) transcription factor [Arabidopsis thaliana]

Seq. No. 197646
Contig ID 33600_1.R1039
5'-most EST uC-gsronu33B101b07b1
Method BLASTX
NCBI GI g1362078
BLAST score 312
E value 1.0e-28
Match length 105
% identity 57

NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi|311835|emb|CAA48324| (X68254) cellulase [Tropaeolum majus]
Seq. No.	197647
Contig ID	33604_1.R1039
5'-most EST	LIB3148-044-Q1-K1-A9
Seq. No.	197648
Contig ID	33608_1.R1039
5'-most EST	LIB3189-007-P1-K1-G2
Method	BLASTX
NCBI GI	g3876865
BLAST score	226
E value	4.0e-18
Match length	177
% identity	35
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
Seq. No.	197649
Contig ID	33612_1.R1039
5'-most EST	uC-gsronu33B021c11b1
Seq. No.	197650
Contig ID	33670_1.R1039
5'-most EST	LIB3166-017-P1-K1-C1
Method	BLASTX
NCBI GI	g3881507
BLAST score	452
E value	9.0e-45
Match length	154
% identity	53
NCBI Description	(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]
Seq. No.	197651
Contig ID	33680_1.R1039
5'-most EST	LIB3189-041-P1-K1-H6
Seq. No.	197652
Contig ID	33687_1.R1039
5'-most EST	LIB3148-045-Q1-K1-C4
Method	BLASTX
NCBI GI	g2160180
BLAST score	174
E value	1.0e-12
Match length	44
% identity	73
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	197653
Contig ID	33690_1.R1039
5'-most EST	LIB3149-037-Q1-K1-H6
Method	BLASTX

NCBI GI g1362162
BLAST score 328
E value 2.0e-30
Match length 76
% identity 75
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi|804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 197654
Contig ID 33695_1.R1039
5'-most EST LIB3189-008-P1-K1-C3
Method BLASTX
NCBI GI g1421730
BLAST score 538
E value 4.0e-55
Match length 138
% identity 78
NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 197655
Contig ID 33729_1.R1039
5'-most EST g3326542
Method BLASTN
NCBI GI g2290682
BLAST score 58
E value 2.0e-23
Match length 532
% identity 83
NCBI Description Citrus sinensis basic cellulase mRNA, complete cds

Seq. No. 197656
Contig ID 33747_1.R1039
5'-most EST LIB3148-046-Q1-K1-C10

Seq. No. 197657
Contig ID 33749_1.R1039
5'-most EST LIB3148-046-Q1-K1-C12

Seq. No. 197658
Contig ID 33764_1.R1039
5'-most EST LIB3165-058-P1-K1-C10
Method BLASTX
NCBI GI g2244756
BLAST score 388
E value 2.0e-39
Match length 137
% identity 65
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 197659
Contig ID 33773_1.R1039
5'-most EST LIB3148-046-Q1-K1-F2

Seq. No. 197660
Contig ID 33777_1.R1039
5'-most EST LIB3148-046-Q1-K1-F8

Seq. No. 197661
Contig ID 33788_1.R1039
5'-most EST LIB3149-059-Q1-K1-F2

Seq. No. 197662
Contig ID 33799_1.R1039
5'-most EST LIB3148-047-Q1-K1-A4

Seq. No. 197663
Contig ID 33826_1.R1039
5'-most EST uC-gsronu33B061a05b1
Method BLASTX
NCBI GI g4539386
BLAST score 352
E value 3.0e-33
Match length 168
% identity 32
NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No. 197664
Contig ID 33850_1.R1039
5'-most EST LIB3196-020-P1-M1-F4
Method BLASTX
NCBI GI g118926
BLAST score 389
E value 2.0e-37
Match length 174
% identity 46
NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi|320600|pir||E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi|167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi|227781|prf||1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No. 197665
Contig ID 33854_1.R1039
5'-most EST uC-gsronu33B141c04b1

Seq. No. 197666
Contig ID 33863_1.R1039
5'-most EST LIB3148-047-Q1-K1-H12
Method BLASTX
NCBI GI g4544408
BLAST score 450
E value 8.0e-45
Match length 111
% identity 73
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 197667
Contig ID 33901_1.R1039
5'-most EST LIB3148-048-Q1-K1-D3

Seq. No. 197668
Contig ID 33902_1.R1039
5'-most EST uC-gsronu33B144c11b1

Method	BLASTX
NCBI GI	g3023432
BLAST score	488
E value	3.0e-49
Match length	162
% identity	64
NCBI Description	CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi|1785477|dbj|BAA19102| (AB000408) caffeoyl-CoA 3-O-methyltransferase [Populus kitakamiensis]

Seq. No.	197669
Contig ID	33906_1.R1039
5'-most EST	LIB3165-002-Q1-K1-F1
Method	BLASTX
NCBI GI	g3355486
BLAST score	560
E value	1.0e-57
Match length	149
% identity	71
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	197670
Contig ID	33916_1.R1039
5'-most EST	LIB3166-042-P1-K1-H1

Seq. No.	197671
Contig ID	33921_1.R1039
5'-most EST	LIB3272-024-P1-K1-A5
Method	BLASTX
NCBI GI	g3360289
BLAST score	514
E value	2.0e-59
Match length	150
% identity	74
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	197672
Contig ID	33922_1.R1039
5'-most EST	uC-gsflnu33B058d08b1

Seq. No.	197673
Contig ID	33927_1.R1039
5'-most EST	LIB3148-048-Q1-K1-G2

Seq. No.	197674
Contig ID	33929_1.R1039
5'-most EST	LIB3148-048-Q1-K1-G4

Seq. No.	197675
Contig ID	33938_1.R1039
5'-most EST	uC-gsronu33B171e07b1
Method	BLASTX
NCBI GI	g1237183
BLAST score	528
E value	5.0e-63

Match length	141
% identity	81
NCBI Description	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No.	197676
Contig ID	33940_1.R1039
5'-most EST	LIB3148-048-Q1-K1-H9
Method	BLASTX
NCBI GI	g1877397
BLAST score	934
E value	1.0e-101
Match length	194
% identity	91
NCBI Description	(Y11591) shaggy-like kinase [Ricinus communis]

Seq. No.	197677
Contig ID	33941_1.R1039
5'-most EST	g5044401
Method	BLASTN
NCBI GI	g1877396
BLAST score	228
E value	1.0e-125
Match length	491
% identity	87
NCBI Description	R.communis mRNA for shaggy-like kinase, partial

Seq. No.	197678
Contig ID	33961_1.R1039
5'-most EST	LIB3148-049-Q1-K1-C10

Seq. No.	197679
Contig ID	33981_1.R1039
5'-most EST	LIB3165-020-P1-K1-H11
Method	BLASTX
NCBI GI	g3986750
BLAST score	973
E value	1.0e-105
Match length	258
% identity	67
NCBI Description	(AF107464) serine/threonine protein phosphatase type 2A [Hevea brasiliensis]

Seq. No.	197680
Contig ID	33984_1.R1039
5'-most EST	LIB3197-023-Q1-M1-F7
Method	BLASTN
NCBI GI	g1912285
BLAST score	143
E value	3.0e-74
Match length	479
% identity	82
NCBI Description	Arabidopsis thaliana type 2A serine/threonine protein phosphatase (PP2A) mRNA, complete cds

Seq. No.	197681
Contig ID	33994_1.R1039
5'-most EST	LIB3149-035-Q1-K1-F1

Method	BLASTX
NCBI GI	g3776559
BLAST score	645
E value	2.0e-67
Match length	198
% identity	66
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi|3482933 cdc2 protein kinase homolog from A. thaliana BAC gb|AC003970. ESTs gb|Z35332 and gb|F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	197682
Contig ID	34004_1.R1039
5'-most EST	g5048993
Method	BLASTX
NCBI GI	g4467123
BLAST score	536
E value	9.0e-55
Match length	193
% identity	58
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197683
Contig ID	34018_1.R1039
5'-most EST	LIB3148-049-Q1-K1-H6
Method	BLASTX
NCBI GI	g4567205
BLAST score	178
E value	1.0e-25
Match length	78
% identity	81
NCBI Description	(AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	197684
Contig ID	34029_1.R1039
5'-most EST	g5045651
Method	BLASTX
NCBI GI	g1255951
BLAST score	960
E value	1.0e-104
Match length	211
% identity	82
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	197685
Contig ID	34036_1.R1039
5'-most EST	uC-gsronu33B178d09b1
Method	BLASTX
NCBI GI	g3687245
BLAST score	568
E value	2.0e-58
Match length	129
% identity	81
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	197686
Contig ID	34038_1.R1039
5'-most EST	LIB3189-052-P1-K1-C7

Seq. No.	197687
Contig ID	34068_1.R1039
5'-most EST	uC-gsflmaxxa046b07b1

Seq. No.	197688
Contig ID	34071_1.R1039
5'-most EST	LIB3166-043-P1-K1-G11
Method	BLASTX
NCBI GI	g4090535
BLAST score	366
E value	4.0e-44
Match length	145
% identity	66
NCBI Description	(U68216) ACC synthase [Carica papaya]

Seq. No.	197689
Contig ID	34076_1.R1039
5'-most EST	LIB3148-050-Q1-K1-F7

Seq. No.	197690
Contig ID	34096_1.R1039
5'-most EST	uC-gsflnu33B029b07b1

Seq. No.	197691
Contig ID	34113_1.R1039
5'-most EST	LIB3148-051-Q1-K1-C12
Method	BLASTX
NCBI GI	g2804278
BLAST score	669
E value	2.0e-70
Match length	154
% identity	82
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	197692
Contig ID	34124_1.R1039
5'-most EST	LIB3149-015-Q1-K1-D5
Method	BLASTX
NCBI GI	g3688170
BLAST score	451
E value	9.0e-45
Match length	162
% identity	61
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	197693
Contig ID	34133_1.R1039
5'-most EST	LIB3148-051-Q1-K1-E12

Seq. No.	197694
Contig ID	34141_1.R1039
5'-most EST	uC-gsflmaxxa055e07b1
Method	BLASTX

NCBI GI	g2281115
BLAST score	875
E value	2.0e-94
Match length	200
% identity	81
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	197695
Contig ID	34152_1.R1039
5'-most EST	g5050708
Method	BLASTX
NCBI GI	g3355471
BLAST score	705
E value	2.0e-74
Match length	187
% identity	65
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	197696
Contig ID	34170_1.R1039
5'-most EST	uC-gsflnu33B013c02b1
Method	BLASTX
NCBI GI	g1076511
BLAST score	507
E value	3.0e-51
Match length	101
% identity	98
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi|758250|emb|CAA59799| (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	197697
Contig ID	34173_1.R1039
5'-most EST	uC-gsronu33B150a08b1

Seq. No.	197698
Contig ID	34197_1.R1039
5'-most EST	LIB3148-052-Q1-K1-D12

Seq. No.	197699
Contig ID	34203_1.R1039
5'-most EST	LIB3148-052-Q1-K1-D8
Method	BLASTX
NCBI GI	g3892056
BLAST score	537
E value	5.0e-55
Match length	120
% identity	86
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	197700
Contig ID	34208_1.R1039
5'-most EST	LIB3165-027-P1-K1-F3
Method	BLASTX
NCBI GI	g4206195

BLAST score	202
E value	9.0e-16
Match length	39
% identity	87
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi|4262169|gb|AAD14469| (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197701
Contig ID	34209_1.R1039
5'-most EST	LIB3166-004-P1-K1-C10
Method	BLASTX
NCBI GI	g2129604
BLAST score	537
E value	8.0e-55
Match length	122
% identity	82
NCBI Description	GTP-binding protein 1 - Arabidopsis thaliana >gi|2129607|pir||S71584 GTP-binding protein ATBG1 - Arabidopsis thaliana >gi|1184981 (U46924) ATGB1 [Arabidopsis thaliana]

Seq. No.	197702
Contig ID	34223_1.R1039
5'-most EST	uC-gsronu33B079d06b1

Seq. No.	197703
Contig ID	34226_1.R1039
5'-most EST	LIB3148-052-Q1-K1-G10
Method	BLASTX
NCBI GI	g3540199
BLAST score	486
E value	4.0e-49
Match length	120
% identity	74
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	197704
Contig ID	34287_1.R1039
5'-most EST	uC-gsronu33B130b12b1
Method	BLASTX
NCBI GI	g4469025
BLAST score	471
E value	4.0e-47
Match length	106
% identity	64
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	197705
Contig ID	34312_1.R1039
5'-most EST	LIB3148-053-Q1-K1-H2
Method	BLASTX
NCBI GI	g169363
BLAST score	337
E value	2.0e-31
Match length	66

% identity	88
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	197706
Contig ID	34320_2.R1039
5'-most EST	uC-gsflnu33B055c11b1

Seq. No.	197707
Contig ID	34342_1.R1039
5'-most EST	uC-gsronu33B057d06b1
Method	BLASTX
NCBI GI	g2340166
BLAST score	362
E value	3.0e-34
Match length	110
% identity	60
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi|2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	197708
Contig ID	34343_1.R1039
5'-most EST	g3325985
Method	BLASTX
NCBI GI	g4538901
BLAST score	437
E value	4.0e-43
Match length	192
% identity	45
NCBI Description	(AL049482) RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]

Seq. No.	197709
Contig ID	34360_1.R1039
5'-most EST	LIB3148-054-Q1-K1-E3

Seq. No.	197710
Contig ID	34362_1.R1039
5'-most EST	LIB3166-030-P1-K1-F8

Seq. No.	197711
Contig ID	34374_1.R1039
5'-most EST	LIB3148-054-Q1-K1-F8

Seq. No.	197712
Contig ID	34402_1.R1039
5'-most EST	g3326571
Method	BLASTX
NCBI GI	g2522534
BLAST score	1000
E value	1.0e-108
Match length	433
% identity	32
NCBI Description	(AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No.	197713

Contig ID	34414_1.R1039
5'-most EST	uC-gsronu33B049e12b1

Seq. No.	197714
Contig ID	34416_1.R1039
5'-most EST	g5045182
Method	BLASTN
NCBI GI	g399614
BLAST score	37
E value	8.0e-11
Match length	145
% identity	81
NCBI Description	Lycopersicon esculentum (DB142) meloidogyne-induced giant cell protein mRNA, 3' end

Seq. No.	197715
Contig ID	34440_1.R1039
5'-most EST	LIB3148-055-Q1-K1-D9

Seq. No.	197716
Contig ID	34441_1.R1039
5'-most EST	uC-gsronu33B032b03b1

Seq. No.	197717
Contig ID	34470_1.R1039
5'-most EST	uC-gsronu33B103c07b1
Method	BLASTX
NCBI GI	g4140326
BLAST score	244
E value	2.0e-20
Match length	95
% identity	44
NCBI Description	(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No.	197718
Contig ID	34473_1.R1039
5'-most EST	uC-gsflmaxxa089d03b1

Seq. No.	197719
Contig ID	34498_1.R1039
5'-most EST	LIB3148-056-Q1-K1-B8

Seq. No.	197720
Contig ID	34501_1.R1039
5'-most EST	g5046699

Seq. No.	197721
Contig ID	34530_1.R1039
5'-most EST	uC-gsronu33B111c11b1

Seq. No.	197722
Contig ID	34574_1.R1039
5'-most EST	uC-gsflmaxxa038d12b1
Method	BLASTX
NCBI GI	g886130

BLAST score	458
E value	1.0e-45
Match length	203
% identity	49
NCBI Description	(U28148) putative pectinesterase [Medicago sativa]

Seq. No.	197723
Contig ID	34575_1.R1039
5'-most EST	LIB3148-057-Q1-K1-C1

Seq. No.	197724
Contig ID	34577_1.R1039
5'-most EST	g5050407
Method	BLASTN
NCBI GI	g2245073
BLAST score	33
E value	9.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	197725
Contig ID	34601_1.R1039
5'-most EST	LIB3148-057-Q1-K1-E6
Method	BLASTX
NCBI GI	g2129767
BLAST score	393
E value	3.0e-41
Match length	131
% identity	63
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi|1805364|dbj|BAA09615| (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	197726
Contig ID	34619_1.R1039
5'-most EST	uC-gsronu33B125e10b1

Seq. No.	197727
Contig ID	34631_1.R1039
5'-most EST	LIB3149-060-Q1-K1-H4
Method	BLASTX
NCBI GI	g4539452
BLAST score	753
E value	4.0e-80
Match length	201
% identity	66
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	197728
Contig ID	34636_1.R1039
5'-most EST	g5047683
Method	BLASTX
NCBI GI	g4206206
BLAST score	303

E value	2.0e-27
Match length	125
% identity	47
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi|4263039|gb|AAD15308| (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	197729
Contig ID	34649_1.R1039
5'-most EST	LIB3148-058-Q1-K1-A9
Method	BLASTX
NCBI GI	g3643610
BLAST score	145
E value	1.0e-09
Match length	32
% identity	81
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	197730
Contig ID	34664_1.R1039
5'-most EST	uC-gsflnu33B138a01b1

Seq. No.	197731
Contig ID	34678_1.R1039
5'-most EST	LIB3189-051-P1-K1-F7
Method	BLASTX
NCBI GI	g3298548
BLAST score	668
E value	1.0e-79
Match length	211
% identity	71
NCBI Description	(AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No.	197732
Contig ID	34694_1.R1039
5'-most EST	LIB3148-058-Q1-K1-F3
Method	BLASTN
NCBI GI	g3152602
BLAST score	53
E value	1.0e-20
Match length	153
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	197733
Contig ID	34702_1.R1039
5'-most EST	LIB3166-010-P1-K1-C9
Method	BLASTX
NCBI GI	g3152605
BLAST score	422
E value	3.0e-41
Match length	93
% identity	84
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197734
Contig ID	34710_1.R1039
5'-most EST	uC-gsflnu33B072b01b1
Method	BLASTX
NCBI GI	g2232354
BLAST score	249
E value	3.0e-21
Match length	109
% identity	46
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	197735
Contig ID	34714_1.R1039
5'-most EST	LIB3148-058-Q1-K1-H4

Seq. No.	197736
Contig ID	34740_1.R1039
5'-most EST	LIB3149-051-Q1-K1-H4
Method	BLASTX
NCBI GI	g2281090
BLAST score	438
E value	3.0e-43
Match length	179
% identity	53
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197737
Contig ID	34761_1.R1039
5'-most EST	LIB3148-059-Q1-K1-E6

Seq. No.	197738
Contig ID	34766_1.R1039
5'-most EST	uC-gsronu33B082e04b1
Method	BLASTX
NCBI GI	g2688830
BLAST score	306
E value	8.0e-28
Match length	72
% identity	86
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	197739
Contig ID	34786_1.R1039
5'-most EST	g5047297
Method	BLASTX
NCBI GI	g3367593
BLAST score	452
E value	9.0e-45
Match length	148
% identity	53
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi|3805841|emb|CAA21461| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	197740
Contig ID	34795_1.R1039

5'-most EST	uC-gsronu33B150f04b1
Method	BLASTX
NCBI GI	g1172555
BLAST score	499
E value	2.0e-50
Match length	119
% identity	77
NCBI Description	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi|629720|pir||S46936 34K porin - potato >gi|1076682|pir||A55364 porin (clone pPOM-34) - potato mitochondrion >gi|516166|emb|CAA56599| (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No.	197741
Contig ID	34795_2.R1039
5'-most EST	LIB3197-060-Q1-M1-H8
Method	BLASTX
NCBI GI	g1172556
BLAST score	384
E value	4.0e-37
Match length	91
% identity	78
NCBI Description	36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi|629729|pir||S46925 porin II, 36K - potato >gi|1076681|pir||B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi|515360|emb|CAA56600| (X80387) 36kDA porin II [Solanum tuberosum]

Seq. No.	197742
Contig ID	34809_1.R1039
5'-most EST	LIB3149-001-P1-K1-C9
Method	BLASTN
NCBI GI	g3868723
BLAST score	35
E value	4.0e-10
Match length	75
% identity	87
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	197743
Contig ID	34809_2.R1039
5'-most EST	LIB3149-001-P1-K1-C11

Seq. No.	197744
Contig ID	34816_1.R1039
5'-most EST	LIB3149-001-P1-K1-C6

Seq. No.	197745
Contig ID	34820_1.R1039
5'-most EST	LIB3149-062-Q1-K1-A12
Method	BLASTX
NCBI GI	g2088652
BLAST score	527
E value	1.0e-53

Match length	141
% identity	72
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi|2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	197746
Contig ID	34820_2.R1039
5'-most EST	uC-gsronu33B037h04b1
Method	BLASTX
NCBI GI	g2088652
BLAST score	525
E value	1.0e-86
Match length	220
% identity	73
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi|2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	197747
Contig ID	34836_1.R1039
5'-most EST	uC-gsronu33B031g12b1
Method	BLASTX
NCBI GI	g1729980
BLAST score	697
E value	2.0e-73
Match length	227
% identity	73
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi|2129751|pir||S71175 thaumatin-like protein - Arabidopsis thaliana >gi|536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi|1094863|prf||2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	197748
Contig ID	34844_1.R1039
5'-most EST	uC-gsflmaxxa095e12b1

Seq. No.	197749
Contig ID	34847_1.R1039
5'-most EST	LIB3149-001-P1-K1-F10
Method	BLASTX
NCBI GI	g2511598
BLAST score	191
E value	1.0e-14
Match length	42
% identity	81
NCBI Description	(Y13696) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana]

Seq. No.	197750
Contig ID	34852_1.R1039
5'-most EST	LIB3149-001-P1-K1-G4
Method	BLASTX
NCBI GI	g565166

BLAST score	229
E value	9.0e-19
Match length	143
% identity	32
NCBI Description	calmodulin {D to N substitution at residue 50, G to E substitution at residue 40} [Paramecium tetraurelia, stocks 51s and nd-6, Peptide Mutant, 148 aa]

Seq. No.	197751
Contig ID	34854_1.R1039
5'-most EST	LIB3166-054-P1-K1-G6
Method	BLASTX
NCBI GI	g123684
BLAST score	539
E value	7.0e-55
Match length	137
% identity	76
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR) >gi|100267|pir||S12361 heat shock transcription factor HSF24 - Peruvian tomato >gi|19488|emb|CAA39034| (X55347) heat stress transcription factor [Lycopersicon peruvianum]

Seq. No.	197752
Contig ID	34869_1.R1039
5'-most EST	LIB3149-002-P1-K2-H6

Seq. No.	197753
Contig ID	34870_1.R1039
5'-most EST	LIB3149-002-P1-K2-A11

Seq. No.	197754
Contig ID	34876_1.R1039
5'-most EST	LIB3149-002-P1-K2-B2
Method	BLASTX
NCBI GI	g4512617
BLAST score	204
E value	6.0e-16
Match length	83
% identity	51
NCBI Description	(AC004793) F28K20.16 [Arabidopsis thaliana]

Seq. No.	197755
Contig ID	34893_1.R1039
5'-most EST	uC-gsronu33B090b02b1
Method	BLASTX
NCBI GI	g2258469
BLAST score	698
E value	1.0e-73
Match length	180
% identity	69
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	197756
Contig ID	34898_1.R1039
5'-most EST	LIB3196-054-P1-M1-E11
Method	BLASTX

NCBI GI g1888357
BLAST score 853
E value 7.0e-92
Match length 206
% identity 76
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi|1890154|emb|CAA72432| (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No. 197757
Contig ID 34900_1.R1039
5'-most EST LIB3149-002-P1-K2-E9

Seq. No. 197758
Contig ID 34916_1.R1039
5'-most EST LIB3166-034-P1-K1-C2
Method BLASTX
NCBI GI g1518540
BLAST score 144
E value 4.0e-09
Match length 33
% identity 82
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 197759
Contig ID 34925_1.R1039
5'-most EST LIB3149-003-P1-K1-A12
Method BLASTX
NCBI GI g322854
BLAST score 275
E value 4.0e-24
Match length 111
% identity 46
NCBI Description pollen-specific protein - rice >gi|20310|emb|CAA78897| (Z16402) pollen specific gene [Oryza sativa]

Seq. No. 197760
Contig ID 34935_1.R1039
5'-most EST uC-gsflnu33B109a12b1
Method BLASTX
NCBI GI g169459
BLAST score 247
E value 8.0e-21
Match length 96
% identity 51
NCBI Description (M18538) pop3 peptide [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No. 197761
Contig ID 34940_1.R1039
5'-most EST g5046348
Method BLASTX
NCBI GI g2129915
BLAST score 466
E value 3.0e-46
Match length 150
% identity 59

NCBI Description	ferredoxin precursor - sweet orange >gi|1360725|emb|CAA87068| (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]
Seq. No.	197762
Contig ID	34940_2.R1039
5'-most EST	uC-gsflmaxxa045g12b1
Method	BLASTX
NCBI GI	g2129915
BLAST score	317
E value	3.0e-29
Match length	97
% identity	62
NCBI Description	ferredoxin precursor - sweet orange >gi|1360725|emb|CAA87068| (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]
Seq. No.	197763
Contig ID	34981_1.R1039
5'-most EST	LIB3149-004-P1-K1-E2
Method	BLASTX
NCBI GI	g4263519
BLAST score	438
E value	2.0e-43
Match length	93
% identity	89
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]
Seq. No.	197764
Contig ID	34988_1.R1039
5'-most EST	LIB3149-004-P1-K1-F1
Seq. No.	197765
Contig ID	35003_1.R1039
5'-most EST	LIB3149-004-P1-K1-H12
Seq. No.	197766
Contig ID	35015_1.R1039
5'-most EST	g5047457
Method	BLASTX
NCBI GI	g2351378
BLAST score	598
E value	6.0e-62
Match length	207
% identity	54
NCBI Description	(U54558) translation initiation factor eIF3 p66 subunit [Homo sapiens] >gi|4200328|emb|CAA18440| (AL022313) EIF3-P66 [Homo sapiens] >gi|4503523|ref|NP_003744.1|pEIF3S7| UNKNOWN
Seq. No.	197767
Contig ID	35025_1.R1039
5'-most EST	LIB3149-005-Q1-K2-D4
Method	BLASTX
NCBI GI	g3928083
BLAST score	583

E value 6.0e-60
Match length 196
% identity 77
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 197768
Contig ID 35032_1.R1039
5'-most EST g3325613
Method BLASTN
NCBI GI g3928074
BLAST score 34
E value 4.0e-09
Match length 202
% identity 83
NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 197769
Contig ID 35054_1.R1039
5'-most EST uC-gsronu33B125e09b1

Seq. No. 197770
Contig ID 35059_1.R1039
5'-most EST LIB3149-029-Q1-K1-A3
Method BLASTX
NCBI GI g133940
BLAST score 475
E value 8.0e-48
Match length 109
% identity 90
NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No. 197771
Contig ID 35065_1.R1039
5'-most EST LIB3149-006-Q1-K1-E2
Method BLASTX
NCBI GI g3023512
BLAST score 308
E value 4.0e-28
Match length 119
% identity 53
NCBI Description PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT PRECURSOR (ENDOPEPTIDASE CLP) >gi|2134793|pir||S68421 ATP-dependent Clp proteinase (EC 3.4.21.92) chain P homolog - human >gi|963048|emb|CAA90705| (Z50853) CLPP [Homo sapiens]

Seq. No. 197772
Contig ID 35066_1.R1039
5'-most EST LIB3149-006-Q1-K1-E3
Method BLASTX
NCBI GI g2407613
BLAST score 360
E value 5.0e-34

Match length	137
% identity	51
NCBI Description	(AF017995) 3-phosphoinositide dependent protein kinase-1 [Homo sapiens] >gi|2505936|emb|CAA75341| (Y15056) PkB kinase [Homo sapiens] >gi|4505695|ref|NP_002604.1|pPDPK1| 3-phosphoinositide dependent protein kinase-1

Seq. No.	197773
Contig ID	35082_1.R1039
5'-most EST	g5049584

Seq. No.	197774
Contig ID	35087_1.R1039
5'-most EST	LIB3149-007-Q1-K1-B11
Method	BLASTX
NCBI GI	g3915039
BLAST score	355
E value	2.0e-57
Match length	135
% identity	81
NCBI Description	SUGAR CARRIER PROTEIN C >gi|169718 (L08196) sugar carrier protein [Ricinus communis]

Seq. No.	197775
Contig ID	35134_1.R1039
5'-most EST	uC-gsflmaxxa088c04b1

Seq. No.	197776
Contig ID	35143_1.R1039
5'-most EST	LIB3196-030-P1-M1-E7
Method	BLASTX
NCBI GI	g421960
BLAST score	525
E value	2.0e-53
Match length	187
% identity	58
NCBI Description	small nuclear ribonucleoprotein U2B'' - potato >gi|169589 (M72892) spliceosomal protein [Solanum tuberosum]

Seq. No.	197777
Contig ID	35152_1.R1039
5'-most EST	LIB3149-061-Q1-K1-E10

Seq. No.	197778
Contig ID	35158_1.R1039
5'-most EST	LIB3149-013-Q1-K1-B7
Method	BLASTX
NCBI GI	g1717949
BLAST score	922
E value	1.0e-100
Match length	186
% identity	91
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) >gi|100375|pir||B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) >gi|170322 (M77225) Rieske Fe-S protein

[Nicotiana tabacum]

Seq. No.	197779
Contig ID	35164_1.R1039
5'-most EST	uC-gsflnu33B037e02b1

Seq. No.	197780
Contig ID	35185_1.R1039
5'-most EST	g5046808
Method	BLASTX
NCBI GI	g4337189
BLAST score	357
E value	1.0e-33
Match length	116
% identity	67
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	197781
Contig ID	35228_1.R1039
5'-most EST	LIB3149-007-Q1-K1-B10
Method	BLASTX
NCBI GI	g1706551
BLAST score	286
E value	1.0e-25
Match length	84
% identity	61
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi|924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	197782
Contig ID	35235_1.R1039
5'-most EST	LIB3149-007-Q1-K1-G5

Seq. No.	197783
Contig ID	35246_1.R1039
5'-most EST	LIB3149-021-Q1-K1-E7
Method	BLASTX
NCBI GI	g1871577
BLAST score	574
E value	4.0e-59
Match length	170
% identity	62
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	197784
Contig ID	35265_1.R1039
5'-most EST	LIB3149-013-Q1-K1-F8
Method	BLASTX
NCBI GI	g2829923
BLAST score	423
E value	9.0e-42
Match length	100
% identity	43
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis

09604704 - 040900

thaliana]

Seq. No. 197785
Contig ID 35280_1.R1039
5'-most EST LIB3165-050-Q1-K1-C6
Method BLASTX
NCBI GI g1753085
BLAST score 163
E value 7.0e-11
Match length 88
% identity 42
NCBI Description (U25283) leucine zipper protein [Oryza sativa]

Seq. No. 197786
Contig ID 35284_1.R1039
5'-most EST uC-gsflnu33B090e02b1

Seq. No. 197787
Contig ID 35286_1.R1039
5'-most EST LIB3149-014-Q1-K1-D11

Seq. No. 197788
Contig ID 35288_1.R1039
5'-most EST LIB3149-014-Q1-K1-D2

Seq. No. 197789
Contig ID 35289_1.R1039
5'-most EST uC-gsflnu33B137b12b1
Method BLASTX
NCBI GI g1711382
BLAST score 382
E value 2.0e-36
Match length 135
% identity 50
NCBI Description SET PROTEIN >gi|940889 (U30470) SET [Drosophila melanogaster]

Seq. No. 197790
Contig ID 35292_1.R1039
5'-most EST LIB3166-017-P1-K1-C5
Method BLASTX
NCBI GI g1679794
BLAST score 303
E value 1.0e-27
Match length 115
% identity 51
NCBI Description (U77627) Allele: hi2 [Danio rerio]

Seq. No. 197791
Contig ID 35293_1.R1039
5'-most EST uC-gsflnu33B137f11b1

Seq. No. 197792
Contig ID 35312_1.R1039
5'-most EST LIB3149-015-Q1-K1-F2

Seq. No. 197793

Contig ID	35317_1.R1039
5'-most EST	uC-gsflnu33B091c10b1
Seq. No.	197794
Contig ID	35318_1.R1039
5'-most EST	LIB3166-010-P1-K1-C8
Method	BLASTX
NCBI GI	g3482973
BLAST score	515
E value	3.0e-52
Match length	199
% identity	62
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	197795
Contig ID	35325_1.R1039
5'-most EST	uC-gsronu33B154b07b2
Method	BLASTX
NCBI GI	g2398531
BLAST score	481
E value	4.0e-48
Match length	155
% identity	70
NCBI Description	(Y13726) Transcription factor [Arabidopsis thaliana]
Seq. No.	197796
Contig ID	35347_1.R1039
5'-most EST	uC-gsflnu33B049g03b1
Method	BLASTX
NCBI GI	g3928095
BLAST score	539
E value	2.0e-55
Match length	129
% identity	78
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]
Seq. No.	197797
Contig ID	35364_1.R1039
5'-most EST	LIB3149-016-Q1-K1-C4
Seq. No.	197798
Contig ID	35371_1.R1039
5'-most EST	uC-gsflnu33B076a04b1
Seq. No.	197799
Contig ID	35371_2.R1039
5'-most EST	LIB3272-017-P1-K1-A7
Seq. No.	197800
Contig ID	35403_1.R1039
5'-most EST	LIB3189-022-P1-K1-E9
Method	BLASTX
NCBI GI	g3860272
BLAST score	666
E value	1.0e-69
Match length	231
% identity	62

NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi|4314399|gb|AAD15609| (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	197801
Contig ID	35403_2.R1039
5'-most EST	LIB3149-016-Q1-K1-F3
Method	BLASTX
NCBI GI	g3860272
BLAST score	507
E value	3.0e-51
Match length	134
% identity	76
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi|4314399|gb|AAD15609| (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	197802
Contig ID	35404_1.R1039
5'-most EST	LIB3149-016-Q1-K1-F4

Seq. No.	197803
Contig ID	35452_1.R1039
5'-most EST	LIB3197-033-Q1-M1-A11
Method	BLASTX
NCBI GI	g3874228
BLAST score	217
E value	2.0e-17
Match length	141
% identity	21
NCBI Description	(Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669 comes from this gene; cDNA EST EMBL:D70979 comes from this gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E

Seq. No.	197804
Contig ID	35464_1.R1039
5'-most EST	LIB3149-017-Q1-K1-E9

Seq. No.	197805
Contig ID	35468_1.R1039
5'-most EST	LIB3149-044-Q1-K1-C9
Method	BLASTX
NCBI GI	g1362078
BLAST score	478
E value	6.0e-48
Match length	124
% identity	69
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi|311835|emb|CAA48324| (X68254) cellulase [Tropaeolum majus]

Seq. No.	197806
Contig ID	35474_1.R1039
5'-most EST	LIB3149-017-Q1-K1-G4
Method	BLASTX
NCBI GI	g2980770

BLAST score 534
E value 2.0e-54
Match length 164
% identity 63
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 197807
Contig ID 35500_1.R1039
5'-most EST LIB3197-026-Q1-M1-F10

Seq. No. 197808
Contig ID 35507_1.R1039
5'-most EST LIB3196-020-P1-M1-E9

Seq. No. 197809
Contig ID 35513_1.R1039
5'-most EST uC-gsflnu33B061a01b1

Seq. No. 197810
Contig ID 35514_1.R1039
5'-most EST uC-gsronu33B113b11b1
Method BLASTX
NCBI GI g484656
BLAST score 562
E value 1.0e-57
Match length 211
% identity 54
NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi|452165|dbj|BAA05408| (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No. 197811
Contig ID 35515_1.R1039
5'-most EST uC-gsflnu33B082d05b1

Seq. No. 197812
Contig ID 35527_1.R1039
5'-most EST LIB3197-060-Q1-M1-F2

Seq. No. 197813
Contig ID 35534_1.R1039
5'-most EST LIB3149-035-Q1-K1-B12

Seq. No. 197814
Contig ID 35544_1.R1039
5'-most EST LIB3149-018-Q1-K1-G7
Method BLASTX
NCBI GI g3157934
BLAST score 350
E value 4.0e-33
Match length 82
% identity 82
NCBI Description (AC002131) Similar to hypothetical protein F09E5.8 gb|U37429 from C. elegans. ESTs gb|T42019 and gb|N97000 come from this gene. [Arabidopsis thaliana]

Seq. No. 197815

Contig ID	35549_1.R1039
5'-most EST	uC-gsf1nu33B018c09b1
Method	BLASTX
NCBI GI	g2407800
BLAST score	478
E value	5.0e-48
Match length	101
% identity	93
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	197816
Contig ID	35581_1.R1039
5'-most EST	LIB3149-019-Q1-K1-C9
Method	BLASTX
NCBI GI	g4454466
BLAST score	244
E value	1.0e-20
Match length	74
% identity	59
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	197817
Contig ID	35608_1.R1039
5'-most EST	LIB3197-039-Q1-M1-D10
Method	BLASTX
NCBI GI	g3776578
BLAST score	359
E value	8.0e-34
Match length	130
% identity	48
NCBI Description	(AC005388) ESTs gb|F13915 and gb|F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	197818
Contig ID	35616_1.R1039
5'-most EST	LIB3149-019-Q1-K1-G6
Method	BLASTX
NCBI GI	g3297819
BLAST score	505
E value	2.0e-51
Match length	123
% identity	78
NCBI Description	(AL031032) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	197819
Contig ID	35627_1.R1039
5'-most EST	LIB3166-026-P1-K1-D10
Method	BLASTX
NCBI GI	g2496731
BLAST score	347
E value	4.0e-60
Match length	207
% identity	63
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN Y4OV >gi|2182566 (AE000089) Y4oV [Rhizobium sp. NGR234]

Seq. No.	197820
Contig ID	35649_1.R1039
5'-most EST	uC-gsronu33B036g04b1
Method	BLASTX
NCBI GI	g3241945
BLAST score	422
E value	3.0e-41
Match length	165
% identity	47
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	197821
Contig ID	35670_1.R1039
5'-most EST	LIB3166-029-P1-K1-D3
Method	BLASTX
NCBI GI	g100535
BLAST score	236
E value	2.0e-19
Match length	62
% identity	76
NCBI Description	hypothetical protein - swollen duckweed >gi|1929057|emb|CAA32236| (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	197822
Contig ID	35681_1.R1039
5'-most EST	LIB3166-046-P1-K1-C7
Method	BLASTX
NCBI GI	g4454484
BLAST score	1546
E value	1.0e-172
Match length	390
% identity	75
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	197823
Contig ID	35686_1.R1039
5'-most EST	LIB3272-045-P1-K1-H5
Method	BLASTX
NCBI GI	g3378491
BLAST score	548
E value	4.0e-56
Match length	184
% identity	57
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	197824
Contig ID	35698_1.R1039
5'-most EST	LIB3149-020-Q1-K1-H6

Seq. No.	197825
Contig ID	35702_1.R1039
5'-most EST	LIB3149-021-Q1-K1-A1
Method	BLASTX
NCBI GI	g1514643
BLAST score	151

E value 8.0e-10
Match length 54
% identity 57
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 197826
Contig ID 35703_1.R1039
5'-most EST LIB3149-021-Q1-K1-A11
Method BLASTX
NCBI GI g4539330
BLAST score 905
E value 9.0e-98
Match length 237
% identity 72
NCBI Description (AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No. 197827
Contig ID 35704_1.R1039
5'-most EST LIB3149-021-Q1-K1-A6

Seq. No. 197828
Contig ID 35717_1.R1039
5'-most EST LIB3149-021-Q1-K1-B9
Method BLASTX
NCBI GI g2582665
BLAST score 330
E value 8.0e-31
Match length 104
% identity 63
NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 197829
Contig ID 35718_1.R1039
5'-most EST LIB3189-034-P1-K1-A11
Method BLASTX
NCBI GI g1730502
BLAST score 241
E value 5.0e-20
Match length 150
% identity 39
NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi|110903|pir||A31351 probable transmembrane protein FT27 - mouse >gi|535682 (M23568) transmembrane protein [Mus musculus]

Seq. No. 197830
Contig ID 35743_1.R1039
5'-most EST g5046094
Method BLASTX
NCBI GI g4559334
BLAST score 854
E value 6.0e-92
Match length 219
% identity 66
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 197831

Contig ID	35755_1.R1039
5'-most EST	LIB3149-021-Q1-K1-G7
Seq. No.	197832
Contig ID	35781_1.R1039
5'-most EST	LIB3189-012-P1-K1-G8
Method	BLASTX
NCBI GI	g2583123
BLAST score	435
E value	2.0e-43
Match length	129
% identity	81
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]
Seq. No.	197833
Contig ID	35785_1.R1039
5'-most EST	LIB3165-018-P1-K1-A5
Method	BLASTX
NCBI GI	g133085
BLAST score	391
E value	1.0e-37
Match length	153
% identity	58
NCBI Description	50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12) >gi|71136|pir||R7SP12 ribosomal protein L12, chloroplast - spinach >gi|170115 (J02849) ribosomal L12 precursor [Spinacia oleracea]
Seq. No.	197834
Contig ID	35807_1.R1039
5'-most EST	LIB3272-007-P1-K1-A7
Method	BLASTX
NCBI GI	g4538993
BLAST score	655
E value	2.0e-68
Match length	253
% identity	67
NCBI Description	(AL049481) putative host response protein [Arabidopsis thaliana]
Seq. No.	197835
Contig ID	35841_1.R1039
5'-most EST	uC-gsflmaxxa040g08b1
Method	BLASTX
NCBI GI	g4544431
BLAST score	277
E value	2.0e-24
Match length	97
% identity	58
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	197836
Contig ID	35844_1.R1039
5'-most EST	LIB3149-043-Q1-K1-D8
Seq. No.	197837

Contig ID	35847_1.R1039
5'-most EST	g5046122
Method	BLASTX
NCBI GI	g3874563
BLAST score	335
E value	5.0e-31
Match length	153
% identity	43
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi|3924825|emb|CAB05549| (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	197838
Contig ID	35861_1.R1039
5'-most EST	LIB3196-018-P1-M1-D6
Method	BLASTX
NCBI GI	g4388728
BLAST score	294
E value	2.0e-26
Match length	180
% identity	42
NCBI Description	(AC006413) putative grr1-like protein [Arabidopsis thaliana]

Seq. No.	197839
Contig ID	35887_1.R1039
5'-most EST	LIB3189-015-P1-K1-F6
Method	BLASTX
NCBI GI	g1009232
BLAST score	204
E value	6.0e-16
Match length	73
% identity	60
NCBI Description	(L38828) EF-1-alpha-related GTP-binding protein [Nicotiana tabacum]

Seq. No.	197840
Contig ID	35902_1.R1039
5'-most EST	g5050336
Method	BLASTX
NCBI GI	g1946361
BLAST score	491
E value	2.0e-49
Match length	152
% identity	66
NCBI Description	(U93215) C3HC4 zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	197841
Contig ID	35905_1.R1039
5'-most EST	LIB3149-024-Q1-K1-A1

Seq. No.	197842
Contig ID	35929_1.R1039
5'-most EST	LIB3149-024-Q1-K1-C12
Method	BLASTX
NCBI GI	g3218410
BLAST score	396
E value	4.0e-38
Match length	187
% identity	48
NCBI Description	(AL023859) putative prolyl-trna synthetase [Schizosaccharomyces pombe]

Seq. No.	197843
Contig ID	35947_1.R1039
5'-most EST	LIB3149-024-Q1-K1-E4
Method	BLASTX
NCBI GI	g1707008
BLAST score	480
E value	3.0e-48
Match length	134
% identity	73
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	197844
Contig ID	35968_1.R1039
5'-most EST	LIB3149-024-Q1-K1-H1
Method	BLASTX
NCBI GI	g3415113
BLAST score	175
E value	3.0e-30
Match length	238
% identity	36
NCBI Description	(AF081201) villin 1 [Arabidopsis thaliana]

Seq. No.	197845
Contig ID	35969_1.R1039
5'-most EST	LIB3149-024-Q1-K1-H2
Method	BLASTX
NCBI GI	g3643610
BLAST score	757
E value	1.0e-80
Match length	181
% identity	83
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	197846
Contig ID	35970_1.R1039
5'-most EST	uC-gsflnu33B029a06b1

Seq. No.	197847
Contig ID	35982_1.R1039
5'-most EST	uC-gsronu33B167g02b1

Seq. No.	197848

Contig ID	35986_1.R1039
5'-most EST	uC-gsflnu33B022c06b1
Seq. No.	197849
Contig ID	35998_1.R1039
5'-most EST	LIB3149-025-Q1-K1-C5
Method	BLASTX
NCBI GI	g4417304
BLAST score	252
E value	1.0e-21
Match length	100
% identity	49
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]
Seq. No.	197850
Contig ID	36016_1.R1039
5'-most EST	LIB3166-033-P1-K1-E6
Method	BLASTX
NCBI GI	g1076809
BLAST score	1124
E value	1.0e-123
Match length	275
% identity	81
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi|758355|emb|CAA59800| (X85805) H(+)-transporting ATPase [Zea mays]
Seq. No.	197851
Contig ID	36032_1.R1039
5'-most EST	LIB3272-017-P1-K1-F6
Method	BLASTX
NCBI GI	g3759184
BLAST score	421
E value	3.0e-41
Match length	190
% identity	48
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]
Seq. No.	197852
Contig ID	36035_1.R1039
5'-most EST	LIB3197-026-Q1-M1-B4
Method	BLASTX
NCBI GI	g82307
BLAST score	791
E value	2.0e-84
Match length	221
% identity	67
NCBI Description	myb protein 306 - garden snapdragon >gi|256828|bbs|115017 Myb oncoprotein homolog {clone 306} [Antirrhinum majus=snapdragons, J1:522, flowers, Peptide, 316 aa]
Seq. No.	197853
Contig ID	36052_1.R1039
5'-most EST	LIB3149-026-Q1-K1-A5
Method	BLASTX

NCBI GI	g4510381
BLAST score	186
E value	1.0e-13
Match length	56
% identity	70
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	197854
Contig ID	36053_1.R1039
5'-most EST	LIB3197-047-Q1-M1-G2
Method	BLASTX
NCBI GI	g2736147
BLAST score	745
E value	3.0e-79
Match length	170
% identity	75
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi|3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	197855
Contig ID	36056_1.R1039
5'-most EST	LIB3149-026-Q1-K1-B9

Seq. No.	197856
Contig ID	36065_1.R1039
5'-most EST	LIB3196-015-P1-M1-D8
Method	BLASTX
NCBI GI	g2583108
BLAST score	370
E value	3.0e-35
Match length	184
% identity	44
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	197857
Contig ID	36066_1.R1039
5'-most EST	uC-gsronu33B104g10b1
Method	BLASTX
NCBI GI	g1363484
BLAST score	175
E value	2.0e-12
Match length	79
% identity	46
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi|972929 (U18415) IAA13 [Arabidopsis thaliana] >gi|2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	197858
Contig ID	36077_1.R1039
5'-most EST	LIB3149-026-Q1-K1-D12

Seq. No.	197859
Contig ID	36081_1.R1039
5'-most EST	uC-gsronu33B087g04b1

Seq. No.	197860

Contig ID	36085_1.R1039
5'-most EST	LIB3166-035-P1-K1-C3
Method	BLASTX
NCBI GI	g4335764
BLAST score	457
E value	2.0e-45
Match length	150
% identity	46
NCBI Description	(AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No.	197861
Contig ID	36106_1.R1039
5'-most EST	LIB3149-026-Q1-K1-H11
Method	BLASTX
NCBI GI	g4249386
BLAST score	524
E value	3.0e-53
Match length	213
% identity	56
NCBI Description	(AC005966) Strong similarity to gb|AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb|H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	197862
Contig ID	36116_1.R1039
5'-most EST	g5048541
Method	BLASTX
NCBI GI	g4206196
BLAST score	275
E value	5.0e-24
Match length	125
% identity	70
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197863
Contig ID	36120_1.R1039
5'-most EST	LIB3149-030-Q1-K1-A3

Seq. No.	197864
Contig ID	36121_1.R1039
5'-most EST	LIB3149-047-Q1-K1-A4
Method	BLASTX
NCBI GI	g3281868
BLAST score	238
E value	9.0e-20
Match length	53
% identity	91
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	197865
Contig ID	36123_1.R1039
5'-most EST	LIB3166-022-P1-K1-C7
Method	BLASTX
NCBI GI	g4512122
BLAST score	545
E value	9.0e-56

Match length	198
% identity	59
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	197866
Contig ID	36125_1.R1039
5'-most EST	LIB3149-030-Q1-K1-B12
Method	BLASTX
NCBI GI	g1899188
BLAST score	246
E value	7.0e-21
Match length	103
% identity	37
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	197867
Contig ID	36134_1.R1039
5'-most EST	LIB3149-030-Q1-K1-C8
Method	BLASTX
NCBI GI	g2501578
BLAST score	734
E value	6.0e-78
Match length	157
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi|2129913|pir||S60047 ethylene-responsive protein 1 - Para rubber tree >gi|1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	197868
Contig ID	36135_1.R1039
5'-most EST	LIB3197-040-Q1-M1-E9
Method	BLASTN
NCBI GI	g3335356
BLAST score	72
E value	4.0e-32
Match length	348
% identity	59
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	197869
Contig ID	36144_1.R1039
5'-most EST	LIB3149-027-Q1-K1-D9
Method	BLASTX
NCBI GI	g417103
BLAST score	275
E value	6.0e-42
Match length	92
% identity	95
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone

H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa] >gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	197870
Contig ID	36146_1.R1039
5'-most EST	LIB3149-030-Q1-K1-E10
Method	BLASTN
NCBI GI	g488568
BLAST score	125
E value	8.0e-64
Match length	273
% identity	87
NCBI Description	Medicago sativa Regen S clone pH3c118 histone H3.2 mRNA, complete cds

Seq. No.	197871
Contig ID	36149_1.R1039
5'-most EST	LIB3149-030-Q1-K1-E5
Method	BLASTX
NCBI GI	g3309243
BLAST score	646
E value	8.0e-68
Match length	136
% identity	91
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	197872
Contig ID	36151_1.R1039
5'-most EST	LIB3149-051-Q1-K1-F8
Method	BLASTX
NCBI GI	g1877397
BLAST score	338
E value	1.0e-31
Match length	73
% identity	86
NCBI Description	(Y11591) shaggy-like kinase [Ricinus communis]

Seq. No.	197873
Contig ID	36152_1.R1039
5'-most EST	LIB3149-027-Q1-K1-F1
Method	BLASTX
NCBI GI	g131276
BLAST score	609
E value	2.0e-63
Match length	127
% identity	88

NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi|72704|pir||QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi|11856|emb|CAA77373| (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi|225224|prf||1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	197874
Contig ID	36154_1.R1039
5'-most EST	LIB3149-030-Q1-K1-F12

Seq. No.	197875
Contig ID	36155_1.R1039
5'-most EST	LIB3149-030-Q1-K1-F4

Seq. No.	197876
Contig ID	36156_1.R1039
5'-most EST	LIB3149-030-Q1-K1-F7
Method	BLASTX
NCBI GI	g4204095
BLAST score	425
E value	5.0e-42
Match length	123
% identity	63
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	197877
Contig ID	36163_1.R1039
5'-most EST	uC-gsflnu33B075g01b1
Method	BLASTX
NCBI GI	g4433048
BLAST score	557
E value	6.0e-57
Match length	147
% identity	76
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	197878
Contig ID	36165_1.R1039
5'-most EST	LIB3149-027-Q1-K1-G5
Method	BLASTX
NCBI GI	g4530066
BLAST score	238
E value	5.0e-20
Match length	119
% identity	39
NCBI Description	(AF060544) androgen receptor associated protein 54 [Homo sapiens]

Seq. No.	197879
Contig ID	36166_1.R1039
5'-most EST	LIB3149-027-Q1-K1-G6

Seq. No.	197880
Contig ID	36173_1.R1039
5'-most EST	uC-gsronu33B141g05b1
Method	BLASTX

NCBI GI	g3005063
BLAST score	953
E value	1.0e-103
Match length	317
% identity	55
NCBI Description	(AF043324) N-myristoyltransferase 1 [Homo sapiens]

Seq. No.	197881
Contig ID	36177_1.R1039
5'-most EST	uC-gsronu33B124a01b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	494
E value	6.0e-50
Match length	146
% identity	64
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	197882
Contig ID	36180_1.R1039
5'-most EST	LIB3149-028-Q1-K1-A7
Method	BLASTX
NCBI GI	g485111
BLAST score	180
E value	3.0e-13
Match length	121
% identity	40
NCBI Description	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]

Seq. No.	197883
Contig ID	36183_1.R1039
5'-most EST	uC-gsronu33B103g12b1
Method	BLASTX
NCBI GI	g3941543
BLAST score	707
E value	1.0e-74
Match length	166
% identity	83
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi|4469016|emb|CAB38277| (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	197884
Contig ID	36217_1.R1039
5'-most EST	uC-gsronu33B108f12b1
Method	BLASTX
NCBI GI	g4006858
BLAST score	648
E value	1.0e-67
Match length	196
% identity	62
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	197885

Contig ID 36227_1.R1039
5'-most EST LIB3272-009-P1-K1-E3

Seq. No. 197886
Contig ID 36231_1.R1039
5'-most EST LIB3149-028-Q1-K1-G3

Seq. No. 197887
Contig ID 36237_1.R1039
5'-most EST uC-gsflnu33B018d11b1

Seq. No. 197888
Contig ID 36243_1.R1039
5'-most EST LIB3149-029-Q1-K1-A11
Method BLASTX
NCBI GI g4455351
BLAST score 260
E value 2.0e-36
Match length 113
% identity 68
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 197889
Contig ID 36284_1.R1039
5'-most EST LIB3149-029-Q1-K1-F3
Method BLASTX
NCBI GI g4128197
BLAST score 375
E value 2.0e-37
Match length 121
% identity 65
NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No. 197890
Contig ID 36293_1.R1039
5'-most EST LIB3149-029-Q1-K1-G2

Seq. No. 197891
Contig ID 36295_1.R1039
5'-most EST LIB3149-029-Q1-K1-G4
Method BLASTX
NCBI GI g114181
BLAST score 183
E value 3.0e-13
Match length 84
% identity 49
NCBI Description 3-DEHYDROQUINATE SYNTHASE >gi|68385|pir||SYECQ
3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli
>gi|40968|emb|CAA27495| (X03867) 3-dehydroquinate synthase
(aa 1-362) [Escherichia coli] >gi|41225|emb|CAA79666|
(Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett.
200:11-17(1986) [Escherichia coli] >gi|606323 (U18997)
3-dehydroquinate synthase [Escherichia coli] >gi|1789791
(AE000414) 3-dehydroquinate synthase [Escherichia coli]

Seq. No. 197892
Contig ID 36299_1.R1039

5'-most EST	LIB3149-029-Q1-K1-G8
Seq. No.	197893
Contig ID	36314_1.R1039
5'-most EST	LIB3166-049-P1-K1-F8
Method	BLASTX
NCBI GI	g399900
BLAST score	308
E value	3.0e-37
Match length	149
% identity	63
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi|99659|pir||S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi|16329|emb|CAA41625| (X58821) Athb-1 protein [Arabidopsis thaliana]
Seq. No.	197894
Contig ID	36377_1.R1039
5'-most EST	LIB3149-030-Q1-K1-H8
Method	BLASTX
NCBI GI	g1173194
BLAST score	342
E value	3.0e-32
Match length	117
% identity	60
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi|2119093|pir||S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi|16767|emb|CAA79013| (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi|662869|emb|CAA88028| (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi|1107483|emb|CAA63021| (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi|1515107|emb|CAA60413| (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]
Seq. No.	197895
Contig ID	36405_1.R1039
5'-most EST	LIB3165-047-Q1-K1-F8
Method	BLASTX
NCBI GI	g3297815
BLAST score	511
E value	9.0e-52
Match length	122
% identity	78
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	197896
Contig ID	36413_1.R1039
5'-most EST	LIB3149-049-Q1-K1-E1
Method	BLASTX
NCBI GI	g3096949
BLAST score	631
E value	7.0e-66
Match length	151
% identity	81

NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi|3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	197897
Contig ID	36417_1.R1039
5'-most EST	LIB3272-026-P1-K1-F11

Seq. No.	197898
Contig ID	36434_1.R1039
5'-most EST	LIB3149-031-Q1-K1-G6

Seq. No.	197899
Contig ID	36457_1.R1039
5'-most EST	LIB3149-032-Q1-K1-B6
Method	BLASTX
NCBI GI	g1710424
BLAST score	205
E value	7.0e-26
Match length	98
% identity	53
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi|2129718|pir||S71282 ribosomal protein L21 - Arabidopsis thaliana >gi|1149573|emb|CAA89887| (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	197900
Contig ID	36462_1.R1039
5'-most EST	uC-gsronu33B178c02b1
Method	BLASTN
NCBI GI	g3128141
BLAST score	33
E value	1.0e-08
Match length	45
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	197901
Contig ID	36464_1.R1039
5'-most EST	LIB3149-032-Q1-K1-C10
Method	BLASTX
NCBI GI	g495725
BLAST score	566
E value	2.0e-58
Match length	161
% identity	68
NCBI Description	(L25042) acetyl-CoA carboxylase [Medicago sativa]

Seq. No.	197902
Contig ID	36470_1.R1039
5'-most EST	g5047841
Method	BLASTX
NCBI GI	g2130521
BLAST score	692
E value	6.0e-73
Match length	194

% identity	66
NCBI Description	(U31565) reversibly glycosylatable polypeptide [Pisum sativum]

Seq. No.	197903
Contig ID	36475_1.R1039
5'-most EST	LIB3272-038-P1-K1-C3

Seq. No.	197904
Contig ID	36479_1.R1039
5'-most EST	LIB3149-032-Q1-K1-D5
Method	BLASTX
NCBI GI	g119530
BLAST score	251
E value	2.0e-21
Match length	126
% identity	18
NCBI Description	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) >gi|87320|pir||A23723 protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor - human >gi|181508 (J05016) protein disulfide isomerase-related protein [Homo sapiens]

Seq. No.	197905
Contig ID	36495_1.R1039
5'-most EST	LIB3149-032-Q1-K1-F2
Method	BLASTX
NCBI GI	g3820648
BLAST score	308
E value	3.0e-28
Match length	78
% identity	71
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	197906
Contig ID	36502_1.R1039
5'-most EST	uC-gsronu33B154d05b2

Seq. No.	197907
Contig ID	36516_1.R1039
5'-most EST	LIB3149-033-Q1-K1-A2
Method	BLASTX
NCBI GI	g1723228
BLAST score	118
E value	3.0e-09
Match length	109
% identity	38
NCBI Description	HYPOTHETICAL 45.5 KD PROTEIN C1D4.05C IN CHROMOSOME I >gi|1177338|emb|CAA93214| (Z69239) unknown [Schizosaccharomyces pombe]

Seq. No.	197908
Contig ID	36523_2.R1039
5'-most EST	g5045666
Method	BLASTX
NCBI GI	g2911044
BLAST score	468
E value	1.0e-46

Match length	133
% identity	69
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	197909
Contig ID	36532_1.R1039
5'-most EST	LIB3149-033-Q1-K1-F11
Method	BLASTX
NCBI GI	g544134
BLAST score	343
E value	3.0e-32
Match length	131
% identity	61
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi|99720|pir||S22863 hypothetical protein - Arabidopsis thaliana >gi|421844|pir||A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	197910
Contig ID	36546_1.R1039
5'-most EST	uC-gsf1nu33B144e03b1
Method	BLASTX
NCBI GI	g2275215
BLAST score	541
E value	3.0e-55
Match length	202
% identity	54
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197911
Contig ID	36551_1.R1039
5'-most EST	g5045629
Method	BLASTX
NCBI GI	g2702268
BLAST score	761
E value	5.0e-81
Match length	198
% identity	69
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	197912
Contig ID	36571_1.R1039
5'-most EST	LIB3149-033-Q1-K1-G4
Method	BLASTX
NCBI GI	g4512667
BLAST score	438
E value	6.0e-72
Match length	215
% identity	67
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	197913
Contig ID	36579_1.R1039
5'-most EST	uC-gsronu33B037d08b1

Seq. No.	197914
Contig ID	36582_1.R1039

5'-most EST	uC-gsflmaxxa011b05b1
Method	BLASTX
NCBI GI	g2582665
BLAST score	738
E value	3.0e-78
Match length	186
% identity	81
NCBI Description	(Z82983) thi [Citrus sinensis]

Seq. No.	197915
Contig ID	36583_1.R1039
5'-most EST	LIB3166-025-P1-K1-G5
Method	BLASTX
NCBI GI	g2435511
BLAST score	503
E value	1.0e-50
Match length	187
% identity	53
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	197916
Contig ID	36591_1.R1039
5'-most EST	LIB3149-034-Q1-K1-A6

Seq. No.	197917
Contig ID	36593_1.R1039
5'-most EST	uC-gsflnu33B055g11b1

Seq. No.	197918
Contig ID	36616_1.R1039
5'-most EST	uC-gsronu33B016f06b1
Method	BLASTX
NCBI GI	g1709455
BLAST score	559
E value	1.0e-109
Match length	290
% identity	67
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT >gi|2147993|pir||S73187 pyruvate dehydrogenase E1 component beta chain - Porphyra purpurea chloroplast >gi|1276732 (U38804) pyruvate dehydrogenase E1 component, beta subunit [Porphyra purpurea]

Seq. No.	197919
Contig ID	36632_1.R1039
5'-most EST	LIB3149-034-Q1-K1-F10

Seq. No.	197920
Contig ID	36661_1.R1039
5'-most EST	LIB3149-035-Q1-K1-G1
Method	BLASTX
NCBI GI	g4580468
BLAST score	560
E value	1.0e-57
Match length	138
% identity	72

NCBI Description	(AC006081) putative protein kinase; similar to human PKX1 and Drosophila DC2 [Arabidopsis thaliana]

Seq. No.	197921
Contig ID	36697_1.R1039
5'-most EST	LIB3272-053-P1-K1-H12
Method	BLASTX
NCBI GI	g3128196
BLAST score	159
E value	1.0e-10
Match length	55
% identity	53
NCBI Description	(AC004521) putative cellulase [Arabidopsis thaliana] >gi|3341674 (AC003672) putative glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	197922
Contig ID	36716_1.R1039
5'-most EST	LIB3197-023-Q1-M1-B2
Method	BLASTX
NCBI GI	g3850089
BLAST score	454
E value	1.0e-44
Match length	320
% identity	41
NCBI Description	(AL033389) putative yeast cell division cycle CDC50 homolog [Schizosaccharomyces pombe]

Seq. No.	197923
Contig ID	36748_1.R1039
5'-most EST	LIB3149-036-Q1-K1-E2
Method	BLASTX
NCBI GI	g1354849
BLAST score	753
E value	4.0e-80
Match length	222
% identity	65
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	197924
Contig ID	36754_1.R1039
5'-most EST	uC-gsflnu33B064h04b1

Seq. No.	197925
Contig ID	36787_1.R1039
5'-most EST	LIB3272-047-P1-K1-B4
Method	BLASTX
NCBI GI	g1352316
BLAST score	472
E value	2.0e-47
Match length	97
% identity	93
NCBI Description	DR1 PROTEIN HOMOLOG >gi|633026|dbj|BAA07288| (D38110) Dr1 [Arabidopsis thaliana]

Seq. No.	197926
Contig ID	36807_1.R1039

5'-most EST	LIB3166-043-P1-K1-F1
Method	BLASTX
NCBI GI	g2098705
BLAST score	308
E value	3.0e-28
Match length	122
% identity	56
NCBI Description	(U82973) pectinesterase [Citrus sinensis]

Seq. No.	197927
Contig ID	36822_1.R1039
5'-most EST	g5047224
Method	BLASTX
NCBI GI	g3914192
BLAST score	830
E value	9.0e-89
Match length	379
% identity	47
NCBI Description	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX PRECURSOR (E2) (PDC-E2) >gi|3150120|emb|CAA19134| (AL023595) dihydrolipoamide acetyltransferase component [Schizosaccharomyces pombe]

Seq. No.	197928
Contig ID	36832_1.R1039
5'-most EST	LIB3149-037-Q1-K1-F2

Seq. No.	197929
Contig ID	36843_1.R1039
5'-most EST	g5047022
Method	BLASTX
NCBI GI	g4206206
BLAST score	400
E value	4.0e-39
Match length	164
% identity	55
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi|4263039|gb|AAD15308| (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	197930
Contig ID	36852_1.R1039
5'-most EST	g5048526
Method	BLASTX
NCBI GI	g3341693
BLAST score	179
E value	8.0e-13
Match length	127
% identity	35
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	197931
Contig ID	36873_1.R1039
5'-most EST	g5045594
Method	BLASTX
NCBI GI	g1931654
BLAST score	370

E value	7.0e-35
Match length	278
% identity	35
NCBI Description	(U95973) BRCA1-associated RING domain protein isolog [Arabidopsis thaliana]

Seq. No.	197932
Contig ID	36881_1.R1039
5'-most EST	g3326682
Method	BLASTX
NCBI GI	g3063706
BLAST score	542
E value	3.0e-55
Match length	229
% identity	72
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	197933
Contig ID	36890_1.R1039
5'-most EST	uC-gsflnu33B015d04b1
Method	BLASTX
NCBI GI	g4522011
BLAST score	220
E value	1.0e-17
Match length	94
% identity	49
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197934
Contig ID	36895_1.R1039
5'-most EST	LIB3149-038-Q1-K1-G5
Method	BLASTX
NCBI GI	g544134
BLAST score	247
E value	4.0e-21
Match length	103
% identity	49
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi|99720|pir||S22863 hypothetical protein - Arabidopsis thaliana >gi|421844|pir||A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	197935
Contig ID	36905_1.R1039
5'-most EST	LIB3149-039-Q1-K1-A1

Seq. No.	197936
Contig ID	36910_1.R1039
5'-most EST	g5046151
Method	BLASTX
NCBI GI	g1922251
BLAST score	632
E value	8.0e-66
Match length	182
% identity	77
NCBI Description	(Y12072) farnesyl pyrophosphate synthase [Gossypium arboreum]

Seq. No.	197937
Contig ID	36921_1.R1039
5'-most EST	LIB3166-046-P1-K1-H1
Method	BLASTX
NCBI GI	g3747050
BLAST score	432
E value	1.0e-42
Match length	106
% identity	79
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	197938
Contig ID	36940_1.R1039
5'-most EST	g5045781
Method	BLASTX
NCBI GI	g3212854
BLAST score	200
E value	2.0e-15
Match length	124
% identity	36
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	197939
Contig ID	36972_1.R1039
5'-most EST	LIB3166-025-P1-K1-G9

Seq. No.	197940
Contig ID	36977_1.R1039
5'-most EST	uC-gsronu33B138e01b1

Seq. No.	197941
Contig ID	36984_1.R1039
5'-most EST	LIB3149-040-Q1-K1-E7
Method	BLASTX
NCBI GI	g2760325
BLAST score	315
E value	5.0e-29
Match length	131
% identity	50
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	197942
Contig ID	36986_1.R1039
5'-most EST	LIB3149-040-Q1-K1-B1
Method	BLASTX
NCBI GI	g1076314
BLAST score	547
E value	3.0e-56
Match length	120
% identity	84
NCBI Description	cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis thaliana (fragment) >gi|499166|emb|CAA56143| (X79707) CYS1 [Arabidopsis thaliana]

Seq. No.	197943
Contig ID	36990_1.R1039

5'-most EST	LIB3149-040-Q1-K1-B4
Seq. No.	197944
Contig ID	36997_1.R1039
5'-most EST	LIB3166-016-P1-K1-D11
Method	BLASTX
NCBI GI	g4406777
BLAST score	174
E value	2.0e-12
Match length	85
% identity	46
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]
Seq. No.	197945
Contig ID	37001_1.R1039
5'-most EST	LIB3149-040-Q1-K1-C5
Seq. No.	197946
Contig ID	37010_1.R1039
5'-most EST	LIB3149-040-Q1-K1-D4
Method	BLASTX
NCBI GI	g4103154
BLAST score	401
E value	8.0e-39
Match length	156
% identity	54
NCBI Description	(AF020717) histidyl-tRNA synthetase [Triticum aestivum]
Seq. No.	197947
Contig ID	37029_1.R1039
5'-most EST	LIB3149-040-Q1-K1-F2
Method	BLASTX
NCBI GI	g4455194
BLAST score	258
E value	2.0e-22
Match length	63
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	197948
Contig ID	37034_1.R1039
5'-most EST	LIB3189-042-P1-K1-B12
Method	BLASTX
NCBI GI	g3582436
BLAST score	1048
E value	1.0e-114
Match length	271
% identity	75
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
Seq. No.	197949
Contig ID	37037_1.R1039
5'-most EST	uC-gsflnu33B130g06b1
Method	BLASTX
NCBI GI	g2275213
BLAST score	425

E value	7.0e-42
Match length	130
% identity	61
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197950
Contig ID	37038_1.R1039
5'-most EST	LIB3149-040-Q1-K1-G2

Seq. No.	197951
Contig ID	37044_1.R1039
5'-most EST	g5045893

Seq. No.	197952
Contig ID	37081_1.R1039
5'-most EST	g5046863
Method	BLASTX
NCBI GI	g4567310
BLAST score	614
E value	2.0e-63
Match length	278
% identity	53
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	197953
Contig ID	37097_1.R1039
5'-most EST	LIB3149-042-Q1-K1-D6

Seq. No.	197954
Contig ID	37100_1.R1039
5'-most EST	LIB3149-042-Q1-K1-D8
Method	BLASTX
NCBI GI	g1710780
BLAST score	660
E value	3.0e-69
Match length	170
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi|1321917|emb|CAA65433| (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	197955
Contig ID	37107_1.R1039
5'-most EST	LIB3149-042-Q1-K1-E5

Seq. No.	197956
Contig ID	37108_1.R1039
5'-most EST	g5049734
Method	BLASTX
NCBI GI	g3451473
BLAST score	259
E value	3.0e-22
Match length	113
% identity	45
NCBI Description	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]

Seq. No.	197957
Contig ID	37143_1.R1039
5'-most EST	LIB3149-043-Q1-K1-A12
Method	BLASTX
NCBI GI	g4432840
BLAST score	326
E value	3.0e-30
Match length	106
% identity	62
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	197958
Contig ID	37156_1.R1039
5'-most EST	uC-gsronu33B144g02b1

Seq. No.	197959
Contig ID	37157_1.R1039
5'-most EST	uC-gsflnu33B012c07b1

Seq. No.	197960
Contig ID	37188_1.R1039
5'-most EST	LIB3149-043-Q1-K1-F1

Seq. No.	197961
Contig ID	37199_1.R1039
5'-most EST	uC-gsflnu33B100a08b1

Seq. No.	197962
Contig ID	37220_1.R1039
5'-most EST	LIB3149-044-Q1-K1-A4
Method	BLASTX
NCBI GI	g3893081
BLAST score	523
E value	2.0e-53
Match length	138
% identity	70
NCBI Description	(AJ012747) MLH1 protein [Arabidopsis thaliana]

Seq. No.	197963
Contig ID	37224_1.R1039
5'-most EST	LIB3149-044-Q1-K1-B1

Seq. No.	197964
Contig ID	37226_1.R1039
5'-most EST	uC-gsronu33B087e05b1
Method	BLASTX
NCBI GI	g2500517
BLAST score	881
E value	3.0e-95
Match length	183
% identity	94
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-9 (EIF-4A-9) >gi|485951|emb|CAA55736| (X79135) NeIF-4A9 [Nicotiana tabacum]

Seq. No.	197965
Contig ID	37229_1.R1039

5'-most EST	LIB3149-044-Q1-K1-B4
Seq. No.	197966
Contig ID	37231_1.R1039
5'-most EST	LIB3197-035-Q1-M1-D1
Method	BLASTX
NCBI GI	g4206210
BLAST score	402
E value	1.0e-56
Match length	172
% identity	70
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi|4263043|gb|AAD15312| (AC005142) putative calcium channel [Arabidopsis thaliana]
Seq. No.	197967
Contig ID	37237_1.R1039
5'-most EST	uC-gsronu33B050f06b1
Method	BLASTN
NCBI GI	g3241927
BLAST score	52
E value	6.0e-20
Match length	175
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.	197968
Contig ID	37271_1.R1039
5'-most EST	LIB3149-044-Q1-K1-G6
Method	BLASTX
NCBI GI	g2842689
BLAST score	227
E value	1.0e-18
Match length	141
% identity	39
NCBI Description	HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I >gi|1638851|emb|CAB03598| (Z81312) unknown [Schizosaccharomyces pombe]
Seq. No.	197969
Contig ID	37277_1.R1039
5'-most EST	uC-gsflmaxxa091g09b1
Seq. No.	197970
Contig ID	37316_1.R1039
5'-most EST	LIB3149-046-Q1-K1-E2
Method	BLASTX
NCBI GI	g2262116
BLAST score	154
E value	8.0e-10
Match length	138
% identity	33
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.	197971
Contig ID	37317_1.R1039

5'-most EST	uC-gsflmaxxa057c09b1
Seq. No.	197972
Contig ID	37344_1.R1039
5'-most EST	uC-gsflnu33B018h03b1
Seq. No.	197973
Contig ID	37362_1.R1039
5'-most EST	LIB3165-033-P1-K1-H4
Method	BLASTX
NCBI GI	g1706110
BLAST score	361
E value	4.0e-34
Match length	180
% identity	44
NCBI Description	NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) >gi|1143713 (U13632) non-green plastid phosphate/triose-phosphate translocator precursor [Brassica oleracea]
Seq. No.	197974
Contig ID	37374_1.R1039
5'-most EST	LIB3166-039-P1-K1-G8
Method	BLASTX
NCBI GI	g4099914
BLAST score	279
E value	9.0e-25
Match length	79
% identity	71
NCBI Description	(U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]
Seq. No.	197975
Contig ID	37383_1.R1039
5'-most EST	LIB3149-047-Q1-K1-D5
Seq. No.	197976
Contig ID	37427_1.R1039
5'-most EST	LIB3149-047-Q1-K1-H9
Method	BLASTX
NCBI GI	g2228773
BLAST score	209
E value	2.0e-16
Match length	73
% identity	63
NCBI Description	(AF001454) Dc3 promoter-binding factor-2 [Helianthus annuus]
Seq. No.	197977
Contig ID	37431_1.R1039
5'-most EST	LIB3149-048-Q1-K1-A3
Seq. No.	197978
Contig ID	37491_1.R1039
5'-most EST	g5046751
Method	BLASTX
NCBI GI	g2414622

BLAST score	298
E value	7.0e-27
Match length	107
% identity	52
NCBI Description	(Z99259) conserved protein [Schizosaccharomyces pombe]

Seq. No.	197979
Contig ID	37494_1.R1039
5'-most EST	uC-gsflmaxxa047e07b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	848
E value	3.0e-91
Match length	214
% identity	73
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	197980
Contig ID	37494_2.R1039
5'-most EST	uC-gsflmaxxa058d06b1
Method	BLASTX
NCBI GI	g537313
BLAST score	363
E value	1.0e-34
Match length	96
% identity	75
NCBI Description	(L36159) unknown protein [Medicago sativa]

Seq. No.	197981
Contig ID	37531_1.R1039
5'-most EST	LIB3149-049-Q1-K1-D6
Method	BLASTX
NCBI GI	g1707657
BLAST score	182
E value	3.0e-13
Match length	79
% identity	54
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	197982
Contig ID	37539_1.R1039
5'-most EST	uC-gsflnu33B050e11b1

Seq. No.	197983
Contig ID	37543_2.R1039
5'-most EST	LIB3149-049-Q1-K1-E4

Seq. No.	197984
Contig ID	37553_1.R1039
5'-most EST	g5047750
Method	BLASTX
NCBI GI	g2244850
BLAST score	338
E value	3.0e-31
Match length	198
% identity	45
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	197985
Contig ID	37557_1.R1039
5'-most EST	LIB3149-049-Q1-K1-G1
Method	BLASTX
NCBI GI	g1363482
BLAST score	466
E value	2.0e-46
Match length	180
% identity	59
NCBI Description	IAA11 protein - Arabidopsis thaliana >gi|972925 (U18413) IAA11 [Arabidopsis thaliana]

Seq. No.	197986
Contig ID	37563_1.R1039
5'-most EST	LIB3197-033-Q1-M1-B9
Method	BLASTX
NCBI GI	g3482967
BLAST score	754
E value	4.0e-80
Match length	178
% identity	79
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|4559345|gb|AAD23006.1|AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	197987
Contig ID	37565_1.R1039
5'-most EST	LIB3149-049-Q1-K1-G6
Method	BLASTN
NCBI GI	g4559344
BLAST score	42
E value	5.0e-14
Match length	130
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	197988
Contig ID	37595_1.R1039
5'-most EST	LIB3149-050-Q1-K1-C4
Method	BLASTX
NCBI GI	g3928543
BLAST score	171
E value	4.0e-12
Match length	109
% identity	39
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	197989
Contig ID	37615_1.R1039
5'-most EST	LIB3149-050-Q1-K1-F1

Seq. No.	197990
Contig ID	37631_1.R1039
5'-most EST	uC-gsflnu33B056h06b1

Method	BLASTX
NCBI GI	g606942
BLAST score	635
E value	5.0e-66
Match length	249
% identity	55
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	197991
Contig ID	37635_1.R1039
5'-most EST	uC-gsflmaxxa061c04b1

Seq. No.	197992
Contig ID	37641_1.R1039
5'-most EST	uC-gsronu33B011c12b1
Method	BLASTX
NCBI GI	g4454048
BLAST score	281
E value	5.0e-25
Match length	88
% identity	57
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	197993
Contig ID	37646_1.R1039
5'-most EST	uC-gsflnu33B115c02b1
Method	BLASTX
NCBI GI	g3882203
BLAST score	283
E value	3.0e-33
Match length	135
% identity	59
NCBI Description	(AB018284) KIAA0741 protein [Homo sapiens]

Seq. No.	197994
Contig ID	37680_1.R1039
5'-most EST	g5048464
Method	BLASTX
NCBI GI	g3037045
BLAST score	203
E value	1.0e-15
Match length	117
% identity	41
NCBI Description	(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No.	197995
Contig ID	37682_1.R1039
5'-most EST	LIB3149-051-Q1-K1-G7

Seq. No.	197996
Contig ID	37683_1.R1039
5'-most EST	uC-gsflnu33B064c07b1
Method	BLASTX
NCBI GI	g3193314
BLAST score	381
E value	6.0e-37
Match length	103

% identity	70
NCBI Description	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

Seq. No.	197997
Contig ID	37702_1.R1039
5'-most EST	g5044264
Method	BLASTX
NCBI GI	g2500026
BLAST score	1291
E value	1.0e-143
Match length	291
% identity	84
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi|1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana]

Seq. No.	197998
Contig ID	37711_1.R1039
5'-most EST	uC-gsflnu33B080h06b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	34
E value	3.0e-09
Match length	282
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	197999
Contig ID	37723_1.R1039
5'-most EST	LIB3149-053-Q1-K1-C8
Method	BLASTX
NCBI GI	g4432863
BLAST score	177
E value	2.0e-12
Match length	190
% identity	25
NCBI Description	(AC006300) putative phosphate/phosphoenolpyruvate translocator protein [Arabidopsis thaliana]

Seq. No.	198000
Contig ID	37730_1.R1039
5'-most EST	LIB3196-016-P1-M1-A3
Method	BLASTX
NCBI GI	g3335359
BLAST score	238
E value	5.0e-20
Match length	128
% identity	45
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	198001
Contig ID	37739_1.R1039
5'-most EST	uC-gsronu33B042g06b1
Method	BLASTX
NCBI GI	g1922242

BLAST score	183
E value	2.0e-13
Match length	67
% identity	60
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198002
Contig ID	37752_1.R1039
5'-most EST	LIB3149-053-Q1-K1-G12
Method	BLASTX
NCBI GI	g3702343
BLAST score	238
E value	1.0e-19
Match length	163
% identity	32
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	198003
Contig ID	37762_1.R1039
5'-most EST	LIB3149-053-Q1-K1-H5
Method	BLASTX
NCBI GI	g4567304
BLAST score	150
E value	1.0e-12
Match length	120
% identity	41
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	198004
Contig ID	37772_1.R1039
5'-most EST	LIB3149-064-Q1-K1-E5
Method	BLASTX
NCBI GI	g4262147
BLAST score	256
E value	5.0e-22
Match length	113
% identity	49
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	198005
Contig ID	37780_1.R1039
5'-most EST	LIB3149-054-Q1-K1-C3

Seq. No.	198006
Contig ID	37787_1.R1039
5'-most EST	LIB3196-045-P1-M1-D2

Seq. No.	198007
Contig ID	37806_1.R1039
5'-most EST	LIB3149-054-Q1-K1-F2

Seq. No.	198008
Contig ID	37808_1.R1039
5'-most EST	uC-gsflnu33B145h08b1

Seq. No.	198009
Contig ID	37817_1.R1039
5'-most EST	LIB3189-010-P1-K1-A7
Method	BLASTX
NCBI GI	g4218120
BLAST score	293
E value	8.0e-26
Match length	301
% identity	31
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	198010
Contig ID	37821_1.R1039
5'-most EST	LIB3149-054-Q1-K1-G5

Seq. No.	198011
Contig ID	37842_1.R1039
5'-most EST	uC-gsflnu33B078a05b1
Method	BLASTX
NCBI GI	g3023847
BLAST score	659
E value	3.0e-69
Match length	134
% identity	50
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi|2385376|emb|CAA69934| (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	198012
Contig ID	37848_1.R1039
5'-most EST	LIB3149-055-Q1-K1-C3
Method	BLASTX
NCBI GI	g3264767
BLAST score	142
E value	2.0e-16
Match length	99
% identity	50
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	198013
Contig ID	37864_1.R1039
5'-most EST	g3326172
Method	BLASTX
NCBI GI	g3924597
BLAST score	260
E value	1.0e-22
Match length	97
% identity	48
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	198014
Contig ID	37877_1.R1039
5'-most EST	uC-gsronu33B137f07b1

Seq. No.	198015
Contig ID	37883_1.R1039

5'-most EST	uC-gsflnu33B059a11b1
Method	BLASTX
NCBI GI	g2245024
BLAST score	173
E value	1.0e-12
Match length	74
% identity	47
NCBI Description	(Z97341) cyanohydrin lyase homolog [Arabidopsis thaliana]

Seq. No.	198016
Contig ID	37900_1.R1039
5'-most EST	uC-gsflmaxxa040f06b1

Seq. No.	198017
Contig ID	37928_1.R1039
5'-most EST	LIB3149-057-Q1-K1-E11
Method	BLASTX
NCBI GI	g3176676
BLAST score	568
E value	3.0e-58
Match length	228
% identity	50
NCBI Description	(AC003671) Similar to carbonic anhydrase gb|L19255 from Nicotiana tabacum. ESTs gb|AA597643, gb|T45390, gb|T43963 and gb|AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	198018
Contig ID	37930_1.R1039
5'-most EST	g5048680

Seq. No.	198019
Contig ID	37932_1.R1039
5'-most EST	uC-gsflmaxxa091g02b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	368
E value	4.0e-35
Match length	81
% identity	83
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	198020
Contig ID	37934_1.R1039
5'-most EST	LIB3166-039-P1-K1-G1
Method	BLASTX
NCBI GI	g4455201
BLAST score	542
E value	2.0e-55
Match length	143
% identity	76
NCBI Description	(AL035440) grpE like protein [Arabidopsis thaliana]

Seq. No.	198021
Contig ID	37951_1.R1039
5'-most EST	g5047812
Method	BLASTX
NCBI GI	g3878412

BLAST score	158
E value	2.0e-10
Match length	120
% identity	33
NCBI Description	(Z77666) cDNA EST EMBL:T01059 comes from this gene; cDNA EST EMBL:D71534 comes from this gene; cDNA EST EMBL:D74514 comes from this gene; cDNA EST EMBL:D66796 comes from this gene; cDNA EST EMBL:C11630 comes from this gene; cDN

Seq. No.	198022
Contig ID	37959_1.R1039
5'-most EST	LIB3149-057-Q1-K1-E1

Seq. No.	198023
Contig ID	37963_1.R1039
5'-most EST	LIB3149-057-Q1-K1-E2

Seq. No.	198024
Contig ID	37973_1.R1039
5'-most EST	LIB3149-057-Q1-K1-F3
Method	BLASTX
NCBI GI	g2795807
BLAST score	159
E value	8.0e-11
Match length	81
% identity	44
NCBI Description	(AC003674) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198025
Contig ID	37993_1.R1039
5'-most EST	LIB3149-057-Q1-K1-H10

Seq. No.	198026
Contig ID	38004_1.R1039
5'-most EST	g5047128
Method	BLASTX
NCBI GI	g2493046
BLAST score	785
E value	8.0e-84
Match length	195
% identity	78
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi|82297|pir||A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato >gi|217938|dbj|BAA01511| (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	198027
Contig ID	38005_1.R1039
5'-most EST	uC-gsflnu33B051d09b1
Method	BLASTX
NCBI GI	g3269289
BLAST score	410
E value	4.0e-40
Match length	105
% identity	75
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	198028
Contig ID	38010_1.R1039
5'-most EST	LIB3149-059-Q1-K1-B9
Method	BLASTX
NCBI GI	g1743354
BLAST score	677
E value	2.0e-71
Match length	157
% identity	77
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	198029
Contig ID	38019_1.R1039
5'-most EST	LIB3149-059-Q1-K1-D11
Method	BLASTX
NCBI GI	g2104446
BLAST score	136
E value	1.0e-09
Match length	165
% identity	25
NCBI Description	(Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	198030
Contig ID	38025_1.R1039
5'-most EST	LIB3189-022-P1-K1-G1
Method	BLASTX
NCBI GI	g1170168
BLAST score	197
E value	3.0e-15
Match length	108
% identity	47
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) >gi|549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi|549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi|2245105|emb|CAB10527| (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	198031
Contig ID	38039_1.R1039
5'-most EST	LIB3166-057-P1-K1-E2
Method	BLASTX
NCBI GI	g2204077
BLAST score	229
E value	1.0e-18
Match length	102
% identity	48
NCBI Description	(D85623) extracellular insoluble cystatin [Daucus carota]

Seq. No.	198032
Contig ID	38047_1.R1039
5'-most EST	uC-gsronu33B126f03b1

Seq. No.	198033
Contig ID	38054_1.R1039
5'-most EST	LIB3165-028-P1-K1-C4
Method	BLASTX

NCBI GI	g2827992
BLAST score	465
E value	3.0e-46
Match length	235
% identity	41
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No.	198034
Contig ID	38056_1.R1039
5'-most EST	LIB3149-059-Q1-K1-H7
Method	BLASTX
NCBI GI	g4263771
BLAST score	398
E value	2.0e-38
Match length	117
% identity	64
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	198035
Contig ID	38057_1.R1039
5'-most EST	LIB3149-059-Q1-K1-H8

Seq. No.	198036
Contig ID	38059_1.R1039
5'-most EST	LIB3149-060-Q1-K1-A5
Method	BLASTX
NCBI GI	g2832682
BLAST score	210
E value	1.0e-16
Match length	119
% identity	46
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198037
Contig ID	38064_1.R1039
5'-most EST	LIB3165-008-P1-K1-C12
Method	BLASTN
NCBI GI	g2832667
BLAST score	35
E value	4.0e-10
Match length	47
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	198038
Contig ID	38067_1.R1039
5'-most EST	uC-gsronu33B158d03b2
Method	BLASTX
NCBI GI	g3687239
BLAST score	611
E value	1.0e-63
Match length	119
% identity	97
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	198039
Contig ID	38076_1.R1039
5'-most EST	LIB3149-060-Q1-K1-C3

Seq. No.	198040
Contig ID	38080_1.R1039
5'-most EST	uC-gsronu33b023e05b1
Method	BLASTX
NCBI GI	g4006886
BLAST score	757
E value	1.0e-80
Match length	200
% identity	74
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	198041
Contig ID	38094_1.R1039
5'-most EST	LIB3196-033-P1-M1-E9

Seq. No.	198042
Contig ID	38098_1.R1039
5'-most EST	LIB3272-032-P1-K1-C4
Method	BLASTX
NCBI GI	g2454182
BLAST score	306
E value	8.0e-28
Match length	79
% identity	72
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	198043
Contig ID	38170_1.R1039
5'-most EST	LIB3149-062-Q1-K1-C4

Seq. No.	198044
Contig ID	38175_1.R1039
5'-most EST	LIB3197-006-P1-M1-D12
Method	BLASTX
NCBI GI	g3941289
BLAST score	398
E value	2.0e-38
Match length	188
% identity	46
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	198045
Contig ID	38181_1.R1039
5'-most EST	uC-gsflnu33B089a02b1
Method	BLASTX
NCBI GI	g3877256
BLAST score	163
E value	7.0e-11
Match length	87
% identity	44
NCBI Description	(Z50177) similar to lipase [Caenorhabditis elegans]

Seq. No.	198046
Contig ID	38188_1.R1039
5'-most EST	LIB3197-052-Q1-M1-E6
Method	BLASTX
NCBI GI	g3075398
BLAST score	551
E value	2.0e-56
Match length	194
% identity	53
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	198047
Contig ID	38193_1.R1039
5'-most EST	LIB3149-062-Q1-K1-F3

Seq. No.	198048
Contig ID	38202_1.R1039
5'-most EST	LIB3149-062-Q1-K1-G3

Seq. No.	198049
Contig ID	38205_1.R1039
5'-most EST	g5048394
Method	BLASTX
NCBI GI	g4262240
BLAST score	679
E value	5.0e-86
Match length	262
% identity	35
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No.	198050
Contig ID	38234_1.R1039
5'-most EST	uC-gsflnu33B146d12b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	203
E value	8.0e-16
Match length	53
% identity	72
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	198051
Contig ID	38239_1.R1039
5'-most EST	uC-gsflmaxxa003h08b1
Method	BLASTX
NCBI GI	g4218120
BLAST score	505
E value	3.0e-51
Match length	145
% identity	66
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	198052
Contig ID	38297_1.R1039
5'-most EST	uC-gsflnu33B073b07b1

Seq. No.	198053
Contig ID	38311_1.R1039
5'-most EST	g5044365
Method	BLASTX
NCBI GI	g4127662
BLAST score	861
E value	1.0e-92
Match length	263
% identity	60
NCBI Description	(Y11176) fructosidase [Cichorium intybus]

Seq. No.	198054
Contig ID	38317_1.R1039
5'-most EST	LIB3149-064-Q1-K1-D6

Seq. No.	198055
Contig ID	38327_1.R1039
5'-most EST	uC-gsflmaxxa002e04b1

Seq. No.	198056
Contig ID	38333_1.R1039
5'-most EST	LIB3165-021-P1-K1-G11
Method	BLASTX
NCBI GI	g1673344
BLAST score	166
E value	3.0e-11
Match length	53
% identity	55
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]

Seq. No.	198057
Contig ID	38336_1.R1039
5'-most EST	LIB3149-064-Q1-K1-G11

Seq. No.	198058
Contig ID	38343_1.R1039
5'-most EST	g5046091
Method	BLASTX
NCBI GI	g4455174
BLAST score	239
E value	1.0e-19
Match length	78
% identity	55
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	198059
Contig ID	38357_1.R1039
5'-most EST	LIB3165-048-Q1-K1-G3

Seq. No.	198060
Contig ID	38395_1.R1039
5'-most EST	LIB3165-037-P1-K1-C4
Method	BLASTX
NCBI GI	g3426051
BLAST score	159
E value	1.0e-10

Match length	63
% identity	56
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198061
Contig ID	38397_1.R1039
5'-most EST	LIB3197-047-Q1-M1-E7

Seq. No.	198062
Contig ID	38407_1.R1039
5'-most EST	LIB3165-001-Q1-K1-F9
Method	BLASTX
NCBI GI	g2496789
BLAST score	843
E value	1.0e-90
Match length	228
% identity	72
NCBI Description	1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) >gi|1001556|dbj|BAA10183| (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	198063
Contig ID	38427_1.R1039
5'-most EST	LIB3272-042-P1-K1-F6

Seq. No.	198064
Contig ID	38451_1.R1039
5'-most EST	uC-gsronu33B044g11b1

Seq. No.	198065
Contig ID	38452_1.R1039
5'-most EST	LIB3165-002-Q1-K1-D12
Method	BLASTX
NCBI GI	g4263710
BLAST score	510
E value	9.0e-52
Match length	104
% identity	52
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	198066
Contig ID	38454_1.R1039
5'-most EST	LIB3165-002-Q1-K1-D3
Method	BLASTX
NCBI GI	g3157952
BLAST score	336
E value	2.0e-31
Match length	120
% identity	60
NCBI Description	(AC002131) F12F1.11 [Arabidopsis thaliana]

Seq. No.	198067
Contig ID	38455_1.R1039
5'-most EST	uC-gsronu33B159f11b1
Method	BLASTX
NCBI GI	g3415117

BLAST score	477
E value	5.0e-54
Match length	303
% identity	42
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	198068
Contig ID	38458_1.R1039
5'-most EST	LIB3165-002-Q1-K1-D7

Seq. No.	198069
Contig ID	38459_1.R1039
5'-most EST	LIB3165-014-P1-K1-D12
Method	BLASTX
NCBI GI	g2618686
BLAST score	130
E value	4.0e-13
Match length	111
% identity	44
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198070
Contig ID	38462_1.R1039
5'-most EST	LIB3165-002-Q1-K1-E11

Seq. No.	198071
Contig ID	38471_1.R1039
5'-most EST	LIB3165-002-Q1-K1-F11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	198072
Contig ID	38474_1.R1039
5'-most EST	uC-gsflnu33B088d10b1
Method	BLASTX
NCBI GI	g2505872
BLAST score	144
E value	6.0e-09
Match length	63
% identity	52
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198073
Contig ID	38476_1.R1039
5'-most EST	LIB3165-043-Q1-K1-E6
Method	BLASTX
NCBI GI	g3334223
BLAST score	510
E value	7.0e-52
Match length	143
% identity	69
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)

	>gi|2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi|2392518 (U89267) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi|3098559 (AF047834) 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
Seq. No.	198074
Contig ID	38527_1.R1039
5'-most EST	LIB3165-003-P1-K1-D11
Method	BLASTX
NCBI GI	g3327394
BLAST score	163
E value	3.0e-11
Match length	50
% identity	56
NCBI Description	(AC004483) putative RNA helicase [Arabidopsis thaliana]
Seq. No.	198075
Contig ID	38533_1.R1039
5'-most EST	LIB3197-023-Q1-M1-G7
Method	BLASTX
NCBI GI	g1931639
BLAST score	234
E value	1.0e-19
Match length	126
% identity	39
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.	198076
Contig ID	38533_2.R1039
5'-most EST	LIB3165-003-P1-K1-E10
Seq. No.	198077
Contig ID	38536_1.R1039
5'-most EST	LIB3165-024-P1-K1-A1
Method	BLASTX
NCBI GI	g119937
BLAST score	390
E value	9.0e-38
Match length	120
% identity	63
NCBI Description	FERREDOXIN I PRECURSOR >gi|65741|pir||FESP1 ferredoxin [2Fe-2S] I precursor - spinach >gi|170109 (M35660) ferredoxin I precursor [Spinacia oleracea] >gi|227453|prf||1704156A ferredoxin I [Spinacia oleracea]
Seq. No.	198078
Contig ID	38541_1.R1039
5'-most EST	uC-gsflnu33B046b01b1
Method	BLASTX
NCBI GI	g1881585
BLAST score	225
E value	2.0e-18
Match length	88
% identity	67
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	198079
Contig ID	38544_1.R1039
5'-most EST	LIB3165-003-P1-K1-F11
Method	BLASTX
NCBI GI	g3288821
BLAST score	557
E value	3.0e-57
Match length	133
% identity	78
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	198080
Contig ID	38545_1.R1039
5'-most EST	LIB3165-003-P1-K1-F2

Seq. No.	198081
Contig ID	38553_1.R1039
5'-most EST	LIB3165-003-P1-K1-G1

Seq. No.	198082
Contig ID	38568_1.R1039
5'-most EST	LIB3165-014-P1-K1-E9

Seq. No.	198083
Contig ID	38570_1.R1039
5'-most EST	LIB3165-020-P1-K1-F3
Method	BLASTX
NCBI GI	g11638
BLAST score	227
E value	4.0e-42
Match length	126
% identity	76
NCBI Description	(X01647) open reading frame (ORF701) pot. membrane protein (aa 1-487) [Marchantia polymorpha]

Seq. No.	198084
Contig ID	38600_1.R1039
5'-most EST	uC-gsronu33B008e01b1
Method	BLASTX
NCBI GI	g541951
BLAST score	516
E value	2.0e-52
Match length	129
% identity	77
NCBI Description	SPCP2 protein - soybean >gi|310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	198085
Contig ID	38600_2.R1039
5'-most EST	LIB3165-004-P1-K1-D7
Method	BLASTX
NCBI GI	g541951
BLAST score	360
E value	3.0e-34
Match length	94
% identity	46

NCBI Description	SPCP2 protein - soybean >gi|310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	198086
Contig ID	38611_1.R1039
5'-most EST	LIB3272-014-P1-K1-A7

Seq. No.	198087
Contig ID	38616_1.R1039
5'-most EST	LIB3165-025-P1-K1-F12
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	6.0e-09
Match length	37
% identity	97
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	198088
Contig ID	38618_1.R1039
5'-most EST	uC-gsf1maxxa006a11b1
Method	BLASTX
NCBI GI	g2580440
BLAST score	231
E value	8.0e-19
Match length	58
% identity	74
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	198089
Contig ID	38631_1.R1039
5'-most EST	LIB3165-004-P1-K1-H1
Method	BLASTX
NCBI GI	g1256595
BLAST score	369
E value	2.0e-35
Match length	106
% identity	65
NCBI Description	(U38915) LytB [Synechocystis PCC6803]

Seq. No.	198090
Contig ID	38632_1.R1039
5'-most EST	LIB3197-060-Q1-M1-F8

Seq. No.	198091
Contig ID	38644_1.R1039
5'-most EST	g5047762
Method	BLASTX
NCBI GI	g3193298
BLAST score	400
E value	9.0e-39
Match length	120
% identity	62
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	198092
Contig ID	38658_1.R1039

5'-most EST	LIB3165-005-P1-K1-C10
Method	BLASTX
NCBI GI	g3785986
BLAST score	161
E value	5.0e-11
Match length	78
% identity	53
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	198093
Contig ID	38663_1.R1039
5'-most EST	LIB3165-005-P1-K1-C6
Method	BLASTX
NCBI GI	g1653242
BLAST score	272
E value	1.0e-23
Match length	264
% identity	29
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	198094
Contig ID	38675_1.R1039
5'-most EST	LIB3165-005-P1-K1-D7
Method	BLASTX
NCBI GI	g4454459
BLAST score	626
E value	2.0e-65
Match length	149
% identity	80
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	198095
Contig ID	38676_1.R1039
5'-most EST	LIB3165-043-Q1-K1-D12

Seq. No.	198096
Contig ID	38680_1.R1039
5'-most EST	LIB3196-053-P1-M1-D2
Method	BLASTX
NCBI GI	g1653016
BLAST score	141
E value	1.0e-08
Match length	84
% identity	39
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	198097
Contig ID	38682_1.R1039
5'-most EST	LIB3166-043-P1-K1-C5
Method	BLASTX
NCBI GI	g3850111
BLAST score	248
E value	1.0e-33
Match length	231
% identity	42
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	198098
Contig ID	38683_1.R1039
5'-most EST	LIB3165-005-P1-K1-E4
Method	BLASTX
NCBI GI	g3861068
BLAST score	278
E value	2.0e-24
Match length	149
% identity	40
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	198099
Contig ID	38683_2.R1039
5'-most EST	LIB3196-053-P1-M1-H9
Method	BLASTX
NCBI GI	g3861068
BLAST score	145
E value	4.0e-09
Match length	65
% identity	45
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	198100
Contig ID	38698_1.R1039
5'-most EST	LIB3165-005-P1-K1-G1

Seq. No.	198101
Contig ID	38710_1.R1039
5'-most EST	g5048267
Method	BLASTN
NCBI GI	g3738275
BLAST score	38
E value	1.0e-11
Match length	118
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	198102
Contig ID	38714_1.R1039
5'-most EST	LIB3165-006-P1-K3-A1

Seq. No.	198103
Contig ID	38719_1.R1039
5'-most EST	LIB3165-006-P1-K4-A8
Method	BLASTX
NCBI GI	g4206122
BLAST score	428
E value	7.0e-42
Match length	232
% identity	42
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	198104
Contig ID	38737_1.R1039

5'-most EST	LIB3165-006-P1-K3-C3
Seq. No.	198105
Contig ID	38738_2.R1039
5'-most EST	LIB3165-006-P1-K1-C5
Seq. No.	198106
Contig ID	38741_1.R1039
5'-most EST	LIB3165-006-P1-K3-D12
Seq. No.	198107
Contig ID	38749_1.R1039
5'-most EST	LIB3165-006-P1-K4-D8
Method	BLASTN
NCBI GI	g3869069
BLAST score	39
E value	2.0e-12
Match length	133
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.	198108
Contig ID	38756_1.R1039
5'-most EST	LIB3165-006-P1-K1-E6
Seq. No.	198109
Contig ID	38759_1.R1039
5'-most EST	LIB3165-006-P1-K3-F1
Method	BLASTX
NCBI GI	g3928543
BLAST score	661
E value	3.0e-69
Match length	201
% identity	59
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]
Seq. No.	198110
Contig ID	38766_1.R1039
5'-most EST	LIB3165-006-P1-K3-F8
Seq. No.	198111
Contig ID	38768_1.R1039
5'-most EST	LIB3165-006-P1-K3-G1
Method	BLASTX
NCBI GI	g231610
BLAST score	141
E value	1.0e-17
Match length	101
% identity	58
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi|67880|pir||PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi|19785|emb|CAA45152| (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	198112
Contig ID	38776_1.R1039
5'-most EST	g3326459
Method	BLASTX
NCBI GI	g4512667
BLAST score	734
E value	6.0e-78
Match length	179
% identity	76
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	198113
Contig ID	38776_2.R1039
5'-most EST	LIB3165-006-P1-K3-H1
Method	BLASTX
NCBI GI	g4512667
BLAST score	792
E value	9.0e-85
Match length	183
% identity	79
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	198114
Contig ID	38781_1.R1039
5'-most EST	LIB3166-008-P1-K1-D5
Method	BLASTX
NCBI GI	g3582333
BLAST score	1204
E value	1.0e-133
Match length	268
% identity	82
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198115
Contig ID	38794_1.R1039
5'-most EST	LIB3165-006-P1-K3-A7

Seq. No.	198116
Contig ID	38853_1.R1039
5'-most EST	LIB3165-006-P1-K2-H2
Method	BLASTX
NCBI GI	g3482918
BLAST score	140
E value	2.0e-17
Match length	111
% identity	58
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	198117
Contig ID	38855_1.R1039
5'-most EST	LIB3165-006-P1-K3-H4

Seq. No.	198118
Contig ID	39011_1.R1039
5'-most EST	LIB3165-007-P1-K1-C8
Method	BLASTX

NCBI GI	g2244797
BLAST score	144
E value	5.0e-09
Match length	52
% identity	58
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198119
Contig ID	39016_1.R1039
5'-most EST	LIB3165-017-P1-K1-H4

Seq. No.	198120
Contig ID	39028_1.R1039
5'-most EST	LIB3165-007-P1-K1-C6

Seq. No.	198121
Contig ID	39029_1.R1039
5'-most EST	LIB3165-007-P1-K1-C7
Method	BLASTX
NCBI GI	g3335378
BLAST score	470
E value	9.0e-47
Match length	138
% identity	67
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	198122
Contig ID	39056_1.R1039
5'-most EST	LIB3165-007-P1-K1-F6
Method	BLASTX
NCBI GI	g2135053
BLAST score	176
E value	3.0e-12
Match length	148
% identity	26
NCBI Description	E1B 19K/Bcl-2-interacting protein Nip2 - human >gi|558844 (U15173) BCL2/adenovirus E1B 19kD-interacting protein 2 [Homo sapiens]

Seq. No.	198123
Contig ID	39059_1.R1039
5'-most EST	LIB3165-007-P1-K1-G10
Method	BLASTX
NCBI GI	g1419090
BLAST score	365
E value	7.0e-35
Match length	104
% identity	70
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	198124
Contig ID	39080_1.R1039
5'-most EST	LIB3165-055-P1-K1-H4

Seq. No.	198125

Contig ID	39099_1.R1039
5'-most EST	LIB3196-025-P1-M1-B11

Seq. No.	198126
Contig ID	39119_1.R1039
5'-most EST	uC-gsflmaxxa040g02b1
Method	BLASTX
NCBI GI	g3335350
BLAST score	422
E value	1.0e-41
Match length	126
% identity	58
NCBI Description	(AC004512) Similar to gb|Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	198127
Contig ID	39131_1.R1039
5'-most EST	LIB3165-031-P1-K1-C12
Method	BLASTX
NCBI GI	g1352683
BLAST score	219
E value	9.0e-18
Match length	60
% identity	73
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi|995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	198128
Contig ID	39137_1.R1039
5'-most EST	LIB3272-026-P1-K1-B4

Seq. No.	198129
Contig ID	39141_1.R1039
5'-most EST	LIB3166-045-P1-K1-E5
Method	BLASTX
NCBI GI	g3355480
BLAST score	453
E value	4.0e-45
Match length	134
% identity	63
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	198130
Contig ID	39145_1.R1039
5'-most EST	LIB3165-009-P1-K1-A1
Method	BLASTX
NCBI GI	g3880432
BLAST score	162
E value	4.0e-11
Match length	60
% identity	48
NCBI Description	(Z66521) similar to kinensin-like protein; cDNA EST yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	198131
Contig ID	39149_1.R1039
5'-most EST	LIB3165-009-P1-K1-A3
Method	BLASTX
NCBI GI	g128194
BLAST score	576
E value	8.0e-74
Match length	195
% identity	65
NCBI Description	NITRATE REDUCTASE (NR) >gi|81572|pir||A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi|167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	198132
Contig ID	39157_1.R1039
5'-most EST	LIB3165-044-Q1-K1-F1
Method	BLASTX
NCBI GI	g4091806
BLAST score	918
E value	2.0e-99
Match length	223
% identity	79
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	198133
Contig ID	39173_1.R1039
5'-most EST	LIB3165-044-Q1-K1-H8
Method	BLASTX
NCBI GI	g4115357
BLAST score	265
E value	4.0e-23
Match length	136
% identity	43
NCBI Description	(AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198134
Contig ID	39179_1.R1039
5'-most EST	LIB3165-009-P1-K1-D7
Method	BLASTX
NCBI GI	g4455256
BLAST score	438
E value	2.0e-43
Match length	112
% identity	72
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	198135
Contig ID	39199_1.R1039
5'-most EST	g5044906
Method	BLASTX
NCBI GI	g3024908
BLAST score	301
E value	6.0e-27
Match length	179
% identity	40
NCBI Description	HYPOTHETICAL 27.2 KD PROTEIN SLL0875

>gi|1652675|dbj|BAA17595| (D90907) hypothetical protein [Synechocystis sp.]

Seq. No. 198136
Contig ID 39238_1.R1039
5'-most EST LIB3165-011-P1-K1-B9

Seq. No. 198137
Contig ID 39246_1.R1039
5'-most EST LIB3165-011-P1-K1-C7

Seq. No. 198138
Contig ID 39252_1.R1039
5'-most EST LIB3165-011-P1-K1-D2
Method BLASTX
NCBI GI g3122232
BLAST score 279
E value 8.0e-25
Match length 105
% identity 58
NCBI Description MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi|1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi|4454008|emb|CAA23061| (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No. 198139
Contig ID 39253_1.R1039
5'-most EST LIB3165-017-P1-K1-F8
Method BLASTX
NCBI GI g3236255
BLAST score 176
E value 2.0e-12
Match length 99
% identity 41
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198140
Contig ID 39264_1.R1039
5'-most EST LIB3165-011-P1-K1-E4
Method BLASTX
NCBI GI g2894568
BLAST score 176
E value 1.0e-12
Match length 62
% identity 60
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 198141
Contig ID 39292_1.R1039
5'-most EST LIB3165-011-P1-K1-H12

Seq. No. 198142
Contig ID 39335_1.R1039
5'-most EST LIB3165-012-P1-K1-E10
Method BLASTX
NCBI GI g3193326

BLAST score 157
E value 3.0e-13
Match length 88
% identity 58
NCBI Description (AF069299) contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R proteins [Arabidopsis thaliana]

Seq. No. 198143
Contig ID 39342_1.R1039
5'-most EST LIB3165-012-P1-K1-E7
Method BLASTX
NCBI GI g2231046
BLAST score 719
E value 3.0e-76
Match length 162
% identity 86
NCBI Description (Y12618) PPF-1 protein [Pisum sativum]

Seq. No. 198144
Contig ID 39356_1.R1039
5'-most EST g2604016
Method BLASTX
NCBI GI g1653089
BLAST score 305
E value 8.0e-28
Match length 89
% identity 63
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]

Seq. No. 198145
Contig ID 39360_1.R1039
5'-most EST LIB3165-022-P1-K1-A5
Method BLASTN
NCBI GI g3241924
BLAST score 48
E value 7.0e-18
Match length 289
% identity 82
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 198146
Contig ID 39361_1.R1039
5'-most EST LIB3165-012-P1-K1-G6
Method BLASTX
NCBI GI g2191169
BLAST score 109
E value 7.0e-11
Match length 85
% identity 58
NCBI Description (AF007270) Similar to shaggy related protein kinase. Belongs to the CDC2/CDKX subfamily [Arabidopsis thaliana]

Seq. No. 198147
Contig ID 39370_1.R1039
5'-most EST LIB3165-012-P1-K1-H6

Method	BLASTX
NCBI GI	g418754
BLAST score	382
E value	1.0e-36
Match length	122
% identity	54
NCBI Description	catechol oxidase (EC 1.10.3.1) precursor - fava bean

Seq. No.	198148
Contig ID	39374_1.R1039
5'-most EST	LIB3165-013-P1-K1-A11

Seq. No.	198149
Contig ID	39400_1.R1039
5'-most EST	LIB3165-034-P1-K5-C4

Seq. No.	198150
Contig ID	39412_1.R1039
5'-most EST	uC-gsflmaxxa054g07b1
Method	BLASTX
NCBI GI	g2829903
BLAST score	361
E value	2.0e-34
Match length	75
% identity	89
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	198151
Contig ID	39418_1.R1039
5'-most EST	g3326683

Seq. No.	198152
Contig ID	39427_1.R1039
5'-most EST	LIB3165-013-P1-K1-F6
Method	BLASTX
NCBI GI	g480082
BLAST score	177
E value	1.0e-12
Match length	156
% identity	31
NCBI Description	catechol O-methyltransferase (EC 2.1.1.6) - common tobacco >gi|396589|emb|CAA52461| (X74452) catechol O-methyltransferase [Nicotiana tabacum]

Seq. No.	198153
Contig ID	39450_1.R1039
5'-most EST	LIB3165-014-P1-K1-A10

Seq. No.	198154
Contig ID	39461_1.R1039
5'-most EST	g5050222
Method	BLASTX
NCBI GI	g2342674
BLAST score	622
E value	1.0e-64
Match length	214
% identity	64

NCBI Description	(AC000106) Similar to ATP-dependent Clp protease (gb|D90915). EST gb|N65461 comes from this gene. [Arabidopsis thaliana]
Seq. No.	198155
Contig ID	39481_1.R1039
5'-most EST	uC-gsflnu33B112c10b1
Method	BLASTX
NCBI GI	g2956671
BLAST score	222
E value	5.0e-18
Match length	110
% identity	51
NCBI Description	(Y09225) beta-carotene hydrolase [Capsicum annuum]
Seq. No.	198156
Contig ID	39484_1.R1039
5'-most EST	uC-gsflnu33B099b03b1
Method	BLASTX
NCBI GI	g3834306
BLAST score	244
E value	7.0e-21
Match length	84
% identity	57
NCBI Description	(AC005679) EST gb|R65024 comes from this gene. [Arabidopsis thaliana]
Seq. No.	198157
Contig ID	39505_1.R1039
5'-most EST	uC-gsronu33b112d09b1
Seq. No.	198158
Contig ID	39511_1.R1039
5'-most EST	LIB3165-048-Q1-K1-H3
Seq. No.	198159
Contig ID	39521_1.R1039
5'-most EST	LIB3165-036-P1-K1-A11
Method	BLASTX
NCBI GI	g117814
BLAST score	781
E value	1.0e-102
Match length	215
% identity	83
NCBI Description	CYTOCHROME B6 >gi|99387|pir||S21253 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - Chlamydomonas reinhardtii chloroplast >gi|12499|emb|CAA44690| (X62905) petB [Chlamydomonas reinhardtii] >gi|288909|emb|CAA51423| (X72918) cytochrome b6 [Chlamydomonas reinhardtii]
Seq. No.	198160
Contig ID	39528_1.R1039
5'-most EST	uC-gsflmaxxa098c10b1
Seq. No.	198161
Contig ID	39546_1.R1039

5'-most EST	LIB3165-040-Q1-K1-D6
Seq. No.	198162
Contig ID	39555_1.R1039
5'-most EST	LIB3197-053-Q1-M1-B6
Seq. No.	198163
Contig ID	39555_2.R1039
5'-most EST	LIB3197-053-Q1-M1-B11
Seq. No.	198164
Contig ID	39558_1.R1039
5'-most EST	LIB3165-016-P1-K1-D9
Method	BLASTX
NCBI GI	g3292814
BLAST score	171
E value	4.0e-12
Match length	98
% identity	46
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	198165
Contig ID	39571_1.R1039
5'-most EST	LIB3165-016-P1-K1-F1
Seq. No.	198166
Contig ID	39603_1.R1039
5'-most EST	LIB3165-017-P1-K1-A1
Seq. No.	198167
Contig ID	39610_1.R1039
5'-most EST	LIB3165-026-P1-K1-F2
Method	BLASTX
NCBI GI	g2582822
BLAST score	382
E value	1.0e-36
Match length	156
% identity	35
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
Seq. No.	198168
Contig ID	39618_1.R1039
5'-most EST	LIB3166-038-P1-K1-G11
Seq. No.	198169
Contig ID	39635_1.R1039
5'-most EST	LIB3165-017-P1-K1-D10
Seq. No.	198170
Contig ID	39636_1.R1039
5'-most EST	LIB3165-017-P1-K1-D11
Method	BLASTX
NCBI GI	g3184258
BLAST score	214
E value	7.0e-17
Match length	154

% identity	31
NCBI Description	(U82130) tumor susceptibility protein [Homo sapiens]

Seq. No.	198171
Contig ID	39637_1.R1039
5'-most EST	LIB3165-033-P1-K1-D6
Method	BLASTX
NCBI GI	g3451068
BLAST score	715
E value	1.0e-75
Match length	188
% identity	77
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	198172
Contig ID	39689_1.R1039
5'-most EST	LIB3165-018-P1-K1-A6
Method	BLASTX
NCBI GI	g4097547
BLAST score	250
E value	2.0e-21
Match length	122
% identity	32
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	198173
Contig ID	39775_1.R1039
5'-most EST	LIB3165-019-P1-K1-B3
Method	BLASTX
NCBI GI	g4263711
BLAST score	284
E value	2.0e-25
Match length	108
% identity	54
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	198174
Contig ID	39792_1.R1039
5'-most EST	LIB3165-019-P1-K1-D6
Method	BLASTX
NCBI GI	g2827548
BLAST score	249
E value	3.0e-21
Match length	90
% identity	54
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	198175
Contig ID	39808_1.R1039
5'-most EST	uC-gsronu33B019g06b1
Method	BLASTN
NCBI GI	g2477521
BLAST score	49
E value	2.0e-18
Match length	65

% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	198176
Contig ID	39840_1.R1039
5'-most EST	LIB3189-021-P1-K1-B7
Method	BLASTX
NCBI GI	g2191191
BLAST score	242
E value	2.0e-20
Match length	114
% identity	54
NCBI Description	(AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No.	198177
Contig ID	39855_1.R1039
5'-most EST	LIB3165-020-P1-K1-C5

Seq. No.	198178
Contig ID	39860_1.R1039
5'-most EST	LIB3165-020-P1-K1-D10
Method	BLASTX
NCBI GI	g407940
BLAST score	644
E value	2.0e-67
Match length	170
% identity	66
NCBI Description	(U02495) epoxide hydrolase [Solanum tuberosum]

Seq. No.	198179
Contig ID	39864_1.R1039
5'-most EST	LIB3165-020-P1-K1-D4

Seq. No.	198180
Contig ID	39879_1.R1039
5'-most EST	LIB3165-020-P1-K1-F4

Seq. No.	198181
Contig ID	39884_1.R1039
5'-most EST	LIB3165-020-P1-K1-F9

Seq. No.	198182
Contig ID	39892_1.R1039
5'-most EST	uC-gsflnu33B013h07b1

Seq. No.	198183
Contig ID	39895_1.R1039
5'-most EST	g5045254
Method	BLASTX
NCBI GI	g3063444
BLAST score	470
E value	6.0e-47
Match length	98
% identity	85
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No. 198184
Contig ID 39926_1.R1039
5'-most EST LIB3165-021-P1-K1-C7

Seq. No. 198185
Contig ID 39932_1.R1039
5'-most EST LIB3165-021-P1-K1-D4
Method BLASTX
NCBI GI g2317910
BLAST score 341
E value 5.0e-32
Match length 130
% identity 48
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]

Seq. No. 198186
Contig ID 39950_1.R1039
5'-most EST LIB3165-021-P1-K1-F5

Seq. No. 198187
Contig ID 39975_1.R1039
5'-most EST LIB3165-032-P1-K1-E5

Seq. No. 198188
Contig ID 39990_1.R1039
5'-most EST uC-gsronu33B145a12b1
Method BLASTX
NCBI GI g2281633
BLAST score 203
E value 6.0e-25
Match length 144
% identity 53
NCBI Description (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No. 198189
Contig ID 39999_1.R1039
5'-most EST LIB3165-022-P1-K1-C5
Method BLASTX
NCBI GI g4510354
BLAST score 232
E value 3.0e-19
Match length 122
% identity 46
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 198190
Contig ID 40009_1.R1039
5'-most EST uC-gsflnu33B139e02b1

Seq. No. 198191
Contig ID 40010_1.R1039
5'-most EST LIB3165-022-P1-K1-D6
Method BLASTX
NCBI GI g1362017
BLAST score 182

E value	2.0e-13
Match length	78
% identity	53
NCBI Description	zinc finger protein 4 - Arabidopsis thaliana >gi|790679 (L39647) zinc finger protein [Arabidopsis thaliana]

Seq. No.	198192
Contig ID	40032_1.R1039
5'-most EST	uC-gsronu33B012g03b1
Method	BLASTX
NCBI GI	g4455364
BLAST score	595
E value	1.0e-61
Match length	187
% identity	56
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	198193
Contig ID	40048_1.R1039
5'-most EST	LIB3165-022-P1-K1-H12

Seq. No.	198194
Contig ID	40066_1.R1039
5'-most EST	LIB3197-041-Q1-M1-F2
Method	BLASTX
NCBI GI	g3183454
BLAST score	247
E value	5.0e-21
Match length	110
% identity	45
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi|2632217|emb|CAA10859| (AJ222587) YkwC protein [Bacillus subtilis] >gi|2633767|emb|CAB13269| (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	198195
Contig ID	40074_1.R1039
5'-most EST	LIB3166-028-P1-K1-G10
Method	BLASTX
NCBI GI	g3402684
BLAST score	402
E value	3.0e-39
Match length	114
% identity	52
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198196
Contig ID	40076_1.R1039
5'-most EST	uC-gsflmaxxa006a05b1

Seq. No.	198197
Contig ID	40090_1.R1039
5'-most EST	LIB3165-058-P1-K1-B11
Method	BLASTX
NCBI GI	g1488043
BLAST score	265

E value	4.0e-23
Match length	84
% identity	67
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	198198
Contig ID	40095_1.R1039
5'-most EST	uC-gsronu33b112e03b1
Method	BLASTN
NCBI GI	g3241924
BLAST score	40
E value	6.0e-13
Match length	160
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	198199
Contig ID	40097_1.R1039
5'-most EST	LIB3165-023-P1-K1-E12
Method	BLASTX
NCBI GI	g3293031
BLAST score	1122
E value	1.0e-123
Match length	281
% identity	80
NCBI Description	(AJ007574) amino acid carrier [Ricinus communis]

Seq. No.	198200
Contig ID	40102_1.R1039
5'-most EST	LIB3165-023-P1-K1-E7
Method	BLASTX
NCBI GI	g1679658
BLAST score	212
E value	6.0e-17
Match length	91
% identity	53
NCBI Description	(U63726) gamma glutamyl hydrolase [Glycine max]

Seq. No.	198201
Contig ID	40109_1.R1039
5'-most EST	LIB3165-023-P1-K1-F7
Method	BLASTX
NCBI GI	g4455369
BLAST score	244
E value	2.0e-20
Match length	139
% identity	40
NCBI Description	(AL035524) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198202
Contig ID	40114_1.R1039
5'-most EST	LIB3165-023-P1-K1-G10

Seq. No.	198203
Contig ID	40134_1.R1039
5'-most EST	LIB3165-024-P1-K1-A4

Seq. No.	198204
Contig ID	40136_1.R1039
5'-most EST	LIB3197-027-Q1-M1-A12
Method	BLASTX
NCBI GI	g4580394
BLAST score	624
E value	1.0e-64
Match length	247
% identity	47
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	198205
Contig ID	40143_1.R1039
5'-most EST	LIB3165-026-P1-K1-A4
Method	BLASTN
NCBI GI	g3985958
BLAST score	41
E value	1.0e-13
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	198206
Contig ID	40185_1.R1039
5'-most EST	LIB3165-024-P1-K1-F2

Seq. No.	198207
Contig ID	40203_1.R1039
5'-most EST	LIB3197-015-P1-M1-B8
Method	BLASTX
NCBI GI	g1061040
BLAST score	678
E value	2.0e-71
Match length	140
% identity	87
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi|1587694|prf||2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	198208
Contig ID	40236_1.R1039
5'-most EST	LIB3165-048-Q1-K1-H1
Method	BLASTX
NCBI GI	g4056456
BLAST score	795
E value	5.0e-85
Match length	226
% identity	71
NCBI Description	(AC005990) Strong similarity to gb|U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF|00107. ESTs gb|T43674, gb|H77006 and gb|AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No. 198209

Contig ID	40251_1.R1039
5'-most EST	LIB3165-025-P1-K1-G12
Method	BLASTX
NCBI GI	g3334115
BLAST score	326
E value	2.0e-30
Match length	90
% identity	76
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi|2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	198210
Contig ID	40264_1.R1039
5'-most EST	LIB3196-031-P1-M1-A9
Method	BLASTX
NCBI GI	g2388583
BLAST score	196
E value	5.0e-15
Match length	87
% identity	55
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb|D90908). [Arabidopsis thaliana]

Seq. No.	198211
Contig ID	40265_1.R1039
5'-most EST	LIB3165-026-P1-K1-H6

Seq. No.	198212
Contig ID	40280_1.R1039
5'-most EST	uC-gsronu33B150c09b1
Method	BLASTX
NCBI GI	g2194137
BLAST score	412
E value	2.0e-40
Match length	132
% identity	68
NCBI Description	(AC002062) ESTs gb|R29947,gb|H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	198213
Contig ID	40283_1.R1039
5'-most EST	LIB3165-026-P1-K1-C4
Method	BLASTX
NCBI GI	g3721926
BLAST score	274
E value	8.0e-30
Match length	139
% identity	52
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	198214
Contig ID	40285_1.R1039
5'-most EST	LIB3165-026-P1-K1-C9
Method	BLASTX
NCBI GI	g4454480

BLAST score 328
E value 1.0e-30
Match length 73
% identity 78
NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No. 198215
Contig ID 40292_1.R1039
5'-most EST LIB3165-026-P1-K1-E11
Method BLASTX
NCBI GI g4325041
BLAST score 856
E value 3.0e-92
Match length 177
% identity 95
NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No. 198216
Contig ID 40293_1.R1039
5'-most EST LIB3165-043-Q1-K1-B3

Seq. No. 198217
Contig ID 40296_1.R1039
5'-most EST LIB3166-017-P1-K1-E1
Method BLASTX
NCBI GI g3953471
BLAST score 238
E value 6.0e-20
Match length 68
% identity 68
NCBI Description (AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 198218
Contig ID 40324_1.R1039
5'-most EST LIB3165-026-P1-K1-H8
Method BLASTX
NCBI GI g2213597
BLAST score 317
E value 4.0e-29
Match length 86
% identity 71
NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No. 198219
Contig ID 40332_1.R1039
5'-most EST LIB3165-032-P1-K1-A12
Method BLASTX
NCBI GI g4539324
BLAST score 278
E value 1.0e-45
Match length 220
% identity 52
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 198220

Contig ID	40335_1.R1039
5'-most EST	LIB3165-027-P1-K1-A8
Method	BLASTN
NCBI GI	g4567259
BLAST score	54
E value	3.0e-21
Match length	106
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	198221
Contig ID	40370_1.R1039
5'-most EST	LIB3165-027-P1-K1-E5

Seq. No.	198222
Contig ID	40373_1.R1039
5'-most EST	LIB3272-022-P1-K1-D4
Method	BLASTX
NCBI GI	g3738324
BLAST score	397
E value	2.0e-38
Match length	158
% identity	49
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	198223
Contig ID	40382_1.R1039
5'-most EST	LIB3165-047-Q1-K1-E10

Seq. No.	198224
Contig ID	40400_1.R1039
5'-most EST	LIB3165-027-P1-K1-H9
Method	BLASTX
NCBI GI	g4106538
BLAST score	152
E value	7.0e-10
Match length	39
% identity	64
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	198225
Contig ID	40416_1.R1039
5'-most EST	uC-gsronu33B057g10b1
Method	BLASTX
NCBI GI	g3063451
BLAST score	320
E value	1.0e-29
Match length	114
% identity	53
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No.	198226
Contig ID	40433_1.R1039
5'-most EST	LIB3165-028-P1-K1-D6
Method	BLASTX

NCBI GI	g4455787
BLAST score	296
E value	8.0e-27
Match length	120
% identity	42
NCBI Description	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]

Seq. No.	198227
Contig ID	40436_1.R1039
5'-most EST	uC-gsronu33B138b01b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	299
E value	6.0e-27
Match length	75
% identity	64
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi|469110|emb|CAA55321| (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	198228
Contig ID	40458_1.R1039
5'-most EST	uC-gsronu33B158a03b2
Method	BLASTX
NCBI GI	g1871577
BLAST score	280
E value	1.0e-24
Match length	117
% identity	50
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	198229
Contig ID	40462_1.R1039
5'-most EST	LIB3165-028-P1-K1-G7
Method	BLASTX
NCBI GI	g128194
BLAST score	637
E value	2.0e-66
Match length	189
% identity	67
NCBI Description	NITRATE REDUCTASE (NR) >gi|81572|pir||A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi|167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	198230
Contig ID	40466_1.R1039
5'-most EST	LIB3165-028-P1-K1-H11
Method	BLASTX
NCBI GI	g2828292
BLAST score	604
E value	1.0e-62
Match length	149
% identity	74
NCBI Description	(AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No.	198231
Contig ID	40477_1.R1039
5'-most EST	LIB3166-040-P1-K1-E3
Method	BLASTX
NCBI GI	g1777443
BLAST score	154
E value	4.0e-10
Match length	132
% identity	37
NCBI Description	(U28422) CCA1 [Arabidopsis thaliana] >gi|3510263 (AC005310) DNA-binding protein CCA1 [Arabidopsis thaliana] >gi|4090569 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No.	198232
Contig ID	40480_1.R1039
5'-most EST	LIB3272-020-P1-K1-F11
Method	BLASTX
NCBI GI	g3687237
BLAST score	501
E value	9.0e-51
Match length	148
% identity	66
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	198233
Contig ID	40524_1.R1039
5'-most EST	LIB3165-031-P1-K1-A4
Method	BLASTX
NCBI GI	g1707019
BLAST score	202
E value	6.0e-16
Match length	68
% identity	53
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198234
Contig ID	40529_1.R1039
5'-most EST	LIB3272-008-P1-K1-B5
Method	BLASTX
NCBI GI	g2465008
BLAST score	349
E value	5.0e-33
Match length	143
% identity	48
NCBI Description	(AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No.	198235
Contig ID	40533_1.R1039
5'-most EST	LIB3165-031-P1-K1-B6

Seq. No.	198236
Contig ID	40546_1.R1039
5'-most EST	uC-gsronu33B076d10b1

Seq. No.	198237
Contig ID	40604_1.R1039

5'-most EST	LIB3165-032-P1-K1-B12
Method	BLASTX
NCBI GI	g3269292
BLAST score	289
E value	5.0e-26
Match length	74
% identity	69
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	198238
Contig ID	40665_1.R1039
5'-most EST	uC-gsflnu33B134f12b1

Seq. No.	198239
Contig ID	40668_1.R1039
5'-most EST	LIB3165-032-P1-K1-H4

Seq. No.	198240
Contig ID	40670_1.R1039
5'-most EST	LIB3165-032-P1-K1-H6
Method	BLASTX
NCBI GI	g3281850
BLAST score	174
E value	2.0e-12
Match length	99
% identity	41
NCBI Description	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No.	198241
Contig ID	40673_1.R1039
5'-most EST	LIB3166-020-P1-K1-A6

Seq. No.	198242
Contig ID	40687_1.R1039
5'-most EST	uC-gsflnu33B011b12b1
Method	BLASTX
NCBI GI	g3080418
BLAST score	260
E value	1.0e-22
Match length	114
% identity	44
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	198243
Contig ID	40722_1.R1039
5'-most EST	LIB3197-043-Q1-M1-A6
Method	BLASTX
NCBI GI	g1418990
BLAST score	302
E value	2.0e-27
Match length	71
% identity	77
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	198244
Contig ID	40732_1.R1039

5'-most EST	LIB3165-033-P1-K1-G3
Method	BLASTX
NCBI GI	g1592545
BLAST score	163
E value	5.0e-11
Match length	100
% identity	38
NCBI Description	(U37486) peroxisomal multifunctional enzyme type II [Rattus norvegicus]

Seq. No.	198245
Contig ID	40757_1.R1039
5'-most EST	uC-gsflmaxxa028g10b1
Method	BLASTX
NCBI GI	g1076627
BLAST score	468
E value	7.0e-47
Match length	132
% identity	70
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi|790479|emb|CAA58701| (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	198246
Contig ID	40759_1.R1039
5'-most EST	LIB3165-034-P1-K6-B2
Method	BLASTX
NCBI GI	g68200
BLAST score	259
E value	2.0e-22
Match length	89
% identity	66
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi|22633|emb|CAA47293| (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	198247
Contig ID	40764_1.R1039
5'-most EST	LIB3165-034-P1-K1-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	341
E value	2.0e-35
Match length	114
% identity	63
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	198248
Contig ID	40765_1.R1039
5'-most EST	LIB3189-018-P1-K1-E11

Seq. No.	198249
Contig ID	40780_1.R1039
5'-most EST	LIB3165-034-P1-K4-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	362

E value	2.0e-34
Match length	97
% identity	68
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	198250
Contig ID	40805_1.R1039
5'-most EST	LIB3165-034-P1-K5-F4

Seq. No.	198251
Contig ID	40811_1.R1039
5'-most EST	LIB3165-034-P1-K3-G10
Method	BLASTX
NCBI GI	g1619602
BLAST score	257
E value	3.0e-22
Match length	78
% identity	56
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	198252
Contig ID	40818_1.R1039
5'-most EST	LIB3165-034-P1-K3-G7
Method	BLASTX
NCBI GI	g3928543
BLAST score	577
E value	1.0e-59
Match length	138
% identity	72
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	198253
Contig ID	40821_1.R1039
5'-most EST	LIB3165-034-P1-K2-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	437
E value	2.0e-43
Match length	96
% identity	89
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	198254
Contig ID	40821_2.R1039
5'-most EST	LIB3165-034-P1-K6-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	459
E value	6.0e-46
Match length	128
% identity	72
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	198255
Contig ID	40822_1.R1039
5'-most EST	LIB3165-034-P1-K4-H10

Seq. No.	198256
Contig ID	40829_1.R1039
5'-most EST	LIB3165-034-P1-K3-H7
Method	BLASTX
NCBI GI	g100332
BLAST score	1718
E value	0.0e+00
Match length	389
% identity	84
NCBI Description	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - common tobacco >gi|19875|emb|CAA46787| (X65974) glutamate-1-semialdehyde 2,1-aminomutase [Nicotiana tabacum]

Seq. No.	198257
Contig ID	41029_1.R1039
5'-most EST	LIB3165-034-P1-K4-D3

Seq. No.	198258
Contig ID	41242_1.R1039
5'-most EST	LIB3165-036-P1-K1-A1
Method	BLASTX
NCBI GI	g710465
BLAST score	490
E value	3.0e-49
Match length	191
% identity	52
NCBI Description	OEP86=outer envelope protein [Peas, Peptide Chloroplast, 878 aa]

Seq. No.	198259
Contig ID	41276_1.R1039
5'-most EST	LIB3165-036-P1-K1-D5
Method	BLASTX
NCBI GI	g20559
BLAST score	843
E value	1.0e-90
Match length	194
% identity	88
NCBI Description	(X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No.	198260
Contig ID	41286_1.R1039
5'-most EST	LIB3165-036-P1-K1-E5
Method	BLASTX
NCBI GI	g2190551
BLAST score	293
E value	3.0e-26
Match length	107
% identity	51
NCBI Description	(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb|Z71181). ESTs gb|H36844,gb|AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No.	198261
Contig ID	41311_1.R1039

5'-most EST	LIB3165-036-P1-K1-H6
Method	BLASTX
NCBI GI	g2245005
BLAST score	269
E value	1.0e-23
Match length	103
% identity	55
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198262
Contig ID	41343_1.R1039
5'-most EST	g5050520
Method	BLASTX
NCBI GI	g4262236
BLAST score	445
E value	5.0e-44
Match length	138
% identity	65
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	198263
Contig ID	41384_1.R1039
5'-most EST	LIB3272-015-P1-K1-C9
Method	BLASTX
NCBI GI	g3482918
BLAST score	745
E value	3.0e-79
Match length	169
% identity	86
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	198264
Contig ID	41396_1.R1039
5'-most EST	LIB3165-038-Q1-K1-B12

Seq. No.	198265
Contig ID	41398_1.R1039
5'-most EST	LIB3165-038-Q1-K1-B4
Method	BLASTX
NCBI GI	g586858
BLAST score	360
E value	5.0e-34
Match length	161
% identity	47
NCBI Description	HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION >gi|2127020|pir||S66042 hypothetical protein - Bacillus subtilis >gi|467402|dbj|BAA05248| (D26185) unknown [Bacillus subtilis] >gi|2632279|emb|CAB11788| (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	198266
Contig ID	41418_1.R1039
5'-most EST	LIB3165-038-Q1-K1-G10

Seq. No.	198267

Contig ID	41423_1.R1039
5'-most EST	LIB3165-046-Q1-K1-G4
Method	BLASTX
NCBI GI	g4572673
BLAST score	701
E value	5.0e-74
Match length	202
% identity	68
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No.	198268
Contig ID	41495_1.R1039
5'-most EST	g5046506
Method	BLASTX
NCBI GI	g1353013
BLAST score	194
E value	2.0e-14
Match length	149
% identity	34
NCBI Description	HYPOTHETICAL 47.4 KD PROTEIN IN RPS25B-MRS3 INTERGENIC REGION >gi|1077836|pir||S55178 hypothetical protein YJL134w - yeast (Saccharomyces cerevisiae) >gi|854562|emb|CAA60821| (X87371) ORF21; homologous to ORF YKR053c [Saccharomyces cerevisiae] >gi|1008341|emb|CAA89430| (Z49410) ORF YJL134w [Saccharomyces cerevisiae]

Seq. No.	198269
Contig ID	41503_1.R1039
5'-most EST	LIB3165-055-P1-K1-A8
Method	BLASTN
NCBI GI	g4455189
BLAST score	33
E value	6.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSAII project)

Seq. No.	198270
Contig ID	41506_1.R1039
5'-most EST	LIB3189-034-P1-K1-F10
Method	BLASTX
NCBI GI	g3059131
BLAST score	517
E value	3.0e-52
Match length	245
% identity	44
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	198271
Contig ID	41519_1.R1039
5'-most EST	LIB3165-039-Q1-K1-G3
Method	BLASTX
NCBI GI	g3885513
BLAST score	259
E value	1.0e-25

Match length	69
% identity	77
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	198272
Contig ID	41537_1.R1039
5'-most EST	LIB3272-019-P1-K1-E10
Method	BLASTX
NCBI GI	g2618721
BLAST score	169
E value	6.0e-12
Match length	77
% identity	56
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	198273
Contig ID	41559_1.R1039
5'-most EST	LIB3165-040-Q1-K1-C4
Method	BLASTX
NCBI GI	g4490297
BLAST score	468
E value	2.0e-75
Match length	221
% identity	63
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	198274
Contig ID	41587_1.R1039
5'-most EST	LIB3165-040-Q1-K1-E9
Method	BLASTX
NCBI GI	g4376592
BLAST score	163
E value	6.0e-11
Match length	121
% identity	11
NCBI Description	(AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae]

Seq. No.	198275
Contig ID	41588_1.R1039
5'-most EST	LIB3165-040-Q1-K1-F1

Seq. No.	198276
Contig ID	41616_1.R1039
5'-most EST	LIB3165-041-Q1-K1-A10
Method	BLASTX
NCBI GI	g4099835
BLAST score	500
E value	1.0e-50
Match length	141
% identity	62
NCBI Description	(U90266) bifunctional nuclease [Zinnia elegans]

Seq. No.	198277
Contig ID	41625_1.R1039
5'-most EST	LIB3165-041-Q1-K1-B10
Method	BLASTX

NCBI GI	g4091806
BLAST score	554
E value	5.0e-57
Match length	128
% identity	83
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	198278
Contig ID	41634_1.R1039
5'-most EST	LIB3165-041-Q1-K1-C11
Method	BLASTX
NCBI GI	g1658193
BLAST score	384
E value	2.0e-39
Match length	172
% identity	49
NCBI Description	(U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum bicolor]

Seq. No.	198279
Contig ID	41634_2.R1039
5'-most EST	uC-gsflnu33B061g10b1
Method	BLASTX
NCBI GI	g2262164
BLAST score	265
E value	4.0e-23
Match length	91
% identity	62
NCBI Description	(AC002329) putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana]

Seq. No.	198280
Contig ID	41649_1.R1039
5'-most EST	uC-gsronu33B179g03b1
Method	BLASTX
NCBI GI	g3165581
BLAST score	283
E value	5.0e-25
Match length	153
% identity	37
NCBI Description	(AF067942) similar to lysosomal acid lipases (SW:P38571) [Caenorhabditis elegans]

Seq. No.	198281
Contig ID	41651_1.R1039
5'-most EST	g3326523
Method	BLASTX
NCBI GI	g3660471
BLAST score	558
E value	3.0e-57
Match length	160
% identity	69
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	198282
Contig ID	41654_1.R1039

5'-most EST	LIB3165-041-Q1-K1-E8
Method	BLASTX
NCBI GI	g4220477
BLAST score	275
E value	2.0e-24
Match length	113
% identity	55
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	198283
Contig ID	41671_1.R1039
5'-most EST	LIB3165-041-Q1-K1-H10
Method	BLASTX
NCBI GI	g3426043
BLAST score	595
E value	9.0e-62
Match length	134
% identity	77
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	198284
Contig ID	41676_1.R1039
5'-most EST	LIB3196-025-P1-M1-G5

Seq. No.	198285
Contig ID	41716_1.R1039
5'-most EST	LIB3165-042-Q1-K1-D6

Seq. No.	198286
Contig ID	41717_1.R1039
5'-most EST	LIB3165-042-Q1-K1-D7
Method	BLASTN
NCBI GI	g2264310
BLAST score	38
E value	1.0e-11
Match length	74
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	198287
Contig ID	41732_1.R1039
5'-most EST	LIB3272-022-P1-K1-C3
Method	BLASTX
NCBI GI	g4115379
BLAST score	265
E value	4.0e-23
Match length	83
% identity	64
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	198288
Contig ID	41745_1.R1039
5'-most EST	LIB3197-028-Q1-M1-A5

Seq. No.	198289

Contig ID	41746_1.R1039
5'-most EST	LIB3197-053-Q1-M1-D4
Seq. No.	198290
Contig ID	41765_1.R1039
5'-most EST	uC-gsronu33B126d06b1
Seq. No.	198291
Contig ID	41825_1.R1039
5'-most EST	uC-gsflnu33B083e01b1
Seq. No.	198292
Contig ID	41825_2.R1039
5'-most EST	LIB3165-043-Q1-K1-H11
Seq. No.	198293
Contig ID	41834_1.R1039
5'-most EST	LIB3165-044-Q1-K1-A1
Seq. No.	198294
Contig ID	41861_1.R1039
5'-most EST	LIB3165-044-Q1-K1-C7
Method	BLASTX
NCBI GI	g2443751
BLAST score	606
E value	6.0e-63
Match length	168
% identity	66
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi|2529676 (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.	198295
Contig ID	41866_1.R1039
5'-most EST	LIB3165-044-Q1-K1-D3
Seq. No.	198296
Contig ID	41895_1.R1039
5'-most EST	LIB3197-021-Q1-M1-A2
Method	BLASTX
NCBI GI	g4033468
BLAST score	397
E value	1.0e-38
Match length	115
% identity	45
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP40 >gi|2582641|emb|CAA67800| (X99437) splicing factor [Arabidopsis thaliana] >gi|2980800|emb|CAA18176| (AL022197) splicing factor At-SRp40 [Arabidopsis thaliana]
Seq. No.	198297
Contig ID	41897_1.R1039
5'-most EST	LIB3165-044-Q1-K1-G5
Method	BLASTX
NCBI GI	g2952433
BLAST score	866
E value	3.0e-93
Match length	212

% identity	79
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	198298
Contig ID	41917_1.R1039
5'-most EST	LIB3165-045-Q1-K1-B10

Seq. No.	198299
Contig ID	41926_1.R1039
5'-most EST	LIB3165-045-Q1-K1-C7
Method	BLASTX
NCBI GI	g541951
BLAST score	612
E value	1.0e-63
Match length	153
% identity	58
NCBI Description	SPCP2 protein - soybean >gi|310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	198300
Contig ID	41926_2.R1039
5'-most EST	uC-gsronu33B015h12b1
Method	BLASTX
NCBI GI	g541951
BLAST score	606
E value	5.0e-63
Match length	133
% identity	62
NCBI Description	SPCP2 protein - soybean >gi|310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	198301
Contig ID	41939_1.R1039
5'-most EST	LIB3165-045-Q1-K1-E8
Method	BLASTX
NCBI GI	g2398679
BLAST score	944
E value	1.0e-102
Match length	199
% identity	88
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	198302
Contig ID	41981_1.R1039
5'-most EST	LIB3165-046-Q1-K1-C1
Method	BLASTX
NCBI GI	g4510348
BLAST score	711
E value	5.0e-75
Match length	237
% identity	55
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	198303
Contig ID	41985_1.R1039

5'-most EST	uC-gsflnu33B051h04b1
Method	BLASTN
NCBI GI	g166626
BLAST score	274
E value	1.0e-152
Match length	535
% identity	88
NCBI Description	Arabidopsis thaliana nucleotide-binding subunit of vacuolar ATPase mRNA, complete cds

Seq. No.	198304
Contig ID	41985_2.R1039
5'-most EST	uC-gsflnu33B114d10b1
Method	BLASTX
NCBI GI	g2493131
BLAST score	917
E value	3.0e-99
Match length	191
% identity	95
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi|167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	198305
Contig ID	42000_1.R1039
5'-most EST	g5048971
Method	BLASTX
NCBI GI	g3334130
BLAST score	123
E value	2.0e-10
Match length	76
% identity	59
NCBI Description	BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) >gi|1143319 (U40666) biotin carboxyl carrier protein precursor [Glycine max]

Seq. No.	198306
Contig ID	42003_1.R1039
5'-most EST	g5046621
Method	BLASTX
NCBI GI	g1168258
BLAST score	745
E value	4.0e-79
Match length	205
% identity	74
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi|693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	198307
Contig ID	42038_1.R1039
5'-most EST	LIB3189-015-P1-K1-F7
Method	BLASTX
NCBI GI	g2245107
BLAST score	363
E value	2.0e-34
Match length	205

% identity 33
NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No. 198308
Contig ID 42045_1.R1039
5'-most EST uC-gsronu33B143a10b1
Method BLASTX
NCBI GI g4262167
BLAST score 169
E value 1.0e-11
Match length 183
% identity 28
NCBI Description (AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No. 198309
Contig ID 42046_1.R1039
5'-most EST LIB3165-047-Q1-K1-A6

Seq. No. 198310
Contig ID 42050_1.R1039
5'-most EST LIB3165-047-Q1-K1-B1
Method BLASTX
NCBI GI g2290528
BLAST score 1677
E value 0.0e+00
Match length 346
% identity 90
NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]

Seq. No. 198311
Contig ID 42064_1.R1039
5'-most EST LIB3165-047-Q1-K1-C5

Seq. No. 198312
Contig ID 42066_1.R1039
5'-most EST uC-gsronu33B047a07b1
Method BLASTX
NCBI GI g2760345
BLAST score 703
E value 2.0e-74
Match length 141
% identity 28
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]

Seq. No. 198313
Contig ID 42070_1.R1039
5'-most EST LIB3189-023-P1-K1-H2

Seq. No. 198314
Contig ID 42098_1.R1039
5'-most EST LIB3165-047-Q1-K1-G10

Seq. No. 198315
Contig ID 42098_2.R1039
5'-most EST LIB3272-031-P1-K1-H4
Method BLASTX

NCBI GI g4580461
BLAST score 162
E value 7.0e-12
Match length 77
% identity 57
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 198316
Contig ID 42114_1.R1039
5'-most EST LIB3165-047-Q1-K1-H5
Method BLASTX
NCBI GI g3269292
BLAST score 245
E value 7.0e-21
Match length 62
% identity 73
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 198317
Contig ID 42129_1.R1039
5'-most EST g5048885
Method BLASTX
NCBI GI g2801536
BLAST score 435
E value 1.0e-42
Match length 162
% identity 54
NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No. 198318
Contig ID 42134_1.R1039
5'-most EST LIB3166-029-P1-K1-B12
Method BLASTX
NCBI GI g2213595
BLAST score 379
E value 2.0e-36
Match length 144
% identity 53
NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No. 198319
Contig ID 42136_1.R1039
5'-most EST LIB3166-042-P1-K1-D5

Seq. No. 198320
Contig ID 42151_1.R1039
5'-most EST LIB3165-048-Q1-K1-D11
Method BLASTX
NCBI GI g2894603
BLAST score 186
E value 8.0e-14
Match length 95
% identity 23
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 198321
Contig ID 42176_1.R1039

5'-most EST	uC-gsflnu33B070f09b1
Method	BLASTX
NCBI GI	g4510373
BLAST score	439
E value	2.0e-43
Match length	134
% identity	63
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	198322
Contig ID	42195_1.R1039
5'-most EST	g5050751
Method	BLASTX
NCBI GI	g3928084
BLAST score	331
E value	1.0e-30
Match length	164
% identity	49
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	198323
Contig ID	42204_1.R1039
5'-most EST	LIB3165-049-Q1-K1-A4
Method	BLASTX
NCBI GI	g4415908
BLAST score	148
E value	2.0e-09
Match length	65
% identity	51
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	198324
Contig ID	42214_1.R1039
5'-most EST	LIB3272-044-P1-K1-H7
Method	BLASTX
NCBI GI	g2792295
BLAST score	487
E value	5.0e-76
Match length	254
% identity	56
NCBI Description	(AF039182) unknown [Fragaria x ananassa]

Seq. No.	198325
Contig ID	42219_1.R1039
5'-most EST	LIB3165-049-Q1-K1-C2
Method	BLASTX
NCBI GI	g3786016
BLAST score	188
E value	3.0e-21
Match length	102
% identity	63
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	198326

Contig ID	42220_1.R1039
5'-most EST	LIB3166-005-P1-K1-D5
Method	BLASTX
NCBI GI	g3249084
BLAST score	259
E value	8.0e-41
Match length	114
% identity	21
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb|X92750 from Mus musculus. ESTs gb|AA712687 and gb|Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	198327
Contig ID	42235_1.R1039
5'-most EST	g5048310
Method	BLASTX
NCBI GI	g4240273
BLAST score	146
E value	6.0e-09
Match length	145
% identity	30
NCBI Description	(AB020699) KIAA0892 protein [Homo sapiens]

Seq. No.	198328
Contig ID	42237_1.R1039
5'-most EST	LIB3166-028-P1-K1-C12
Method	BLASTX
NCBI GI	g4510375
BLAST score	289
E value	1.0e-25
Match length	147
% identity	56
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	198329
Contig ID	42239_1.R1039
5'-most EST	LIB3165-049-Q1-K1-E4
Method	BLASTX
NCBI GI	g2462781
BLAST score	509
E value	2.0e-51
Match length	152
% identity	68
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	198330
Contig ID	42242_1.R1039
5'-most EST	LIB3165-049-Q1-K1-E8
Method	BLASTX
NCBI GI	g2642154
BLAST score	197
E value	4.0e-15
Match length	124
% identity	43
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana]

>gi|3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	198331
Contig ID	42275_1.R1039
5'-most EST	LIB3189-027-P1-K1-F6

Seq. No.	198332
Contig ID	42276_1.R1039
5'-most EST	LIB3165-050-Q1-K1-B12

Seq. No.	198333
Contig ID	42336_1.R1039
5'-most EST	LIB3165-050-Q1-K1-H8
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	8.0e-09
Match length	36
% identity	97
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	198334
Contig ID	42394_1.R1039
5'-most EST	LIB3165-051-Q1-K1-F9

Seq. No.	198335
Contig ID	42420_1.R1039
5'-most EST	LIB3189-042-P1-K1-G6
Method	BLASTX
NCBI GI	g1350930
BLAST score	719
E value	3.0e-76
Match length	148
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	198336
Contig ID	42432_1.R1039
5'-most EST	LIB3165-052-Q1-K1-C1

Seq. No.	198337
Contig ID	42442_1.R1039
5'-most EST	g5048299
Method	BLASTN
NCBI GI	g3449326
BLAST score	59
E value	3.0e-24
Match length	272
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	198338
Contig ID	42462_1.R1039
5'-most EST	LIB3165-052-Q1-K1-F1
Method	BLASTX

NCBI GI	g3395429
BLAST score	231
E value	9.0e-19
Match length	160
% identity	37
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198339
Contig ID	42466_1.R1039
5'-most EST	LIB3165-052-Q1-K1-F6
Method	BLASTX
NCBI GI	g2982463
BLAST score	998
E value	1.0e-108
Match length	315
% identity	66
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	198340
Contig ID	42471_1.R1039
5'-most EST	LIB3166-044-P1-K1-C7

Seq. No.	198341
Contig ID	42477_1.R1039
5'-most EST	LIB3165-055-P1-K1-G4
Method	BLASTX
NCBI GI	g3688123
BLAST score	369
E value	3.0e-35
Match length	128
% identity	63
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	198342
Contig ID	42484_1.R1039
5'-most EST	g5048354
Method	BLASTX
NCBI GI	g2388689
BLAST score	295
E value	2.0e-26
Match length	115
% identity	54
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	198343
Contig ID	42506_1.R1039
5'-most EST	LIB3166-025-P1-K1-E8
Method	BLASTX
NCBI GI	g1706318
BLAST score	279
E value	1.0e-24
Match length	117
% identity	51
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) >gi|1362098|pir||S56177 probable glutamate decarboxylase - tomato >gi|995555|emb|CAA56812| (X80840) homology to

pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]

Seq. No.	198344
Contig ID	42514_1.R1039
5'-most EST	uC-gsronu33B137g11b1
Method	BLASTX
NCBI GI	g3258571
BLAST score	522
E value	3.0e-53
Match length	139
% identity	79
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	198345
Contig ID	42546_1.R1039
5'-most EST	uC-gsronu33B099f08b1

Seq. No.	198346
Contig ID	42557_2.R1039
5'-most EST	g5047103
Method	BLASTX
NCBI GI	g2673914
BLAST score	808
E value	1.0e-86
Match length	179
% identity	80
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198347
Contig ID	42558_1.R1039
5'-most EST	LIB3166-029-P1-K1-E6
Method	BLASTX
NCBI GI	g4056507
BLAST score	287
E value	2.0e-25
Match length	99
% identity	57
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	198348
Contig ID	42561_1.R1039
5'-most EST	LIB3165-055-P1-K1-A4

Seq. No.	198349
Contig ID	42577_1.R1039
5'-most EST	LIB3165-055-P1-K1-C10

Seq. No.	198350
Contig ID	42619_1.R1039
5'-most EST	uC-gsflnu33B078b08b1
Method	BLASTX
NCBI GI	g549706
BLAST score	178
E value	7.0e-13
Match length	106

% identity	41
NCBI Description	KTI12 PROTEIN >gi|539197|pir||S37937 KTI12 protein - yeast (Saccharomyces cerevisiae) >gi|486185|emb|CAA81950| (Z28110) ORF YKL110c [Saccharomyces cerevisiae] >gi|536816|emb|CAA54646| (X77511) KTI12 [Saccharomyces cerevisiae]
Seq. No.	198351
Contig ID	42624_1.R1039
5'-most EST	uC-gsronu33B117a02b1
Seq. No.	198352
Contig ID	42640_1.R1039
5'-most EST	LIB3166-047-P1-K1-C3
Method	BLASTX
NCBI GI	g1076748
BLAST score	234
E value	2.0e-19
Match length	98
% identity	28
NCBI Description	major intrinsic protein - rice >gi|440869|dbj|BAA04257| (D17443) major intrinsic protein [Oryza sativa]
Seq. No.	198353
Contig ID	42664_1.R1039
5'-most EST	LIB3165-057-P1-K1-A3
Seq. No.	198354
Contig ID	42674_1.R1039
5'-most EST	LIB3166-018-P1-K1-F11
Seq. No.	198355
Contig ID	42675_1.R1039
5'-most EST	uC-gsronu33b023d12b1
Seq. No.	198356
Contig ID	42761_1.R1039
5'-most EST	LIB3165-060-Q1-K1-B2
Method	BLASTX
NCBI GI	g2832643
BLAST score	353
E value	2.0e-33
Match length	105
% identity	75
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.	198357
Contig ID	42772_1.R1039
5'-most EST	LIB3197-044-Q1-M1-H11
Seq. No.	198358
Contig ID	42811_1.R1039
5'-most EST	uC-gsflmaxxa005a02b1
Method	BLASTX
NCBI GI	g1871192
BLAST score	156
E value	2.0e-10

Match length	75
% identity	43
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	198359
Contig ID	42833_1.R1039
5'-most EST	LIB3166-001-Q1-K1-A6
Method	BLASTX
NCBI GI	g4455202
BLAST score	384
E value	4.0e-37
Match length	119
% identity	64
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	198360
Contig ID	42835_1.R1039
5'-most EST	LIB3166-001-Q1-K1-A8
Method	BLASTX
NCBI GI	g2191129
BLAST score	258
E value	2.0e-22
Match length	135
% identity	50
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No.	198361
Contig ID	42837_1.R1039
5'-most EST	LIB3166-001-Q1-K1-B1
Method	BLASTX
NCBI GI	g3122116
BLAST score	294
E value	1.0e-26
Match length	132
% identity	48
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG >gi|2660540|emb|CAA05102| (AJ001932) cell cycle protein [Helicobacter felis]

Seq. No.	198362
Contig ID	42847_1.R1039
5'-most EST	LIB3166-058-P1-K1-C2
Method	BLASTX
NCBI GI	g3790567
BLAST score	252
E value	1.0e-21
Match length	135
% identity	39
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	198363
Contig ID	42850_1.R1039
5'-most EST	LIB3189-003-P1-K1-A1
Method	BLASTX

NCBI GI g1170504
BLAST score 175
E value 2.0e-12
Match length 68
% identity 49
NCBI Description EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi|452440 (M95747) initiation factor (iso)4f p82 subunit [Triticum aestivum]

Seq. No. 198364
Contig ID 42853_1.R1039
5'-most EST LIB3166-001-Q1-K1-C4
Method BLASTX
NCBI GI g4314378
BLAST score 533
E value 3.0e-54
Match length 216
% identity 49
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 198365
Contig ID 42856_1.R1039
5'-most EST LIB3166-001-Q1-K1-C8

Seq. No. 198366
Contig ID 42858_1.R1039
5'-most EST LIB3166-001-Q1-K1-D1
Method BLASTN
NCBI GI g2687434
BLAST score 47
E value 2.0e-17
Match length 215
% identity 81
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No. 198367
Contig ID 42864_1.R1039
5'-most EST LIB3166-001-Q1-K1-D4

Seq. No. 198368
Contig ID 42865_1.R1039
5'-most EST LIB3166-001-Q1-K1-D5
Method BLASTX
NCBI GI g2501572
BLAST score 387
E value 2.0e-37
Match length 107
% identity 63
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi|1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No. 198369
Contig ID 42868_1.R1039
5'-most EST LIB3166-001-Q1-K1-D8
Method BLASTX
NCBI GI g4249410

BLAST score 598
E value 6.0e-62
Match length 139
% identity 80
NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 198370
Contig ID 42870_1.R1039
5'-most EST g3326057

Seq. No. 198371
Contig ID 42875_1.R1039
5'-most EST LIB3272-039-P1-K1-D11
Method BLASTX
NCBI GI g4206789
BLAST score 457
E value 6.0e-56
Match length 147
% identity 75
NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No. 198372
Contig ID 42876_1.R1039
5'-most EST LIB3166-001-Q1-K1-E4

Seq. No. 198373
Contig ID 42878_1.R1039
5'-most EST uC-gsflmaxxa091f07b1
Method BLASTX
NCBI GI g4204313
BLAST score 627
E value 2.0e-65
Match length 140
% identity 84
NCBI Description (AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 198374
Contig ID 42879_1.R1039
5'-most EST LIB3166-001-Q1-K1-E8

Seq. No. 198375
Contig ID 42881_1.R1039
5'-most EST LIB3166-001-Q1-K1-F1

Seq. No. 198376
Contig ID 42884_1.R1039
5'-most EST LIB3166-001-Q1-K1-F12
Method BLASTX
NCBI GI g3281848
BLAST score 177
E value 1.0e-12
Match length 129
% identity 43
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 198377
Contig ID 42886_1.R1039
5'-most EST uC-gsronu33B019h12b1

Seq. No. 198378
Contig ID 42887_1.R1039
5'-most EST LIB3272-016-P1-K1-C12
Method BLASTX
NCBI GI g4417300
BLAST score 153
E value 1.0e-09
Match length 104
% identity 31
NCBI Description (AC006446) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198379
Contig ID 42890_1.R1039
5'-most EST LIB3166-001-Q1-K1-F8

Seq. No. 198380
Contig ID 42895_1.R1039
5'-most EST LIB3166-005-P1-K1-E10
Method BLASTX
NCBI GI g3218467
BLAST score 276
E value 4.0e-24
Match length 225
% identity 35
NCBI Description (AJ006529) putative phosphatase [Gallus gallus]

Seq. No. 198381
Contig ID 42898_1.R1039
5'-most EST uC-gsflmaxxa058d02b1

Seq. No. 198382
Contig ID 42900_1.R1039
5'-most EST LIB3166-001-Q1-K1-G6
Method BLASTX
NCBI GI g3859116
BLAST score 204
E value 6.0e-26
Match length 111
% identity 59
NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 198383
Contig ID 42901_1.R1039
5'-most EST LIB3166-001-Q1-K1-G7

Seq. No. 198384
Contig ID 42902_1.R1039
5'-most EST LIB3166-001-Q1-K1-G8

Seq. No. 198385
Contig ID 42903_1.R1039
5'-most EST LIB3166-001-Q1-K1-G9
Method BLASTX

NCBI GI	g3043760
BLAST score	910
E value	2.0e-98
Match length	244
% identity	66
NCBI Description	(AB012759) rPOP [Rattus norvegicus]

Seq. No.	198386
Contig ID	42907_1.R1039
5'-most EST	LIB3166-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g3402704
BLAST score	344
E value	2.0e-32
Match length	119
% identity	66
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198387
Contig ID	42910_1.R1039
5'-most EST	LIB3166-055-P1-K1-C8
Method	BLASTX
NCBI GI	g2252631
BLAST score	317
E value	8.0e-29
Match length	101
% identity	62
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198388
Contig ID	42910_2.R1039
5'-most EST	LIB3189-053-P1-K1-G6
Method	BLASTX
NCBI GI	g2252631
BLAST score	158
E value	2.0e-10
Match length	63
% identity	49
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198389
Contig ID	42911_1.R1039
5'-most EST	LIB3166-001-Q1-K1-H6
Method	BLASTX
NCBI GI	g3319342
BLAST score	164
E value	2.0e-11
Match length	45
% identity	64
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	198390
Contig ID	42912_1.R1039
5'-most EST	LIB3166-001-Q1-K1-H7
Method	BLASTX

NCBI GI g1352076
BLAST score 162
E value 4.0e-11
Match length 134
% identity 33
NCBI Description BETA-GALACTOSIDASE (LACTASE) >gi|144746 (M35107) beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]

Seq. No. 198391
Contig ID 42913_1.R1039
5'-most EST LIB3272-026-P1-K1-C2
Method BLASTX
NCBI GI g4262225
BLAST score 295
E value 3.0e-42
Match length 147
% identity 55
NCBI Description (AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No. 198392
Contig ID 42976_1.R1039
5'-most EST LIB3166-002-Q1-K1-A10
Method BLASTX
NCBI GI g4539301
BLAST score 423
E value 1.0e-41
Match length 110
% identity 73
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 198393
Contig ID 42977_1.R1039
5'-most EST LIB3272-016-P1-K1-G9
Method BLASTX
NCBI GI g3319340
BLAST score 701
E value 7.0e-74
Match length 206
% identity 66
NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 198394
Contig ID 42981_1.R1039
5'-most EST LIB3166-002-Q1-K1-A7
Method BLASTX
NCBI GI g4105782
BLAST score 422
E value 2.0e-41
Match length 97
% identity 85
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 198395
Contig ID 42983_1.R1039

5'-most EST	uC-gsflmaxxa047f06b1
Method	BLASTX
NCBI GI	g1762428
BLAST score	568
E value	2.0e-58
Match length	159
% identity	17
NCBI Description	(U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No.	198396
Contig ID	42985_1.R1039
5'-most EST	LIB3166-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g418507
BLAST score	329
E value	3.0e-30
Match length	163
% identity	41
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi|541097|pir||S40872 hypothetical protein f161 - Escherichia coli >gi|305032 (L19201) ORF_f161 [Escherichia coli] >gi|1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi|1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	198397
Contig ID	42989_1.R1039
5'-most EST	LIB3166-002-Q1-K1-B3
Method	BLASTX
NCBI GI	g3559811
BLAST score	486
E value	4.0e-49
Match length	137
% identity	71
NCBI Description	(AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No.	198398
Contig ID	43005_1.R1039
5'-most EST	LIB3197-008-P1-M1-A4

Seq. No.	198399
Contig ID	43026_1.R1039
5'-most EST	LIB3166-002-Q1-K1-E6
Method	BLASTX
NCBI GI	g4432857
BLAST score	205
E value	9.0e-19
Match length	136
% identity	46
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198400
Contig ID	43036_1.R1039
5'-most EST	uC-gsflnu33B006a03b1
Method	BLASTX

NCBI GI g3434973
BLAST score 219
E value 1.0e-17
Match length 76
% identity 61
NCBI Description (AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No. 198401
Contig ID 43049_1.R1039
5'-most EST g3326556

Seq. No. 198402
Contig ID 43062_1.R1039
5'-most EST LIB3166-003-P1-K1-A10
Method BLASTX
NCBI GI g3757521
BLAST score 577
E value 2.0e-59
Match length 217
% identity 54
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 198403
Contig ID 43064_1.R1039
5'-most EST LIB3166-026-P1-K1-D1
Method BLASTX
NCBI GI g4539370
BLAST score 337
E value 2.0e-31
Match length 86
% identity 73
NCBI Description (AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No. 198404
Contig ID 43085_1.R1039
5'-most EST LIB3197-005-P1-M1-H2
Method BLASTX
NCBI GI g3183421
BLAST score 208
E value 3.0e-16
Match length 136
% identity 40
NCBI Description HYPOTHETICAL PROTEIN MJ1541 >gi|2129138|pir||D64492 N-ethylammeline chlorohydrolase homolog - Methanococcus jannaschii >gi|1592173 (U67595) N-ethylammeline chlorohydrolase (trzA) [Methanococcus jannaschii]

Seq. No. 198405
Contig ID 43093_1.R1039
5'-most EST uC-gsflmaxxa006a02b1

Seq. No. 198406
Contig ID 43101_1.R1039
5'-most EST LIB3196-018-P1-M1-A2
Method BLASTX

NCBI GI	g4204912
BLAST score	204
E value	1.0e-15
Match length	91
% identity	51
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]

Seq. No.	198407
Contig ID	43111_1.R1039
5'-most EST	LIB3166-003-P1-K1-F5
Method	BLASTX
NCBI GI	g3142290
BLAST score	616
E value	4.0e-64
Match length	176
% identity	74
NCBI Description	(AC002411) Contains similarity to gb|Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	198408
Contig ID	43112_1.R1039
5'-most EST	uC-gsronu33B089e06b1
Method	BLASTX
NCBI GI	g2244865
BLAST score	286
E value	2.0e-25
Match length	192
% identity	39
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198409
Contig ID	43116_1.R1039
5'-most EST	LIB3166-003-P1-K1-G10
Method	BLASTX
NCBI GI	g3860263
BLAST score	283
E value	3.0e-25
Match length	126
% identity	51
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	198410
Contig ID	43116_2.R1039
5'-most EST	LIB3166-016-P1-K1-F11
Method	BLASTX
NCBI GI	g3860263
BLAST score	248
E value	7.0e-41
Match length	114
% identity	64
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	198411
Contig ID	43125_1.R1039
5'-most EST	LIB3166-024-P1-K1-D2

Method	BLASTX
NCBI GI	g1142621
BLAST score	196
E value	1.0e-14
Match length	120
% identity	49
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No.	198412
Contig ID	43125_2.R1039
5'-most EST	LIB3166-011-P1-K1-C3
Method	BLASTX
NCBI GI	g1142621
BLAST score	231
E value	1.0e-23
Match length	183
% identity	44
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No.	198413
Contig ID	43140_1.R1039
5'-most EST	LIB3166-057-P1-K1-G7
Method	BLASTX
NCBI GI	g2190548
BLAST score	244
E value	1.0e-22
Match length	81
% identity	68
NCBI Description	(AC001229) EST gb|ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	198414
Contig ID	43161_1.R1039
5'-most EST	g3325773
Method	BLASTX
NCBI GI	g1237250
BLAST score	943
E value	1.0e-102
Match length	262
% identity	72
NCBI Description	(X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No.	198415
Contig ID	43171_1.R1039
5'-most EST	LIB3272-035-P1-K1-E8
Method	BLASTN
NCBI GI	g1171578
BLAST score	69
E value	4.0e-30
Match length	421
% identity	79
NCBI Description	N.tabacum mRNA for HSR515 protein

Seq. No.	198416
Contig ID	43172_1.R1039

5'-most EST	g3326004
Method	BLASTX
NCBI GI	g4185740
BLAST score	566
E value	3.0e-58
Match length	184
% identity	62
NCBI Description	(AF079999) putative glutamate receptor [Arabidopsis thaliana]

Seq. No.	198417
Contig ID	43183_1.R1039
5'-most EST	uC-gsflnu33B036a07b1

Seq. No.	198418
Contig ID	43194_1.R1039
5'-most EST	LIB3272-029-P1-K1-C12
Method	BLASTX
NCBI GI	g1174592
BLAST score	629
E value	8.0e-66
Match length	118
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi|2119270|pir||S60233 alpha-tubulin - garden pea >gi|525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	198419
Contig ID	43196_1.R1039
5'-most EST	LIB3166-004-P1-K1-G8
Method	BLASTX
NCBI GI	g4512625
BLAST score	217
E value	2.0e-17
Match length	158
% identity	34
NCBI Description	(AC004793) ESTs gb|T20423, gb|AA712864, gb|H76323 and gb|Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No.	198420
Contig ID	43203_1.R1039
5'-most EST	LIB3166-007-P1-K1-G10
Method	BLASTX
NCBI GI	g3582342
BLAST score	271
E value	8.0e-24
Match length	139
% identity	43
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	198421
Contig ID	43205_1.R1039
5'-most EST	g3325897
Method	BLASTX
NCBI GI	g3046696
BLAST score	820

E value 8.0e-88
Match length 196
% identity 79
NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No. 198422
Contig ID 43206_1.R1039
5'-most EST LIB3166-005-P1-K1-A10
Method BLASTX
NCBI GI g4097587
BLAST score 246
E value 2.0e-20
Match length 75
% identity 59
NCBI Description (U64926) NTGP5 [Nicotiana tabacum]

Seq. No. 198423
Contig ID 43207_1.R1039
5'-most EST LIB3197-046-Q1-M1-B11
Method BLASTX
NCBI GI g4056494
BLAST score 451
E value 7.0e-45
Match length 108
% identity 78
NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No. 198424
Contig ID 43217_1.R1039
5'-most EST g5044500
Method BLASTX
NCBI GI g1399271
BLAST score 904
E value 7.0e-98
Match length 199
% identity 85
NCBI Description (U31833) calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana]

Seq. No. 198425
Contig ID 43221_1.R1039
5'-most EST LIB3166-005-P1-K1-B6

Seq. No. 198426
Contig ID 43232_1.R1039
5'-most EST LIB3166-031-P1-K1-D3

Seq. No. 198427
Contig ID 43239_1.R1039
5'-most EST LIB3166-049-P1-K1-G4

Seq. No. 198428
Contig ID 43242_1.R1039
5'-most EST LIB3272-013-P1-K1-H3

Seq. No. 198429

Contig ID	43245_1.R1039
5'-most EST	LIB3166-005-P1-K1-D7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	198430
Contig ID	43251_1.R1039
5'-most EST	LIB3272-034-P1-K1-F8
Method	BLASTX
NCBI GI	g3928095
BLAST score	506
E value	6.0e-66
Match length	229
% identity	59
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	198431
Contig ID	43258_1.R1039
5'-most EST	uC-gsflnu33B083h04b1
Method	BLASTX
NCBI GI	g4105794
BLAST score	298
E value	5.0e-27
Match length	79
% identity	62
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	198432
Contig ID	43266_1.R1039
5'-most EST	LIB3166-036-P1-K1-F10

Seq. No.	198433
Contig ID	43275_1.R1039
5'-most EST	LIB3166-005-P1-K1-H11

Seq. No.	198434
Contig ID	43279_1.R1039
5'-most EST	g5048051
Method	BLASTX
NCBI GI	g2924503
BLAST score	219
E value	2.0e-17
Match length	177
% identity	32
NCBI Description	(AL022019) glucosyltransferase [Schizosaccharomyces pombe]

Seq. No.	198435
Contig ID	43298_1.R1039
5'-most EST	LIB3166-006-P1-K1-B12
Method	BLASTX
NCBI GI	g4263507
BLAST score	366

E value	5.0e-35
Match length	133
% identity	56
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198436
Contig ID	43302_1.R1039
5'-most EST	LIB3166-006-P1-K1-B5
Method	BLASTX
NCBI GI	g4218122
BLAST score	633
E value	9.0e-66
Match length	266
% identity	56
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	198437
Contig ID	43305_1.R1039
5'-most EST	LIB3166-006-P1-K1-B8

Seq. No.	198438
Contig ID	43306_1.R1039
5'-most EST	g5047485
Method	BLASTX
NCBI GI	g2213643
BLAST score	503
E value	1.0e-74
Match length	180
% identity	77
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	198439
Contig ID	43315_1.R1039
5'-most EST	LIB3166-006-P1-K1-C8

Seq. No.	198440
Contig ID	43320_1.R1039
5'-most EST	LIB3166-006-P1-K1-D2
Method	BLASTX
NCBI GI	g3123165
BLAST score	181
E value	6.0e-13
Match length	101
% identity	43
NCBI Description	ZINC FINGER PROTEIN 183 >gi|2274982|emb|CAA66907| (X98253) ZNF183 [Homo sapiens] >gi|2341022 (AC002477) zinc-finger protein [Homo sapiens]

Seq. No.	198441
Contig ID	43326_1.R1039
5'-most EST	LIB3189-011-P1-K1-C11
Method	BLASTX
NCBI GI	g4539340
BLAST score	254
E value	1.0e-21
Match length	166
% identity	36

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 198442
Contig ID 43330_1.R1039
5'-most EST LIB3166-017-P1-K1-D4
Method BLASTX
NCBI GI g322787
BLAST score 586
E value 1.0e-60
Match length 134
% identity 84
NCBI Description pyruvate kinase (EC 2.7.1.40), cytosolic - potato

Seq. No. 198443
Contig ID 43337_1.R1039
5'-most EST LIB3166-045-P1-K1-D10

Seq. No. 198444
Contig ID 43344_1.R1039
5'-most EST LIB3166-040-P1-K1-H9

Seq. No. 198445
Contig ID 43346_1.R1039
5'-most EST LIB3166-006-P1-K1-F9
Method BLASTX
NCBI GI g1871192
BLAST score 291
E value 7.0e-26
Match length 117
% identity 50
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 198446
Contig ID 43354_1.R1039
5'-most EST LIB3166-006-P1-K1-G5
Method BLASTX
NCBI GI g2245131
BLAST score 394
E value 6.0e-38
Match length 154
% identity 51
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198447
Contig ID 43356_1.R1039
5'-most EST LIB3166-006-P1-K1-G7
Method BLASTX
NCBI GI g3915023
BLAST score 162
E value 2.0e-20
Match length 107
% identity 58
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi|2588888|dbj|BAA23213| (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	198448
Contig ID	43362_1.R1039
5'-most EST	g5044961
Method	BLASTX
NCBI GI	g3668089
BLAST score	307
E value	8.0e-28
Match length	104
% identity	52
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	198449
Contig ID	43365_1.R1039
5'-most EST	g3325922
Method	BLASTX
NCBI GI	g4263777
BLAST score	217
E value	1.0e-19
Match length	124
% identity	48
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi|4510391|gb|AAD21479.1| (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	198450
Contig ID	43372_1.R1039
5'-most EST	LIB3166-007-P1-K1-A6

Seq. No.	198451
Contig ID	43380_1.R1039
5'-most EST	LIB3166-054-P1-K1-C8

Seq. No.	198452
Contig ID	43384_1.R1039
5'-most EST	LIB3272-024-P1-K1-G12

Seq. No.	198453
Contig ID	43406_1.R1039
5'-most EST	LIB3166-007-P1-K1-E1
Method	BLASTX
NCBI GI	g3128215
BLAST score	215
E value	3.0e-17
Match length	113
% identity	49
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198454
Contig ID	43414_1.R1039
5'-most EST	LIB3166-007-P1-K1-E7
Method	BLASTX
NCBI GI	g2558660
BLAST score	335
E value	5.0e-31
Match length	153
% identity	44

NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.	198455
Contig ID	43418_1.R1039
5'-most EST	g3325752
Seq. No.	198456
Contig ID	43418_2.R1039
5'-most EST	uC-gsflmaxxa060h10b1
Method	BLASTX
NCBI GI	g1706186
BLAST score	249
E value	5.0e-21
Match length	100
% identity	49
NCBI Description	HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi|110721|pir||A32742 murine ecotropic retrovirus receptor protein - mouse >gi|532612 (M26687) ecotropic retrovirus receptor [Mus musculus]
Seq. No.	198457
Contig ID	43428_1.R1039
5'-most EST	LIB3197-014-P1-M1-E1
Method	BLASTX
NCBI GI	g2160156
BLAST score	1175
E value	0.0e+00
Match length	375
% identity	80
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb|Z73100). [Arabidopsis thaliana]
Seq. No.	198458
Contig ID	43434_1.R1039
5'-most EST	LIB3166-034-P1-K1-H4
Method	BLASTX
NCBI GI	g2464855
BLAST score	673
E value	9.0e-71
Match length	147
% identity	84
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.	198459
Contig ID	43444_1.R1039
5'-most EST	LIB3166-027-P1-K1-F8
Method	BLASTX
NCBI GI	g2618721
BLAST score	189
E value	3.0e-14
Match length	70
% identity	66
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]
Seq. No.	198460

Contig ID	43445_1.R1039
5'-most EST	LIB3166-007-P1-K1-H4

Seq. No.	198461
Contig ID	43462_1.R1039
5'-most EST	LIB3166-008-P1-K1-B3
Method	BLASTX
NCBI GI	g3913047
BLAST score	532
E value	1.0e-72
Match length	178
% identity	80
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA1 (MADS C) >gi|1076477|pir||S52236 Saap1 protein - white mustard >gi|609253|emb|CAA57233| (X81480) Saap1 [Sinapis alba]

Seq. No.	198462
Contig ID	43481_1.R1039
5'-most EST	LIB3166-008-P1-K1-D3
Method	BLASTX
NCBI GI	g3402716
BLAST score	186
E value	1.0e-13
Match length	178
% identity	37
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	198463
Contig ID	43484_1.R1039
5'-most EST	LIB3166-008-P1-K1-D6
Method	BLASTX
NCBI GI	g3986750
BLAST score	687
E value	2.0e-72
Match length	140
% identity	91
NCBI Description	(AF107464) serine/threonine protein phosphatase type 2A [Hevea brasiliensis]

Seq. No.	198464
Contig ID	43485_1.R1039
5'-most EST	LIB3189-046-P1-K1-G12
Method	BLASTX
NCBI GI	g2245037
BLAST score	222
E value	8.0e-18
Match length	153
% identity	43
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]

Seq. No.	198465
Contig ID	43504_1.R1039
5'-most EST	LIB3272-033-P1-K1-A3
Method	BLASTX
NCBI GI	g2809246
BLAST score	203
E value	1.0e-15

Match length	64
% identity	55
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	198466
Contig ID	43519_1.R1039
5'-most EST	g5049851
Method	BLASTX
NCBI GI	g4220538
BLAST score	901
E value	2.0e-97
Match length	218
% identity	78
NCBI Description	(AL035356) NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana]

Seq. No.	198467
Contig ID	43523_1.R1039
5'-most EST	uC-gsflmaxxa001g01b1

Seq. No.	198468
Contig ID	43538_1.R1039
5'-most EST	LIB3166-009-P1-K1-B10
Method	BLASTX
NCBI GI	g2996012
BLAST score	267
E value	1.0e-48
Match length	128
% identity	77
NCBI Description	(AF054455) cytosolic phosphoglucose isomerase; PgiC [Leavenworthia crassa]

Seq. No.	198469
Contig ID	43541_1.R1039
5'-most EST	LIB3196-058-P1-M1-E2
Method	BLASTN
NCBI GI	g871767
BLAST score	35
E value	4.0e-10
Match length	103
% identity	83
NCBI Description	V.unguiculata mRNA for chitinase clase 4 (partial)

Seq. No.	198470
Contig ID	43572_1.R1039
5'-most EST	LIB3166-022-P1-K1-F10
Method	BLASTX
NCBI GI	g1403522
BLAST score	336
E value	2.0e-31
Match length	107
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	198471
Contig ID	43574_1.R1039
5'-most EST	uC-gsflmaxxa004d11b1

Method	BLASTX
NCBI GI	g3287691
BLAST score	417
E value	8.0e-41
Match length	176
% identity	50
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb|X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	198472
Contig ID	43575_1.R1039
5'-most EST	LIB3166-024-P1-K1-E6
Method	BLASTX
NCBI GI	g1871192
BLAST score	395
E value	3.0e-38
Match length	160
% identity	54
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	198473
Contig ID	43594_1.R1039
5'-most EST	uC-gsronu33B163c08b2
Method	BLASTX
NCBI GI	g3176726
BLAST score	659
E value	6.0e-73
Match length	190
% identity	74
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	198474
Contig ID	43596_1.R1039
5'-most EST	g5049565
Method	BLASTX
NCBI GI	g2109293
BLAST score	1169
E value	1.0e-129
Match length	264
% identity	83
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	198475
Contig ID	43598_1.R1039
5'-most EST	LIB3166-009-P1-K1-G5
Method	BLASTX
NCBI GI	g3334659
BLAST score	207
E value	4.0e-21
Match length	118
% identity	54
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	198476

Contig ID	43604_1.R1039
5'-most EST	LIB3196-015-P1-M1-D6
Seq. No.	198477
Contig ID	43621_1.R1039
5'-most EST	LIB3166-010-P1-K1-B10
Method	BLASTX
NCBI GI	g19464
BLAST score	329
E value	1.0e-30
Match length	85
% identity	62
NCBI Description	(X54464) ribulose bisphosphate carboxylase [Larix laricina]
Seq. No.	198478
Contig ID	43648_1.R1039
5'-most EST	LIB3166-010-P1-K1-D5
Method	BLASTX
NCBI GI	g3643611
BLAST score	250
E value	2.0e-21
Match length	59
% identity	78
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.	198479
Contig ID	43656_1.R1039
5'-most EST	LIB3166-058-P1-K1-H10
Method	BLASTX
NCBI GI	g1871192
BLAST score	224
E value	2.0e-18
Match length	91
% identity	48
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
Seq. No.	198480
Contig ID	43659_1.R1039
5'-most EST	g5049354
Method	BLASTX
NCBI GI	g1495259
BLAST score	278
E value	2.0e-24
Match length	135
% identity	39
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]
Seq. No.	198481
Contig ID	43665_1.R1039
5'-most EST	LIB3166-058-P1-K1-A11
Method	BLASTX
NCBI GI	g4049410
BLAST score	322
E value	1.0e-29
Match length	115

% identity 57
NCBI Description (Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No. 198482
Contig ID 43666_1.R1039
5'-most EST uC-gsflnu33B101c06b1

Seq. No. 198483
Contig ID 43676_1.R1039
5'-most EST g5044362

Seq. No. 198484
Contig ID 43681_1.R1039
5'-most EST LIB3166-010-P1-K1-G9
Method BLASTX
NCBI GI g3183316
BLAST score 110
E value 7.0e-12
Match length 80
% identity 49
NCBI Description HYPOTHETICAL 24.4 KD PROTEIN C16E8.14C IN CHROMOSOME I >gi|2330702|emb|CAB11042| (Z98529) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 198485
Contig ID 43695_1.R1039
5'-most EST LIB3166-011-P1-K1-H9
Method BLASTX
NCBI GI g2632252
BLAST score 246
E value 6.0e-21
Match length 134
% identity 43
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 198486
Contig ID 43715_1.R1039
5'-most EST LIB3166-011-P1-K1-C2
Method BLASTX
NCBI GI g409756
BLAST score 143
E value 5.0e-09
Match length 88
% identity 30
NCBI Description (L25643) ATP/GTP nucleotide-binding protein [Leishmania infantum]

Seq. No. 198487
Contig ID 43742_1.R1039
5'-most EST g5049402
Method BLASTX
NCBI GI g498038
BLAST score 743
E value 1.0e-82
Match length 231
% identity 61
NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No.	198488
Contig ID	43761_1.R1039
5'-most EST	LIB3197-021-Q1-M1-H7

Seq. No.	198489
Contig ID	43762_1.R1039
5'-most EST	LIB3272-012-P1-K1-C6
Method	BLASTX
NCBI GI	g3941543
BLAST score	246
E value	7.0e-21
Match length	72
% identity	69
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi|4469016|emb|CAB38277| (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	198490
Contig ID	43763_1.R1039
5'-most EST	LIB3166-021-P1-K1-E12
Method	BLASTX
NCBI GI	g3434967
BLAST score	227
E value	1.0e-18
Match length	85
% identity	55
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	198491
Contig ID	43764_1.R1039
5'-most EST	LIB3166-011-P1-K1-H10

Seq. No.	198492
Contig ID	43775_1.R1039
5'-most EST	LIB3166-012-P1-K1-F12
Method	BLASTX
NCBI GI	g2894106
BLAST score	835
E value	8.0e-90
Match length	177
% identity	88
NCBI Description	(Z78279) Collagen alpha1 [Rattus norvegicus]

Seq. No.	198493
Contig ID	43783_1.R1039
5'-most EST	LIB3166-012-P1-K1-B4

Seq. No.	198494
Contig ID	43823_1.R1039
5'-most EST	LIB3166-012-P1-K1-G5

Seq. No.	198495
Contig ID	43825_1.R1039
5'-most EST	LIB3196-001-P1-M1-H4
Method	BLASTX

NCBI GI	g399413
BLAST score	1739
E value	0.0e+00
Match length	343
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi|72869|pir||EFRB1 translation elongation factor eEF-1 alpha chain - rabbit >gi|1070665|pir||EFHU1 translation elongation factor eEF-1 alpha-1 chain - human >gi|1551|emb|CAA44162| (X62245) elongation factor 1 alpha [Oryctolagus cuniculus] >gi|31098|emb|CAA27245| (X03558) EF-1 alpha (aa 1-463) [Homo sapiens] >gi|181963 (J04617) elongation factor EF-1-alpha [Homo sapiens] >gi|495221 (U09823) elongation factor 1 alpha [Oryctolagus cuniculus] >gi|4503471|ref|NP_001393.1|pEEF1A1| eukaryotic translation elongation factor 1 alpha

Seq. No.	198496
Contig ID	43830_1.R1039
5'-most EST	LIB3196-002-P1-M1-C12
Method	BLASTX
NCBI GI	g113270
BLAST score	1199
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi|71618|pir||ATHUB actin beta - human >gi|71619|pir||ATMSB actin beta - mouse >gi|279669|pir||ATCHB actin beta - chicken >gi|28252|emb|CAA25099| (X00351) beta-actin [Homo sapiens] >gi|49866|emb|CAA27307| (X03672) beta-actin (aa 1-375) [Mus musculus] >gi|55575|emb|CAA24528| (V01217) beta-actin [Rattus norvegicus] >gi|177968 (M10277) cytoplasmic beta actin [Homo sapiens] >gi|211237 (L08165) beta-actin [Gallus gallus] >gi|2116655|dbj|BAA20266| (AB004047) beta-actin [Homo sapiens] >gi|2182269 (U39357) beta actin [Ovis aries] >gi|2661136 (AF035774) beta actin [Equus caballus] >gi|3320892 (AF076190) beta-actin [Trichosurus vulpecula] >gi|4501885|ref|NP_001092.1|pACTB| actin, beta

Seq. No.	198497
Contig ID	43830_3.R1039
5'-most EST	LIB3196-025-P1-M1-H3
Method	BLASTX
NCBI GI	g113271
BLAST score	445
E value	3.0e-45
Match length	103
% identity	94
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA ACTIN) >gi|85691|pir||S01077 actin beta, cytoskeletal - Kenyan clawed frog >gi|1334642|emb|CAA30390| (X07507) actin [Xenopus borealis]

Seq. No.	198498
Contig ID	43830_4.R1039
5'-most EST	LIB3196-065-P1-M1-A1

Method	BLASTX
NCBI GI	g1703121
BLAST score	300
E value	2.0e-45
Match length	109
% identity	81
NCBI Description	ACTIN, CYTOPLASMIC TYPE 5 >gi|63007|emb|CAA26486| (X02648) put. type 5 nonmuscle actin [Gallus gallus]

Seq. No.	198499
Contig ID	43840_1.R1039
5'-most EST	LIB3166-013-P1-K1-A2
Method	BLASTX
NCBI GI	g3184275
BLAST score	136
E value	6.0e-11
Match length	249
% identity	27
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198500
Contig ID	43855_1.R1039
5'-most EST	LIB3272-001-P1-K1-B5
Method	BLASTX
NCBI GI	g4314355
BLAST score	656
E value	2.0e-68
Match length	187
% identity	61
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	198501
Contig ID	43858_1.R1039
5'-most EST	uC-gsronu33B106a05b2
Method	BLASTX
NCBI GI	g3269293
BLAST score	557
E value	5.0e-57
Match length	206
% identity	58
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	198502
Contig ID	43872_1.R1039
5'-most EST	LIB3166-013-P1-K1-D2
Method	BLASTX
NCBI GI	g3367593
BLAST score	600
E value	3.0e-62
Match length	162
% identity	65
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi|3805841|emb|CAA21461| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	198503
Contig ID	43874_1.R1039

5'-most EST	LIB3166-013-P1-K1-D4
Seq. No.	198504
Contig ID	43876_1.R1039
5'-most EST	LIB3197-047-Q1-M1-E6
Seq. No.	198505
Contig ID	43881_1.R1039
5'-most EST	g5050609
Method	BLASTX
NCBI GI	g3894173
BLAST score	315
E value	7.0e-29
Match length	71
% identity	79
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]
Seq. No.	198506
Contig ID	43888_1.R1039
5'-most EST	LIB3197-060-Q1-M1-C12
Seq. No.	198507
Contig ID	43899_1.R1039
5'-most EST	LIB3166-013-P1-K1-F6
Method	BLASTX
NCBI GI	g2146739
BLAST score	224
E value	2.0e-18
Match length	70
% identity	63
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi|881521 (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.	198508
Contig ID	43911_1.R1039
5'-most EST	uC-gsronu33B155c06b2
Method	BLASTX
NCBI GI	g3892059
BLAST score	408
E value	2.0e-39
Match length	211
% identity	50
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]
Seq. No.	198509
Contig ID	43919_1.R1039
5'-most EST	uC-gsflnu33B024b10b1
Method	BLASTX
NCBI GI	g4512694
BLAST score	238
E value	6.0e-20
Match length	133
% identity	41
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	198510

Contig ID 43935_1.R1039
5'-most EST uC-gsronu33B015e04b1
Method BLASTX
NCBI GI g4559382
BLAST score 321
E value 1.0e-29
Match length 145
% identity 47
NCBI Description (AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 198511
Contig ID 43936_1.R1039
5'-most EST LIB3197-052-Q1-M1-E1
Method BLASTX
NCBI GI g2190419
BLAST score 217
E value 2.0e-17
Match length 110
% identity 42
NCBI Description (Y13632) dem [Lycopersicon esculentum]

Seq. No. 198512
Contig ID 43940_1.R1039
5'-most EST LIB3166-014-P1-K1-B4

Seq. No. 198513
Contig ID 43945_1.R1039
5'-most EST LIB3166-014-P1-K1-B9
Method BLASTX
NCBI GI g1814424
BLAST score 575
E value 2.0e-59
Match length 134
% identity 78
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No. 198514
Contig ID 43963_1.R1039
5'-most EST LIB3166-014-P1-K1-D6

Seq. No. 198515
Contig ID 43972_1.R1039
5'-most EST LIB3166-014-P1-K1-E6
Method BLASTX
NCBI GI g3927831
BLAST score 622
E value 1.0e-72
Match length 222
% identity 46
NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No. 198516
Contig ID 43975_1.R1039
5'-most EST LIB3166-014-P1-K1-E9
Method BLASTX

NCBI GI g3738325
BLAST score 516
E value 2.0e-52
Match length 191
% identity 54
NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No. 198517
Contig ID 43992_1.R1039
5'-most EST LIB3166-014-P1-K1-G6
Method BLASTX
NCBI GI g2088651
BLAST score 420
E value 6.0e-43
Match length 123
% identity 64
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 198518
Contig ID 44001_1.R1039
5'-most EST LIB3166-014-P1-K1-H3

Seq. No. 198519
Contig ID 44003_1.R1039
5'-most EST LIB3197-026-Q1-M1-B9

Seq. No. 198520
Contig ID 44009_1.R1039
5'-most EST LIB3166-015-P1-K1-A11

Seq. No. 198521
Contig ID 44015_1.R1039
5'-most EST LIB3272-031-P1-K1-E8

Seq. No. 198522
Contig ID 44026_1.R1039
5'-most EST LIB3166-015-P1-K1-B4
Method BLASTX
NCBI GI g3420049
BLAST score 169
E value 7.0e-12
Match length 131
% identity 39
NCBI Description (AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 198523
Contig ID 44035_1.R1039
5'-most EST uC-gsronu33B061e08b1
Method BLASTX
NCBI GI g548852
BLAST score 349
E value 5.0e-33
Match length 82
% identity 79

NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi|481227|pir||S38357 ribosomal protein S21 - rice >gi|303839|dbj|BAA02158| (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	198524
Contig ID	44049_1.R1039
5'-most EST	LIB3166-015-P1-K1-D5
Method	BLASTX
NCBI GI	g2088662
BLAST score	153
E value	1.0e-09
Match length	128
% identity	24
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	198525
Contig ID	44055_1.R1039
5'-most EST	LIB3197-043-Q1-M1-B5
Method	BLASTX
NCBI GI	g2832658
BLAST score	164
E value	4.0e-11
Match length	114
% identity	33
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	198526
Contig ID	44062_1.R1039
5'-most EST	LIB3166-015-P1-K1-E8
Method	BLASTX
NCBI GI	g2739376
BLAST score	262
E value	9.0e-23
Match length	68
% identity	72
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	198527
Contig ID	44065_1.R1039
5'-most EST	g5048864
Method	BLASTX
NCBI GI	g134970
BLAST score	270
E value	2.0e-23
Match length	101
% identity	47
NCBI Description	STELLACYANIN >gi|65849|pir||SSUL stellacyanin - Japanese lacquer-tree

Seq. No.	198528
Contig ID	44081_1.R1039
5'-most EST	LIB3166-015-P1-K1-G4
Method	BLASTX
NCBI GI	g2384696
BLAST score	489
E value	7.0e-49
Match length	202

% identity	51
NCBI Description	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq. No.	198529
Contig ID	44084_1.R1039
5'-most EST	g5049410
Method	BLASTX
NCBI GI	g1255951
BLAST score	1371
E value	1.0e-152
Match length	326
% identity	80
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	198530
Contig ID	44097_1.R1039
5'-most EST	LIB3166-016-P1-K1-A1
Method	BLASTX
NCBI GI	g1871185
BLAST score	525
E value	1.0e-53
Match length	127
% identity	73
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	198531
Contig ID	44106_1.R1039
5'-most EST	uC-gsflnu33B002c11b1
Method	BLASTX
NCBI GI	g629600
BLAST score	451
E value	2.0e-71
Match length	160
% identity	73
NCBI Description	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - wild cabbage >gi|562280|emb|CAA57724| (X82273) 1-aminocyclopropane-1-carboxylate synthase [Brassica oleracea]

Seq. No.	198532
Contig ID	44107_1.R1039
5'-most EST	LIB3166-016-P1-K1-A8
Method	BLASTX
NCBI GI	g1707922
BLAST score	733
E value	9.0e-78
Match length	161
% identity	86
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi|1076255|pir||S51944 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi|556624|emb|CAA55516| (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No.	198533

Contig ID	44122_1.R1039
5'-most EST	LIB3166-016-P1-K1-C10
Method	BLASTX
NCBI GI	g3249105
BLAST score	624
E value	7.0e-65
Match length	183
% identity	65
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb|X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	198534
Contig ID	44141_1.R1039
5'-most EST	uC-gsronu33B178f06b1
Method	BLASTX
NCBI GI	g4056480
BLAST score	338
E value	3.0e-31
Match length	167
% identity	51
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	198535
Contig ID	44150_1.R1039
5'-most EST	LIB3166-016-P1-K1-E6
Method	BLASTX
NCBI GI	g1174199
BLAST score	357
E value	2.0e-33
Match length	159
% identity	51
NCBI Description	(U44760) S25-PR6 [Nicotiana tabacum]

Seq. No.	198536
Contig ID	44160_1.R1039
5'-most EST	LIB3166-016-P1-K1-F7
Method	BLASTX
NCBI GI	g2088653
BLAST score	214
E value	3.0e-17
Match length	109
% identity	41
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]

Seq. No.	198537
Contig ID	44168_1.R1039
5'-most EST	LIB3272-002-P1-K1-G4
Method	BLASTX
NCBI GI	g2213536
BLAST score	180
E value	5.0e-13
Match length	161
% identity	35
NCBI Description	(X98738) DNA-binding protein PD1 [Pisum sativum]

Seq. No. 198538

Contig ID 44175_1.R1039
5'-most EST LIB3166-016-P1-K1-H12
Method BLASTX
NCBI GI g3859659
BLAST score 455
E value 5.0e-45
Match length 160
% identity 57
NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No. 198539
Contig ID 44178_1.R1039
5'-most EST LIB3166-016-P1-K1-H4
Method BLASTX
NCBI GI g4538905
BLAST score 585
E value 1.0e-60
Match length 132
% identity 83
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 198540
Contig ID 44181_1.R1039
5'-most EST LIB3197-033-Q1-M1-B7
Method BLASTX
NCBI GI g3599491
BLAST score 244
E value 1.0e-20
Match length 57
% identity 79
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 198541
Contig ID 44183_1.R1039
5'-most EST LIB3166-017-P1-K1-A1
Method BLASTX
NCBI GI g541816
BLAST score 425
E value 6.0e-42
Match length 130
% identity 63
NCBI Description protein kinase - common ice plant >gi|457689|emb|CAA82990| (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 198542
Contig ID 44196_1.R1039
5'-most EST LIB3196-050-P1-M1-C2
Method BLASTX
NCBI GI g2792220
BLAST score 314
E value 6.0e-29
Match length 136
% identity 46
NCBI Description (AF032688) NBS-LRR type resistance protein [Oryza sativa]

Seq. No. 198543

Contig ID	44228_1.R1039
5'-most EST	LIB3189-048-P1-K1-G8
Method	BLASTX
NCBI GI	g3834307
BLAST score	1182
E value	1.0e-130
Match length	334
% identity	68
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi|2832679 putative protein from Arabidopsis thaliana BAC gb|AL021712. ESTs gb|N65887 and gb|N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	198544
Contig ID	44238_1.R1039
5'-most EST	LIB3166-017-P1-K1-F10
Method	BLASTX
NCBI GI	g3367568
BLAST score	333
E value	2.0e-33
Match length	108
% identity	64
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	198545
Contig ID	44241_1.R1039
5'-most EST	g5048989
Method	BLASTX
NCBI GI	g4115918
BLAST score	393
E value	1.0e-37
Match length	155
% identity	57
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	198546
Contig ID	44249_1.R1039
5'-most EST	LIB3166-017-P1-K1-G11
Method	BLASTX
NCBI GI	g1172441
BLAST score	380
E value	4.0e-50
Match length	187
% identity	65
NCBI Description	POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi|99685|pir||S21883 DNA-binding protein POSF21 - Arabidopsis thaliana >gi|16429|emb|CAA43366| (X61031) posF21 [Arabidopsis thaliana]

Seq. No.	198547
Contig ID	44251_1.R1039
5'-most EST	uC-gsronu33B169c08b1

Seq. No.	198548
Contig ID	44254_1.R1039

5'-most EST	g5049812
Seq. No.	198549
Contig ID	44272_1.R1039
5'-most EST	LIB3166-018-P1-K1-A3
Seq. No.	198550
Contig ID	44278_1.R1039
5'-most EST	LIB3166-018-P1-K1-A9
Method	BLASTX
NCBI GI	g2961384
BLAST score	892
E value	4.0e-96
Match length	412
% identity	44
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
Seq. No.	198551
Contig ID	44281_1.R1039
5'-most EST	LIB3166-018-P1-K1-E12
Seq. No.	198552
Contig ID	44283_1.R1039
5'-most EST	LIB3166-018-P1-K1-B2
Seq. No.	198553
Contig ID	44286_1.R1039
5'-most EST	LIB3166-018-P1-K1-B6
Seq. No.	198554
Contig ID	44322_1.R1039
5'-most EST	LIB3166-018-P1-K1-E7
Seq. No.	198555
Contig ID	44326_1.R1039
5'-most EST	LIB3166-049-P1-K1-C10
Seq. No.	198556
Contig ID	44333_1.R1039
5'-most EST	uC-gsflnu33B009e11b1
Method	BLASTX
NCBI GI	g3775989
BLAST score	351
E value	4.0e-33
Match length	95
% identity	75
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]
Seq. No.	198557
Contig ID	44337_1.R1039
5'-most EST	uC-gsflmaxxa067e10b1
Method	BLASTX
NCBI GI	g3445207
BLAST score	1469
E value	1.0e-166
Match length	456

% identity	63
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	198558
Contig ID	44340_1.R1039
5'-most EST	LIB3189-003-P1-K1-C8

Seq. No.	198559
Contig ID	44341_1.R1039
5'-most EST	LIB3166-018-P1-K1-G3
Method	BLASTX
NCBI GI	g2136258
BLAST score	183
E value	1.0e-13
Match length	75
% identity	45
NCBI Description	template activating factor-I, splice form alpha - human >gi|971272|dbj|BAA08139| (D45198) template acyivating factor-I alpha [Homo sapiens]

Seq. No.	198560
Contig ID	44342_1.R1039
5'-most EST	LIB3166-018-P1-K1-G5
Method	BLASTX
NCBI GI	g4539333
BLAST score	907
E value	6.0e-98
Match length	266
% identity	64
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	198561
Contig ID	44381_1.R1039
5'-most EST	LIB3189-048-P1-K1-G10
Method	BLASTX
NCBI GI	g2605621
BLAST score	366
E value	3.0e-45
Match length	122
% identity	76
NCBI Description	(D88619) OSMYB3 [Oryza sativa]

Seq. No.	198562
Contig ID	44389_1.R1039
5'-most EST	LIB3166-019-P1-K1-D4
Method	BLASTN
NCBI GI	g2605620
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Oryza sativa mRNA for OSMYB3, complete cds

Seq. No.	198563
Contig ID	44394_1.R1039
5'-most EST	LIB3166-019-P1-K1-D9

Method	BLASTX
NCBI GI	g2160189
BLAST score	764
E value	2.0e-81
Match length	246
% identity	61
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475,gb|ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	198564
Contig ID	44407_1.R1039
5'-most EST	g3325866

Seq. No.	198565
Contig ID	44417_1.R1039
5'-most EST	LIB3166-019-P1-K1-F9
Method	BLASTX
NCBI GI	g2467274
BLAST score	295
E value	2.0e-26
Match length	126
% identity	50
NCBI Description	(Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	198566
Contig ID	44419_1.R1039
5'-most EST	LIB3166-019-P1-K1-G11

Seq. No.	198567
Contig ID	44436_1.R1039
5'-most EST	LIB3166-020-P1-K1-A10
Method	BLASTX
NCBI GI	g417103
BLAST score	140
E value	6.0e-19
Match length	60
% identity	80
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa] >gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	198568
Contig ID	44446_1.R1039
5'-most EST	LIB3166-020-P1-K1-B10

Seq. No.	198569
Contig ID	44452_1.R1039
5'-most EST	uC-gsronu33B168f09b1
Method	BLASTX
NCBI GI	g710626
BLAST score	160
E value	1.0e-10
Match length	133
% identity	37
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi|3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi|3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	198570
Contig ID	44453_1.R1039
5'-most EST	LIB3166-020-P1-K1-B6
Method	BLASTX
NCBI GI	g128194
BLAST score	537
E value	5.0e-55
Match length	129
% identity	80
NCBI Description	NITRATE REDUCTASE (NR) >gi|81572|pir||A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi|167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	198571
Contig ID	44464_1.R1039
5'-most EST	LIB3166-020-P1-K1-C9
Method	BLASTX
NCBI GI	g2244811
BLAST score	208
E value	2.0e-16
Match length	88
% identity	56
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	198572
Contig ID	44485_1.R1039
5'-most EST	g5045079
Method	BLASTX
NCBI GI	g3341687
BLAST score	226
E value	3.0e-18
Match length	75
% identity	63
NCBI Description	(AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No.	198573
Contig ID	44485_2.R1039
5'-most EST	LIB3166-039-P1-K1-H11

Method	BLASTX
NCBI GI	g3341687
BLAST score	179
E value	6.0e-13
Match length	86
% identity	47
NCBI Description	(AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No.	198574
Contig ID	44486_1.R1039
5'-most EST	LIB3166-020-P1-K1-E9
Method	BLASTX
NCBI GI	g1771160
BLAST score	1087
E value	1.0e-119
Match length	287
% identity	72
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi|3687305|emb|CAA06999| (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	198575
Contig ID	44503_1.R1039
5'-most EST	g3326274
Method	BLASTX
NCBI GI	g4567228
BLAST score	257
E value	1.0e-25
Match length	83
% identity	77
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	198576
Contig ID	44524_1.R1039
5'-most EST	LIB3166-021-P1-K1-A2
Method	BLASTX
NCBI GI	g1553133
BLAST score	197
E value	7.0e-15
Match length	192
% identity	12
NCBI Description	(U64722) actin-fragmin kinase [Physarum polycephalum]

Seq. No.	198577
Contig ID	44539_1.R1039
5'-most EST	uC-gsronu33B011b11b1
Method	BLASTX
NCBI GI	g4559331
BLAST score	400
E value	6.0e-39
Match length	83
% identity	83
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	198578
Contig ID	44566_1.R1039
5'-most EST	LIB3166-021-P1-K1-E1

Seq. No.	198579
Contig ID	44568_1.R1039
5'-most EST	LIB3166-021-P1-K1-E11
Method	BLASTX
NCBI GI	g2558664
BLAST score	217
E value	2.0e-17
Match length	70
% identity	59
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198580
Contig ID	44571_1.R1039
5'-most EST	LIB3272-049-P1-K1-C8
Method	BLASTX
NCBI GI	g2507300
BLAST score	507
E value	6.0e-52
Match length	132
% identity	78
NCBI Description	ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi|159011 (M87338) replication factor C, 40-kDa subunit [Homo sapiens] >gi|2914760 (AF045555) replication factor C subunit 2 [Homo sapiens] >gi|4506487|ref|NP_002905.1|pRFC2| replication factor C (activator 1) 2 (40kD)

Seq. No.	198581
Contig ID	44577_1.R1039
5'-most EST	LIB3166-021-P1-K1-E9
Method	BLASTX
NCBI GI	g2281635
BLAST score	237
E value	1.0e-19
Match length	60
% identity	75
NCBI Description	(AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]

Seq. No.	198582
Contig ID	44578_1.R1039
5'-most EST	uC-gsronu33B061h08b1

Seq. No.	198583
Contig ID	44580_1.R1039
5'-most EST	LIB3166-026-P1-K1-F5

Seq. No.	198584
Contig ID	44582_1.R1039
5'-most EST	LIB3166-021-P1-K1-F2

Seq. No.	198585
Contig ID	44585_1.R1039
5'-most EST	LIB3196-041-P1-M1-D3
Method	BLASTX
NCBI GI	g2660676

BLAST score 980
E value 1.0e-106
Match length 214
% identity 82
NCBI Description (AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No. 198586
Contig ID 44590_1.R1039
5'-most EST LIB3166-035-P1-K1-F3

Seq. No. 198587
Contig ID 44596_1.R1039
5'-most EST g5048294
Method BLASTX
NCBI GI g3335378
BLAST score 437
E value 5.0e-43
Match length 107
% identity 74
NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No. 198588
Contig ID 44600_1.R1039
5'-most EST LIB3166-028-P1-K1-E2
Method BLASTX
NCBI GI g4220481
BLAST score 186
E value 6.0e-14
Match length 71
% identity 55
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 198589
Contig ID 44616_1.R1039
5'-most EST LIB3189-048-P1-K1-D10
Method BLASTX
NCBI GI g4371290
BLAST score 708
E value 9.0e-75
Match length 218
% identity 61
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 198590
Contig ID 44617_1.R1039
5'-most EST LIB3197-051-Q1-M1-C9
Method BLASTX
NCBI GI g2642153
BLAST score 172
E value 4.0e-12
Match length 133
% identity 35
NCBI Description (AC003000) unknown protein [Arabidopsis thaliana] >gi|2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	198591
Contig ID	44618_2.R1039
5'-most EST	LIB3166-022-P1-K1-A2
Method	BLASTX
NCBI GI	g1363484
BLAST score	545
E value	9.0e-56
Match length	202
% identity	58
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi|972929 (U18415) IAA13 [Arabidopsis thaliana] >gi|2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	198592
Contig ID	44624_1.R1039
5'-most EST	uC-gsflnu33B101e10b1

Seq. No.	198593
Contig ID	44646_1.R1039
5'-most EST	LIB3166-022-P1-K1-D1

Seq. No.	198594
Contig ID	44650_1.R1039
5'-most EST	LIB3166-028-P1-K1-G4
Method	BLASTX
NCBI GI	g780658
BLAST score	163
E value	6.0e-11
Match length	176
% identity	29
NCBI Description	(U23040) putative alcohol dehydrogenase [Rhizobium leguminosarum bv. viciae]

Seq. No.	198595
Contig ID	44659_1.R1039
5'-most EST	LIB3166-022-P1-K1-E12

Seq. No.	198596
Contig ID	44664_1.R1039
5'-most EST	LIB3166-037-P1-K1-F12

Seq. No.	198597
Contig ID	44676_1.R1039
5'-most EST	LIB3197-015-P1-M1-E4
Method	BLASTX
NCBI GI	g2462825
BLAST score	561
E value	2.0e-57
Match length	188
% identity	64
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	198598
Contig ID	44678_1.R1039
5'-most EST	LIB3166-022-P1-K1-G10
Method	BLASTN

NCBI GI	g3941288
BLAST score	47
E value	5.0e-17
Match length	257
% identity	82
NCBI Description	Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete cds

Seq. No.	198599
Contig ID	44684_1.R1039
5'-most EST	uC-gsronu33B143e01b1
Method	BLASTX
NCBI GI	g2443878
BLAST score	332
E value	8.0e-42
Match length	229
% identity	45
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	198600
Contig ID	44702_1.R1039
5'-most EST	uC-gsflmaxxa061d06b1
Method	BLASTX
NCBI GI	g1695882
BLAST score	210
E value	5.0e-24
Match length	106
% identity	55
NCBI Description	(U63743) mitotic centromere-associated kinesin [Homo sapiens]

Seq. No.	198601
Contig ID	44706_1.R1039
5'-most EST	LIB3166-033-P1-K1-H4

Seq. No.	198602
Contig ID	44718_1.R1039
5'-most EST	LIB3189-036-P1-K1-C7
Method	BLASTX
NCBI GI	g3785972
BLAST score	805
E value	4.0e-86
Match length	231
% identity	72
NCBI Description	(AC005560) putative auxin transport protein [Arabidopsis thaliana] >gi|4262249|gb|AAD14542| (AC006200) putative auxin transport protein [Arabidopsis thaliana]

Seq. No.	198603
Contig ID	44719_1.R1039
5'-most EST	LIB3196-004-P1-M1-F7

Seq. No.	198604
Contig ID	44726_1.R1039
5'-most EST	LIB3197-047-Q1-M1-H9

Seq. No.	198605

Contig ID	44730_1.R1039
5'-most EST	uC-gsflmaxxa040f10b1
Method	BLASTX
NCBI GI	g544134
BLAST score	329
E value	2.0e-30
Match length	107
% identity	50
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi|99720|pir||S22863 hypothetical protein - Arabidopsis thaliana >gi|421844|pir||A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	198606
Contig ID	44739_1.R1039
5'-most EST	uC-gsflnu33B091f03b1
Method	BLASTX
NCBI GI	g3885338
BLAST score	223
E value	3.0e-18
Match length	110
% identity	38
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	198607
Contig ID	44755_1.R1039
5'-most EST	LIB3166-023-P1-K1-F2

Seq. No.	198608
Contig ID	44758_1.R1039
5'-most EST	LIB3166-023-P1-K1-F5
Method	BLASTX
NCBI GI	g2827549
BLAST score	1628
E value	0.0e+00
Match length	346
% identity	89
NCBI Description	(AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	198609
Contig ID	44760_1.R1039
5'-most EST	LIB3166-023-P1-K1-F8

Seq. No.	198610
Contig ID	44765_1.R1039
5'-most EST	LIB3166-023-P1-K1-G2

Seq. No.	198611
Contig ID	44788_1.R1039
5'-most EST	LIB3166-024-P1-K1-A2

Seq. No.	198612
Contig ID	44801_1.R1039
5'-most EST	LIB3196-043-P1-M1-F2
Method	BLASTX
NCBI GI	g1310677

BLAST score 281
E value 8.0e-35
Match length 178
% identity 44
NCBI Description (X97636) protein z-type serpin [Hordeum vulgare]

Seq. No. 198613
Contig ID 44815_1.R1039
5'-most EST LIB3166-027-P1-K1-F5

Seq. No. 198614
Contig ID 44817_1.R1039
5'-most EST uC-gsronu33B117b05b1

Seq. No. 198615
Contig ID 44825_1.R1039
5'-most EST LIB3166-024-P1-K1-D5
Method BLASTX
NCBI GI g4544409
BLAST score 680
E value 1.0e-71
Match length 175
% identity 67
NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No. 198616
Contig ID 44849_1.R1039
5'-most EST LIB3166-024-P1-K1-F8
Method BLASTX
NCBI GI g4263795
BLAST score 249
E value 6.0e-21
Match length 73
% identity 63
NCBI Description (AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 198617
Contig ID 44870_1.R1039
5'-most EST LIB3166-024-P1-K1-H7
Method BLASTX
NCBI GI g1568664
BLAST score 319
E value 3.0e-29
Match length 156
% identity 44
NCBI Description (U70873) O-methyltransferase [Pinus radiata]

Seq. No. 198618
Contig ID 44894_1.R1039
5'-most EST LIB3166-025-P1-K1-B8
Method BLASTX
NCBI GI g3643085
BLAST score 398
E value 2.0e-38
Match length 165

% identity	51
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	198619
Contig ID	44899_1.R1039
5'-most EST	uC-gsflnu33B094d05b1

Seq. No.	198620
Contig ID	44923_1.R1039
5'-most EST	LIB3166-025-P1-K1-E5
Method	BLASTX
NCBI GI	g4559342
BLAST score	602
E value	1.0e-62
Match length	122
% identity	90
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	198621
Contig ID	44941_1.R1039
5'-most EST	LIB3272-033-P1-K1-G9
Method	BLASTX
NCBI GI	g3367522
BLAST score	333
E value	4.0e-31
Match length	126
% identity	57
NCBI Description	(AC004392) EST gb|T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	198622
Contig ID	44944_1.R1039
5'-most EST	LIB3166-025-P1-K1-G6
Method	BLASTX
NCBI GI	g1173137
BLAST score	498
E value	1.0e-50
Match length	98
% identity	94
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi|322700|pir||B44457 RNA polymerase II fifth largest subunit - Glycine max=soybeans >gi|170052 (M90504) RNA polymerase II [Glycine max]

Seq. No.	198623
Contig ID	44945_1.R1039
5'-most EST	LIB3272-052-P1-K1-F7

Seq. No.	198624
Contig ID	44945_2.R1039
5'-most EST	LIB3166-025-P1-K1-G7

Seq. No.	198625
Contig ID	44953_1.R1039
5'-most EST	LIB3166-027-P1-K1-D6

Seq. No.	198626
Contig ID	44963_1.R1039
5'-most EST	g5044413
Method	BLASTX
NCBI GI	g3927916
BLAST score	471
E value	5.0e-47
Match length	88
% identity	98
NCBI Description	(AJ130887) glycine-rich protein 2 [Fagus sylvatica]

Seq. No.	198627
Contig ID	44963_2.R1039
5'-most EST	g5050372
Method	BLASTX
NCBI GI	g1076626
BLAST score	466
E value	2.0e-46
Match length	120
% identity	75
NCBI Description	glycine rich protein - common tobacco >gi|790473|emb|CAA58702| (X83731) soluble, glycine rich protein [Nicotiana tabacum]

Seq. No.	198628
Contig ID	44986_1.R1039
5'-most EST	LIB3166-026-P1-K1-C6
Method	BLASTX
NCBI GI	g2129583
BLAST score	330
E value	1.0e-30
Match length	89
% identity	74
NCBI Description	ferritin - Arabidopsis thaliana >gi|1246401|emb|CAA63932| (X94248) ferritin [Arabidopsis thaliana]

Seq. No.	198629
Contig ID	44987_1.R1039
5'-most EST	LIB3166-051-P1-K1-D1
Method	BLASTX
NCBI GI	g2829862
BLAST score	402
E value	5.0e-39
Match length	187
% identity	47
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	198630
Contig ID	44993_1.R1039
5'-most EST	LIB3166-057-P1-K1-G9
Method	BLASTX
NCBI GI	g439489
BLAST score	270
E value	3.0e-38
Match length	178

% identity	47
NCBI Description	(D26084) zinc-finger DNA binding protein [Petunia x hybrida]

Seq. No.	198631
Contig ID	44993_2.R1039
5'-most EST	LIB3166-026-P1-K1-D12
Method	BLASTX
NCBI GI	g439493
BLAST score	312
E value	1.0e-28
Match length	140
% identity	44
NCBI Description	(D26086) zinc-finger protein [Petunia x hybrida]

Seq. No.	198632
Contig ID	45002_1.R1039
5'-most EST	LIB3166-026-P1-K1-E10
Method	BLASTN
NCBI GI	g4220638
BLAST score	71
E value	1.0e-31
Match length	179
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	198633
Contig ID	45015_1.R1039
5'-most EST	LIB3189-001-P1-K1-A7
Method	BLASTX
NCBI GI	g3176725
BLAST score	189
E value	3.0e-14
Match length	64
% identity	48
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	198634
Contig ID	45031_1.R1039
5'-most EST	LIB3166-026-P1-K1-H1
Method	BLASTX
NCBI GI	g4220534
BLAST score	538
E value	2.0e-55
Match length	214
% identity	57
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	198635
Contig ID	45035_1.R1039
5'-most EST	LIB3166-026-P1-K1-H3
Method	BLASTX
NCBI GI	g2244898
BLAST score	190
E value	2.0e-14
Match length	55

% identity	69
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	198636
Contig ID	45045_1.R1039
5'-most EST	uC-gsf1maxxa098g02b1
Method	BLASTX
NCBI GI	g3395423
BLAST score	293
E value	3.0e-26
Match length	101
% identity	59
NCBI Description	(AC004683) putative protein kinase [Arabidopsis thaliana] >gi|3786023 (AC005499) putative protein kinase [Arabidopsis thaliana]

Seq. No.	198637
Contig ID	45053_1.R1039
5'-most EST	LIB3166-052-P1-K1-A7
Method	BLASTX
NCBI GI	g4164408
BLAST score	752
E value	5.0e-80
Match length	172
% identity	79
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	198638
Contig ID	45055_1.R1039
5'-most EST	LIB3272-003-P1-K1-H4
Method	BLASTX
NCBI GI	g3549679
BLAST score	151
E value	8.0e-10
Match length	39
% identity	82
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	198639
Contig ID	45064_1.R1039
5'-most EST	uC-gsronu33B126f08b1
Method	BLASTX
NCBI GI	g4388834
BLAST score	177
E value	1.0e-12
Match length	188
% identity	18
NCBI Description	(AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]

Seq. No.	198640
Contig ID	45067_1.R1039
5'-most EST	LIB3166-027-P1-K1-C3

Seq. No.	198641
Contig ID	45071_1.R1039

5'-most EST	uC-gsflmaxxa026h05b1
Seq. No.	198642
Contig ID	45077_1.R1039
5'-most EST	LIB3189-005-P1-K1-F5
Seq. No.	198643
Contig ID	45081_1.R1039
5'-most EST	LIB3166-027-P1-K1-D9
Seq. No.	198644
Contig ID	45085_1.R1039
5'-most EST	uC-gsronu33b025c11b1
Method	BLASTX
NCBI GI	g728949
BLAST score	268
E value	4.0e-23
Match length	105
% identity	50
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi|99665|pir||S25555 blue copper protein - Arabidopsis thaliana >gi|2147156|pir||I39698 blue copper-binding protein - Arabidopsis thaliana >gi|16203|emb|CAA78771| (Z15058) blue copper-binding protein [unidentified bacterium] >gi|739987|prf||2004275A blue copper-binding protein [Arabidopsis thaliana]
Seq. No.	198645
Contig ID	45107_1.R1039
5'-most EST	LIB3166-040-P1-K1-B11
Method	BLASTX
NCBI GI	g2464855
BLAST score	436
E value	5.0e-43
Match length	100
% identity	76
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.	198646
Contig ID	45114_1.R1039
5'-most EST	LIB3166-027-P1-K1-H1
Method	BLASTX
NCBI GI	g3702368
BLAST score	405
E value	2.0e-39
Match length	104
% identity	75
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]
Seq. No.	198647
Contig ID	45123_1.R1039
5'-most EST	LIB3166-028-P1-K1-A11
Method	BLASTX
NCBI GI	g4325372
BLAST score	227
E value	1.0e-18

Match length	99
% identity	42
NCBI Description	(AF128396) contains similarity to protein disulfide isomerases [Arabidopsis thaliana]

Seq. No.	198648
Contig ID	45137_1.R1039
5'-most EST	uC-gsflnu33B022e04b1

Seq. No.	198649
Contig ID	45138_1.R1039
5'-most EST	LIB3166-028-P1-K1-B6
Method	BLASTX
NCBI GI	g3785990
BLAST score	467
E value	1.0e-46
Match length	182
% identity	58
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi|4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198650
Contig ID	45143_1.R1039
5'-most EST	uC-gsflnu33B059d05b1
Method	BLASTX
NCBI GI	g1906002
BLAST score	803
E value	4.0e-86
Match length	178
% identity	87
NCBI Description	(U90429) nitrite reductase [Glycine max]

Seq. No.	198651
Contig ID	45175_1.R1039
5'-most EST	LIB3166-045-P1-K1-F8

Seq. No.	198652
Contig ID	45177_1.R1039
5'-most EST	g5048021
Method	BLASTX
NCBI GI	g4006891
BLAST score	155
E value	3.0e-10
Match length	38
% identity	76
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	198653
Contig ID	45188_1.R1039
5'-most EST	LIB3166-028-P1-K1-G11

Seq. No.	198654
Contig ID	45195_1.R1039
5'-most EST	LIB3166-028-P1-K1-G7

Seq. No.	198655

Contig ID 45207_1.R1039
5'-most EST LIB3166-028-P1-K1-H8

Seq. No. 198656
Contig ID 45268_1.R1039
5'-most EST LIB3272-020-P1-K1-C8

Seq. No. 198657
Contig ID 45279_1.R1039
5'-most EST LIB3197-043-Q1-M1-G9
Method BLASTX
NCBI GI g3150402
BLAST score 206
E value 2.0e-22
Match length 75
% identity 81
NCBI Description (AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No. 198658
Contig ID 45304_1.R1039
5'-most EST LIB3272-023-P1-K1-G4
Method BLASTX
NCBI GI g2245108
BLAST score 678
E value 3.0e-71
Match length 166
% identity 74
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 198659
Contig ID 45306_1.R1039
5'-most EST LIB3166-030-P1-K1-C3
Method BLASTX
NCBI GI g3482967
BLAST score 401
E value 1.0e-38
Match length 163
% identity 38
NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|4559345|gb|AAD23006.1|AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 198660
Contig ID 45325_1.R1039
5'-most EST uC-gsflnu33B035h11b1

Seq. No. 198661
Contig ID 45325_2.R1039
5'-most EST uC-gsflnu33B009g06b1

Seq. No. 198662
Contig ID 45325_4.R1039
5'-most EST uC-gsflnu33B132b01b1

Seq. No. 198663
Contig ID 45325_5.R1039

5'-most EST	uC-gsflnu33B056c12b1
Seq. No.	198664
Contig ID	45327_1.R1039
5'-most EST	LIB3197-039-Q1-M1-E4
Method	BLASTX
NCBI GI	g2494625
BLAST score	222
E value	5.0e-18
Match length	130
% identity	39
NCBI Description	HYPOTHETICAL PROTEIN KIAA0107 >gi|285951|dbj|BAA03497| (D14663) KIAA0107 [Homo sapiens]
Seq. No.	198665
Contig ID	45337_1.R1039
5'-most EST	uC-gsflnu33B001c10b1
Seq. No.	198666
Contig ID	45395_1.R1039
5'-most EST	LIB3166-031-P1-K1-E1
Method	BLASTX
NCBI GI	g3859598
BLAST score	311
E value	1.0e-51
Match length	133
% identity	78
NCBI Description	(AF104919) contains similarity to Myb DNA-binding domains (Pfam: PF00249, E=3.7e-27 N=3) [Arabidopsis thaliana]
Seq. No.	198667
Contig ID	45397_1.R1039
5'-most EST	LIB3166-031-P1-K1-E11
Seq. No.	198668
Contig ID	45402_1.R1039
5'-most EST	uC-gsronu33B136d11b1
Method	BLASTX
NCBI GI	g4204277
BLAST score	465
E value	1.0e-46
Match length	109
% identity	73
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	198669
Contig ID	45424_1.R1039
5'-most EST	LIB3166-031-P1-K1-G9
Method	BLASTX
NCBI GI	g4249385
BLAST score	522
E value	3.0e-53
Match length	106
% identity	89
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.	198670

Contig ID	45459_2.R1039
5'-most EST	g5045933
Method	BLASTX
NCBI GI	g4538923
BLAST score	361
E value	1.0e-53
Match length	199
% identity	50
NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]

Seq. No.	198671
Contig ID	45461_1.R1039
5'-most EST	LIB3272-058-P1-K1-H6
Method	BLASTX
NCBI GI	g1076660
BLAST score	546
E value	7.0e-56
Match length	139
% identity	78
NCBI Description	D13F(MYBST1) protein - potato >gi|786426|bbs|159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	198672
Contig ID	45468_1.R1039
5'-most EST	uC-gsflnu33B005e09b1
Method	BLASTX
NCBI GI	g3868857
BLAST score	408
E value	8.0e-40
Match length	93
% identity	82
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]

Seq. No.	198673
Contig ID	45475_1.R1039
5'-most EST	LIB3166-032-P1-K1-G12
Method	BLASTX
NCBI GI	g1143445
BLAST score	307
E value	4.0e-28
Match length	74
% identity	78
NCBI Description	(X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]

Seq. No.	198674
Contig ID	45476_1.R1039
5'-most EST	uC-gsflmaxxa046g06b1
Method	BLASTX
NCBI GI	g3461848
BLAST score	218
E value	2.0e-17
Match length	126
% identity	43
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 198675
Contig ID 45477_1.R1039
5'-most EST LIB3166-055-P1-K1-G6

Seq. No. 198676
Contig ID 45486_1.R1039
5'-most EST uC-gsronu33B057g01b1

Seq. No. 198677
Contig ID 45508_1.R1039
5'-most EST uC-gsronu33B107e11b1
Method BLASTX
NCBI GI g1142619
BLAST score 118
E value 1.0e-11
Match length 59
% identity 73
NCBI Description (U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No. 198678
Contig ID 45518_1.R1039
5'-most EST LIB3166-033-P1-K1-D2
Method BLASTX
NCBI GI g1732517
BLAST score 539
E value 5.0e-55
Match length 224
% identity 51
NCBI Description (U62745) putative cytoskeletal protein [Arabidopsis thaliana]

Seq. No. 198679
Contig ID 45537_1.R1039
5'-most EST uC-gsflnu33B076b09b1
Method BLASTX
NCBI GI g1293835
BLAST score 153
E value 1.0e-09
Match length 124
% identity 31
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 198680
Contig ID 45545_1.R1039
5'-most EST LIB3166-033-P1-K1-F7

Seq. No. 198681
Contig ID 45549_1.R1039
5'-most EST LIB3272-012-P1-K1-A8

Seq. No. 198682
Contig ID 45566_1.R1039
5'-most EST LIB3166-033-P1-K1-H9
Method BLASTX
NCBI GI g2980790

BLAST score	303
E value	2.0e-27
Match length	134
% identity	48
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198683
Contig ID	45599_1.R1039
5'-most EST	LIB3166-034-P1-K1-D11
Method	BLASTX
NCBI GI	g1778376
BLAST score	676
E value	3.0e-71
Match length	179
% identity	70
NCBI Description	(U81288) PsRT17-1 [Pisum sativum]

Seq. No.	198684
Contig ID	45601_1.R1039
5'-most EST	LIB3166-034-P1-K1-D2

Seq. No.	198685
Contig ID	45609_1.R1039
5'-most EST	LIB3166-034-P1-K1-E3
Method	BLASTX
NCBI GI	g2828296
BLAST score	360
E value	3.0e-34
Match length	75
% identity	91
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	198686
Contig ID	45611_1.R1039
5'-most EST	LIB3189-017-P1-K1-B1

Seq. No.	198687
Contig ID	45617_1.R1039
5'-most EST	LIB3166-055-P1-K1-F7

Seq. No.	198688
Contig ID	45627_1.R1039
5'-most EST	LIB3272-020-P1-K1-H11

Seq. No.	198689
Contig ID	45658_1.R1039
5'-most EST	g5049153
Method	BLASTX
NCBI GI	g421989
BLAST score	713
E value	2.0e-75
Match length	214
% identity	63
NCBI Description	serpin - barley >gi|19071|emb|CAA78822| (Z15116) protein zx [Hordeum vulgare] >gi|444778|prf||1908213A protein Zx [Hordeum vulgare]

Seq. No.	198690
Contig ID	45660_1.R1039
5'-most EST	LIB3166-050-P1-K1-E1
Method	BLASTX
NCBI GI	g4262157
BLAST score	169
E value	8.0e-12
Match length	102
% identity	23
NCBI Description	(AC005275) putative calmodulin [Arabidopsis thaliana]

Seq. No.	198691
Contig ID	45674_1.R1039
5'-most EST	LIB3166-035-P1-K1-C9

Seq. No.	198692
Contig ID	45684_1.R1039
5'-most EST	uC-gsflnu33B016e12b1
Method	BLASTX
NCBI GI	g3036840
BLAST score	336
E value	2.0e-31
Match length	137
% identity	47
NCBI Description	(AJ222967) cystinosin [Homo sapiens] >gi|3036851|emb|CAA75882| (Y15924) cystinosin [Homo sapiens]

Seq. No.	198693
Contig ID	45687_1.R1039
5'-most EST	LIB3166-045-P1-K1-D11
Method	BLASTX
NCBI GI	g4098331
BLAST score	1033
E value	1.0e-121
Match length	255
% identity	84
NCBI Description	(U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No.	198694
Contig ID	45690_1.R1039
5'-most EST	LIB3166-035-P1-K1-E8
Method	BLASTX
NCBI GI	g4567250
BLAST score	202
E value	4.0e-19
Match length	113
% identity	42
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198695
Contig ID	45752_1.R1039
5'-most EST	uC-gsflnu33B114a12b1
Method	BLASTX
NCBI GI	g4115936
BLAST score	762
E value	4.0e-81

Match length	171
% identity	84
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	198696
Contig ID	45752_2.R1039
5'-most EST	LIB3166-036-P1-K1-D4
Method	BLASTX
NCBI GI	g4115936
BLAST score	620
E value	1.0e-64
Match length	144
% identity	82
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	198697
Contig ID	45791_1.R1039
5'-most EST	LIB3166-036-P1-K1-H9

Seq. No.	198698
Contig ID	45804_1.R1039
5'-most EST	LIB3166-037-P1-K1-A5
Method	BLASTX
NCBI GI	g530088
BLAST score	194
E value	6.0e-15
Match length	59
% identity	67
NCBI Description	(U12735) aminoalcoholphosphotransferase [Glycine max]

Seq. No.	198699
Contig ID	45805_1.R1039
5'-most EST	LIB3166-039-P1-K1-H1
Method	BLASTX
NCBI GI	g439487
BLAST score	137
E value	3.0e-10
Match length	68
% identity	51
NCBI Description	(D26083) zinc-finger DNA binding protein [Petunia x hybrida]

Seq. No.	198700
Contig ID	45833_1.R1039
5'-most EST	uC-gsflmaxxa054g09b1

Seq. No.	198701
Contig ID	45864_1.R1039
5'-most EST	g3326209

Seq. No.	198702
Contig ID	45875_1.R1039
5'-most EST	LIB3166-037-P1-K1-H7

Seq. No.	198703
Contig ID	45914_1.R1039
5'-most EST	LIB3272-034-P1-K1-B9

Method	BLASTX
NCBI GI	g927025
BLAST score	458
E value	9.0e-46
Match length	146
% identity	47
NCBI Description	(L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No.	198704
Contig ID	45916_1.R1039
5'-most EST	LIB3166-052-P1-K1-H2
Method	BLASTX
NCBI GI	g3123295
BLAST score	301
E value	3.0e-27
Match length	151
% identity	42
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi|2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	198705
Contig ID	45933_1.R1039
5'-most EST	uC-gsflnu33B057e08b1

Seq. No.	198706
Contig ID	45934_1.R1039
5'-most EST	LIB3166-038-P1-K1-F3

Seq. No.	198707
Contig ID	45946_1.R1039
5'-most EST	LIB3166-038-P1-K1-G5
Method	BLASTX
NCBI GI	g4455246
BLAST score	345
E value	2.0e-32
Match length	95
% identity	71
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	198708
Contig ID	45954_1.R1039
5'-most EST	LIB3166-038-P1-K1-H3
Method	BLASTX
NCBI GI	g2582381
BLAST score	665
E value	1.0e-69
Match length	152
% identity	81
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No.	198709
Contig ID	45979_1.R1039
5'-most EST	LIB3166-039-P1-K1-C4

Seq. No.	198710

Contig ID	45982_1.R1039
5'-most EST	LIB3166-039-P1-K1-C2
Seq. No.	198711
Contig ID	45994_1.R1039
5'-most EST	g5044363
Seq. No.	198712
Contig ID	46023_1.R1039
5'-most EST	LIB3196-058-P1-M1-E7
Method	BLASTX
NCBI GI	g1373125
BLAST score	297
E value	6.0e-27
Match length	106
% identity	60
NCBI Description	(U43709) similar to the metB gene product of Escherichia coli; cloned by functional complementation of a metB mutant strain of Escherichia coli LE392 [Arabidopsis thaliana]
Seq. No.	198713
Contig ID	46067_1.R1039
5'-most EST	LIB3166-042-P1-K1-D12
Seq. No.	198714
Contig ID	46069_1.R1039
5'-most EST	uC-gsronu33B104h07b1
Seq. No.	198715
Contig ID	46069_2.R1039
5'-most EST	LIB3197-044-Q1-M1-C10
Seq. No.	198716
Contig ID	46075_1.R1039
5'-most EST	uC-gsflnu33B036f09b1
Method	BLASTX
NCBI GI	g4263787
BLAST score	546
E value	7.0e-56
Match length	174
% identity	62
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.	198717
Contig ID	46077_1.R1039
5'-most EST	uC-gsflnu33B109h01b1
Method	BLASTX
NCBI GI	g1293835
BLAST score	263
E value	2.0e-22
Match length	197
% identity	31
NCBI Description	(U56965) C15H9.5 gene product [Caenorhabditis elegans]
Seq. No.	198718
Contig ID	46092_1.R1039
5'-most EST	LIB3166-040-P1-K1-E6

Method	BLASTX
NCBI GI	g4220482
BLAST score	226
E value	1.0e-18
Match length	88
% identity	52
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198719
Contig ID	46102_1.R1039
5'-most EST	g5047943
Method	BLASTX
NCBI GI	g2739000
BLAST score	475
E value	2.0e-47
Match length	185
% identity	52
NCBI Description	(AF022459) CYP71D10p [Glycine max]

Seq. No.	198720
Contig ID	46103_1.R1039
5'-most EST	uC-gsflmaxxa090b07b1

Seq. No.	198721
Contig ID	46112_1.R1039
5'-most EST	uC-gsflmaxxa002d07b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	585
E value	3.0e-82
Match length	172
% identity	94
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	198722
Contig ID	46112_2.R1039
5'-most EST	LIB3197-027-Q1-M1-D3
Method	BLASTX
NCBI GI	g2369714
BLAST score	569
E value	1.0e-58
Match length	122
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	198723
Contig ID	46112_3.R1039
5'-most EST	uC-gsflmaxxa076c02b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	248
E value	1.0e-23
Match length	111
% identity	61
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	198724

Contig ID	46134_1.R1039
5'-most EST	LIB3166-042-P1-K1-A11
Method	BLASTX
NCBI GI	g4512652
BLAST score	182
E value	4.0e-13
Match length	186
% identity	28
NCBI Description	(AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198725
Contig ID	46144_1.R1039
5'-most EST	LIB3197-008-P1-M1-B4
Method	BLASTX
NCBI GI	g2493321
BLAST score	440
E value	5.0e-57
Match length	191
% identity	56
NCBI Description	L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO) >gi|2129952|pir||S66353 L-ascorbate oxidase (EC 1.10.3.3) precursor - common tobacco >gi|599594|dbj|BAA07734| (D43624) ascorbate oxidase precursor [Nicotiana tabacum]

Seq. No.	198726
Contig ID	46145_1.R1039
5'-most EST	uC-gsronu33B162e12b2
Method	BLASTN
NCBI GI	g599593
BLAST score	35
E value	5.0e-10
Match length	71
% identity	87
NCBI Description	Tobacco mRNA for ascorbate oxidase precursor, complete cds

Seq. No.	198727
Contig ID	46150_1.R1039
5'-most EST	LIB3166-042-P1-K1-B4

Seq. No.	198728
Contig ID	46151_1.R1039
5'-most EST	LIB3166-042-P1-K1-B5
Method	BLASTX
NCBI GI	g2244898
BLAST score	344
E value	7.0e-36
Match length	123
% identity	63
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	198729
Contig ID	46194_1.R1039
5'-most EST	uC-gsflnu33B143a11b1
Method	BLASTX
NCBI GI	g1150406
BLAST score	194

E value	9.0e-15
Match length	100
% identity	39
NCBI Description	(Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase [Pichia angusta]

Seq. No.	198730
Contig ID	46205_1.R1039
5'-most EST	LIB3166-042-P1-K1-G7

Seq. No.	198731
Contig ID	46225_1.R1039
5'-most EST	LIB3166-043-P1-K1-A5
Method	BLASTX
NCBI GI	g3618214
BLAST score	188
E value	7.0e-14
Match length	189
% identity	31
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	198732
Contig ID	46235_1.R1039
5'-most EST	LIB3166-043-P1-K1-B7

Seq. No.	198733
Contig ID	46251_1.R1039
5'-most EST	g5046107
Method	BLASTX
NCBI GI	g3858935
BLAST score	661
E value	2.0e-69
Match length	150
% identity	83
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi|4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	198734
Contig ID	46263_1.R1039
5'-most EST	g3326001
Method	BLASTX
NCBI GI	g4558661
BLAST score	174
E value	2.0e-30
Match length	190
% identity	51
NCBI Description	(AC007063) putative malate oxidoreductase (NAD) [Arabidopsis thaliana]

Seq. No.	198735
Contig ID	46304_1.R1039
5'-most EST	LIB3166-043-P1-K1-H9
Method	BLASTX
NCBI GI	g2281645

BLAST score 231
E value 3.0e-19
Match length 87
% identity 55
NCBI Description (AF003103) AP2 domain containing protein RAP2.10 [Arabidopsis thaliana] >gi|2632063|emb|CAA05630| (AJ002598) TINY-like protein [Arabidopsis thaliana]

Seq. No. 198736
Contig ID 46319_1.R1039
5'-most EST uC-gsflnu33B109c04b1

Seq. No. 198737
Contig ID 46325_1.R1039
5'-most EST LIB3166-044-P1-K1-B7

Seq. No. 198738
Contig ID 46327_1.R1039
5'-most EST LIB3197-022-Q1-M1-D5
Method BLASTX
NCBI GI g2104681
BLAST score 240
E value 5.0e-20
Match length 180
% identity 38
NCBI Description (X97907) transcription factor [Vicia faba]

Seq. No. 198739
Contig ID 46327_2.R1039
5'-most EST uC-gsflnu33B101d01b1

Seq. No. 198740
Contig ID 46331_1.R1039
5'-most EST LIB3272-049-P1-K1-D11
Method BLASTX
NCBI GI g1362103
BLAST score 554
E value 4.0e-57
Match length 126
% identity 83
NCBI Description ubiquitin conjugating enzyme - tomato >gi|886679|emb|CAA58111| (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No. 198741
Contig ID 46344_1.R1039
5'-most EST LIB3166-044-P1-K1-D5
Method BLASTX
NCBI GI g2833379
BLAST score 234
E value 2.0e-19
Match length 62
% identity 68
NCBI Description RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi|1076397|pir||S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi|633140|emb|CAA58717| (X83764)

phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi|3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	198742
Contig ID	46349_1.R1039
5'-most EST	uC-gsflmaxxa096e03b1
Method	BLASTX
NCBI GI	g4468991
BLAST score	214
E value	9.0e-17
Match length	137
% identity	37
NCBI Description	(AL035605) ribosomal-like protein [Arabidopsis thaliana]

Seq. No.	198743
Contig ID	46358_1.R1039
5'-most EST	LIB3166-044-P1-K1-F1

Seq. No.	198744
Contig ID	46372_1.R1039
5'-most EST	LIB3166-044-P1-K1-G2
Method	BLASTX
NCBI GI	g3033389
BLAST score	213
E value	7.0e-17
Match length	185
% identity	6
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	198745
Contig ID	46388_1.R1039
5'-most EST	LIB3166-044-P1-K1-H9
Method	BLASTX
NCBI GI	g4567201
BLAST score	949
E value	1.0e-103
Match length	262
% identity	74
NCBI Description	(AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	198746
Contig ID	46444_1.R1039
5'-most EST	uC-gsronu33b112c04b1
Method	BLASTX
NCBI GI	g3395436
BLAST score	441
E value	2.0e-43
Match length	191
% identity	43
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	198747
Contig ID	46467_1.R1039
5'-most EST	LIB3166-046-P1-K1-A6

Seq. No.	198748
Contig ID	46475_1.R1039
5'-most EST	g5045790
Method	BLASTX
NCBI GI	g1711512
BLAST score	928
E value	1.0e-100
Match length	222
% identity	83
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) >gi|1076577|pir||S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) >gi|556902|emb|CAA84288| (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]

Seq. No.	198749
Contig ID	46476_1.R1039
5'-most EST	g5044729
Method	BLASTX
NCBI GI	g3493131
BLAST score	593
E value	2.0e-61
Match length	143
% identity	76
NCBI Description	(AF081570) thymidylate kinase [Arabidopsis thaliana]

Seq. No.	198750
Contig ID	46517_1.R1039
5'-most EST	uC-gsronu33B124a08b1
Method	BLASTX
NCBI GI	g3023522
BLAST score	688
E value	2.0e-79
Match length	304
% identity	47
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi|2454309 (AF002705) beta prime COP [Rattus norvegicus]

Seq. No.	198751
Contig ID	46531_1.R1039
5'-most EST	g3326293
Method	BLASTX
NCBI GI	g1255951
BLAST score	631
E value	1.0e-65
Match length	186
% identity	69
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	198752
Contig ID	46555_1.R1039
5'-most EST	LIB3197-005-P1-M1-E10
Method	BLASTX
NCBI GI	g4467144
BLAST score	442
E value	7.0e-44

Match length	101
% identity	79
NCBI Description	(AL035540) putative phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	198753
Contig ID	46571_1.R1039
5'-most EST	g5050311
Method	BLASTX
NCBI GI	g2832680
BLAST score	715
E value	1.0e-75
Match length	191
% identity	40
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	198754
Contig ID	46574_1.R1039
5'-most EST	LIB3166-047-P1-K1-E3
Method	BLASTX
NCBI GI	g2213592
BLAST score	482
E value	2.0e-48
Match length	153
% identity	32
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	198755
Contig ID	46575_1.R1039
5'-most EST	g5049273
Method	BLASTX
NCBI GI	g4220489
BLAST score	165
E value	3.0e-11
Match length	59
% identity	56
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198756
Contig ID	46575_2.R1039
5'-most EST	uC-gsronu33B041c01b1

Seq. No.	198757
Contig ID	46617_1.R1039
5'-most EST	LIB3166-048-P1-K1-A9
Method	BLASTX
NCBI GI	g3785986
BLAST score	445
E value	2.0e-44
Match length	101
% identity	84
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	198758
Contig ID	46618_1.R1039
5'-most EST	uC-gsflnu33B101e07b1

Seq. No.	198759
Contig ID	46641_1.R1039
5'-most EST	uC-gsflmaxxa027a09b1
Method	BLASTX
NCBI GI	g2244970
BLAST score	200
E value	3.0e-15
Match length	63
% identity	57
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi|2326365|emb|CAA74765| (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	198760
Contig ID	46666_1.R1039
5'-most EST	LIB3166-048-P1-K1-G5
Method	BLASTX
NCBI GI	g1838976
BLAST score	165
E value	2.0e-11
Match length	78
% identity	54
NCBI Description	(X73635) vsf-1 [Lycopersicon esculentum]

Seq. No.	198761
Contig ID	46675_1.R1039
5'-most EST	LIB3166-049-P1-K1-A1
Method	BLASTX
NCBI GI	g1871577
BLAST score	376
E value	6.0e-36
Match length	165
% identity	44
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	198762
Contig ID	46740_1.R1039
5'-most EST	uC-gsronu33B157d11b1
Method	BLASTX
NCBI GI	g3080442
BLAST score	409
E value	4.0e-40
Match length	104
% identity	68
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	198763
Contig ID	46766_1.R1039
5'-most EST	LIB3166-050-P1-K1-B11

Seq. No.	198764
Contig ID	46816_1.R1039
5'-most EST	LIB3166-050-P1-K1-G9
Method	BLASTX
NCBI GI	g3236254
BLAST score	287
E value	8.0e-26

Match length	119
% identity	48
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	198765
Contig ID	46833_1.R1039
5'-most EST	uC-gsronu33B110c08b1
Method	BLASTX
NCBI GI	g3702339
BLAST score	302
E value	3.0e-27
Match length	140
% identity	46
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	198766
Contig ID	46845_1.R1039
5'-most EST	g5047044
Method	BLASTX
NCBI GI	g2462745
BLAST score	557
E value	3.0e-63
Match length	213
% identity	54
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	198767
Contig ID	46855_1.R1039
5'-most EST	LIB3272-052-P1-K1-D4
Method	BLASTX
NCBI GI	g3335341
BLAST score	522
E value	4.0e-53
Match length	180
% identity	63
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	198768
Contig ID	46902_1.R1039
5'-most EST	LIB3196-032-P1-M1-E1
Method	BLASTX
NCBI GI	g3915009
BLAST score	767
E value	1.0e-81
Match length	214
% identity	69
NCBI Description	ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi|1163181 (U35367) arginine decarboxylase [Glycine max]

Seq. No.	198769
Contig ID	46942_1.R1039
5'-most EST	LIB3166-052-P1-K1-C7
Method	BLASTX
NCBI GI	g2832677
BLAST score	526
E value	2.0e-53
Match length	216

% identity	50
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198770
Contig ID	46962_1.R1039
5'-most EST	LIB3166-052-P1-K1-E4
Method	BLASTX
NCBI GI	g4455223
BLAST score	236
E value	1.0e-19
Match length	64
% identity	37
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	198771
Contig ID	46985_1.R1039
5'-most EST	g5048259
Method	BLASTX
NCBI GI	g3283072
BLAST score	946
E value	1.0e-102
Match length	276
% identity	67
NCBI Description	(AF056022) p60 katanin [Homo sapiens]

Seq. No.	198772
Contig ID	46991_1.R1039
5'-most EST	LIB3197-013-P1-M1-C6

Seq. No.	198773
Contig ID	47001_1.R1039
5'-most EST	LIB3189-004-P1-K1-H2
Method	BLASTX
NCBI GI	g3785989
BLAST score	462
E value	4.0e-46
Match length	104
% identity	86
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	198774
Contig ID	47004_1.R1039
5'-most EST	LIB3166-053-P1-K1-A3

Seq. No.	198775
Contig ID	47011_1.R1039
5'-most EST	uC-gsronu33B141g12b1

Seq. No.	198776
Contig ID	47021_1.R1039
5'-most EST	uC-gsflnu33B137f04b1

Seq. No.	198777
Contig ID	47034_1.R1039
5'-most EST	g5044427

Seq. No. 198778
Contig ID 47070_1.R1039
5'-most EST LIB3166-053-P1-K1-H10

Seq. No. 198779
Contig ID 47073_1.R1039
5'-most EST uC-gsflmaxxa005a12b1

Seq. No. 198780
Contig ID 47100_1.R1039
5'-most EST uC-gsflmaxxa003e05b1

Seq. No. 198781
Contig ID 47117_1.R1039
5'-most EST uC-gsronu33B077g10b1

Seq. No. 198782
Contig ID 47181_1.R1039
5'-most EST LIB3272-042-P1-K1-B10
Method BLASTX
NCBI GI g3249066
BLAST score 466
E value 1.0e-46
Match length 145
% identity 68
NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein gb|984964. ESTs gb|F15433 and gb|AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No. 198783
Contig ID 47187_1.R1039
5'-most EST LIB3166-055-P1-K1-B8
Method BLASTX
NCBI GI g2160169
BLAST score 250
E value 3.0e-21
Match length 92
% identity 55
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 198784
Contig ID 47203_1.R1039
5'-most EST uC-gsflmaxxa047h08b1
Method BLASTX
NCBI GI g3402684
BLAST score 692
E value 5.0e-73
Match length 168
% identity 74
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198785
Contig ID 47212_1.R1039
5'-most EST LIB3197-025-Q1-M1-B9
Method BLASTX
NCBI GI g2961357
BLAST score 929

E value	1.0e-101
Match length	217
% identity	81
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	198786
Contig ID	47223_1.R1039
5'-most EST	g3326087
Method	BLASTX
NCBI GI	g3355465
BLAST score	470
E value	4.0e-57
Match length	201
% identity	58
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	198787
Contig ID	47229_1.R1039
5'-most EST	LIB3166-055-P1-K1-F4

Seq. No.	198788
Contig ID	47238_1.R1039
5'-most EST	uC-gsronu33B040c01b1
Method	BLASTX
NCBI GI	g2194142
BLAST score	667
E value	3.0e-70
Match length	161
% identity	73
NCBI Description	(AC002062) ESTs gb|N38288,gb|T43486,gb|AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	198789
Contig ID	47253_1.R1039
5'-most EST	LIB3196-048-P1-M1-E11
Method	BLASTX
NCBI GI	g2129832
BLAST score	598
E value	4.0e-62
Match length	116
% identity	93
NCBI Description	heat shock transcription factor 5 - soybean >gi|671868|emb|CAA87080| (Z46956) heat shock transcription factor 5 [Glycine max]

Seq. No.	198790
Contig ID	47303_1.R1039
5'-most EST	LIB3166-057-P1-K1-B2
Method	BLASTX
NCBI GI	g100673
BLAST score	483
E value	3.0e-48
Match length	179
% identity	56
NCBI Description	DNA-binding protein GT-2 - rice (fragment)

Seq. No.	198791
Contig ID	47305_1.R1039
5'-most EST	LIB3166-057-P1-K1-B6
Method	BLASTX
NCBI GI	g1168314
BLAST score	155
E value	3.0e-10
Match length	115
% identity	21
NCBI Description	REGULATOR OF ACETYL-COA SYNTHETASE ACTIVITY >gi|1084627|pir||S57116 probable carrier protein ACR1 - yeast (Saccharomyces cerevisiae) >gi|1015794|emb|CAA89624| (Z49595) ORF YJR095w [Saccharomyces cerevisiae]

Seq. No.	198792
Contig ID	47314_1.R1039
5'-most EST	LIB3166-057-P1-K1-C5
Method	BLASTX
NCBI GI	g4415931
BLAST score	455
E value	2.0e-45
Match length	122
% identity	70
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi|4559393|gb|AAD23053.1|AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	198793
Contig ID	47322_1.R1039
5'-most EST	LIB3166-057-P1-K1-D2
Method	BLASTX
NCBI GI	g1350783
BLAST score	384
E value	5.0e-37
Match length	135
% identity	58
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi|282883|pir||S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi|166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi|2842492|emb|CAA16889| (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	198794
Contig ID	47345_1.R1039
5'-most EST	g3326342
Method	BLASTX
NCBI GI	g967125
BLAST score	430
E value	2.0e-70
Match length	162
% identity	80
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	198795
Contig ID	47346_1.R1039
5'-most EST	LIB3166-057-P1-K1-F8

Method	BLASTX
NCBI GI	g3482967
BLAST score	251
E value	2.0e-21
Match length	57
% identity	81
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|4559345|gb|AAD23006.1|AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	198796
Contig ID	47354_1.R1039
5'-most EST	LIB3166-057-P1-K1-G6
Method	BLASTX
NCBI GI	g100226
BLAST score	615
E value	4.0e-64
Match length	145
% identity	81
NCBI Description	hypothetical protein - tomato >gi|19275|emb|CAA78112| (Z12127) protein of unknown function [Lycopersicon esculentum] >gi|445619|prf||1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	198797
Contig ID	47360_1.R1039
5'-most EST	LIB3166-057-P1-K1-H11
Method	BLASTX
NCBI GI	g2648355
BLAST score	148
E value	3.0e-09
Match length	138
% identity	32
NCBI Description	(AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]

Seq. No.	198798
Contig ID	47361_1.R1039
5'-most EST	LIB3272-003-P1-K1-B7
Method	BLASTX
NCBI GI	g2914698
BLAST score	218
E value	2.0e-17
Match length	120
% identity	42
NCBI Description	(AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198799
Contig ID	47363_1.R1039
5'-most EST	LIB3189-028-P1-K1-E12
Method	BLASTX
NCBI GI	g2583130
BLAST score	155
E value	2.0e-10
Match length	114
% identity	32
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No.	198800
Contig ID	47374_1.R1039
5'-most EST	LIB3166-058-P1-K1-A6
Method	BLASTX
NCBI GI	g3121867
BLAST score	99
E value	3.0e-09
Match length	103
% identity	37
NCBI Description	COP1 REGULATORY PROTEIN >gi|1694900|emb|CAA70768| (Y09579) Cop1 protein [Pisum sativum]

Seq. No.	198801
Contig ID	47382_1.R1039
5'-most EST	uC-gsronu33B143e10b1
Method	BLASTX
NCBI GI	g3047125
BLAST score	369
E value	2.0e-35
Match length	107
% identity	67
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	198802
Contig ID	47408_1.R1039
5'-most EST	LIB3189-050-P1-K1-G1
Method	BLASTX
NCBI GI	g2275217
BLAST score	194
E value	1.0e-14
Match length	75
% identity	45
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	198803
Contig ID	47452_1.R1039
5'-most EST	LIB3166-059-P1-K1-B4
Method	BLASTX
NCBI GI	g2495179
BLAST score	634
E value	4.0e-66
Match length	140
% identity	85
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi|1084340|pir||S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi|313150|emb|CAA51941| (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi|313838|emb|CAA52061| (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	198804
Contig ID	47456_1.R1039

5'-most EST	LIB3166-059-P1-K1-C3
Method	BLASTX
NCBI GI	g1914685
BLAST score	387
E value	3.0e-37
Match length	139
% identity	83
NCBI Description	(Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No.	198805
Contig ID	47468_1.R1039
5'-most EST	uC-gsronu33B087e10b1

Seq. No.	198806
Contig ID	47473_1.R1039
5'-most EST	g5050489
Method	BLASTX
NCBI GI	g3831443
BLAST score	332
E value	9.0e-31
Match length	105
% identity	62
NCBI Description	(AC005819) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	198807
Contig ID	47489_1.R1039
5'-most EST	uC-gsflmaxxa043f08b1
Method	BLASTX
NCBI GI	g4467151
BLAST score	1040
E value	1.0e-113
Match length	395
% identity	54
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	198808
Contig ID	47513_1.R1039
5'-most EST	LIB3189-017-P1-K1-D8

Seq. No.	198809
Contig ID	47521_1.R1039
5'-most EST	LIB3189-017-P1-K1-F4
Method	BLASTX
NCBI GI	g2979559
BLAST score	276
E value	2.0e-24
Match length	84
% identity	73
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	198810
Contig ID	47559_1.R1039
5'-most EST	g5046640
Method	BLASTX
NCBI GI	g100535

BLAST score	250
E value	4.0e-21
Match length	65
% identity	78
NCBI Description	hypothetical protein - swollen duckweed >gi|1929057|emb|CAA32236| (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	198811
Contig ID	47577_1.R1039
5'-most EST	g5048318

Seq. No.	198812
Contig ID	47583_1.R1039
5'-most EST	uC-gsflnu33B138a03b1
Method	BLASTN
NCBI GI	g435038
BLAST score	61
E value	2.0e-25
Match length	165
% identity	31
NCBI Description	Gossypium hirsutum proline-rich cell wall protein mRNA, complete cds

Seq. No.	198813
Contig ID	47583_2.R1039
5'-most EST	uC-gsflnu33B023d01b1
Method	BLASTN
NCBI GI	g451543
BLAST score	42
E value	4.0e-14
Match length	290
% identity	43
NCBI Description	Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi|1598725|gb|I18370|I18370 Sequence 25 from patent US

Seq. No.	198814
Contig ID	47583_3.R1039
5'-most EST	LIB3189-051-P1-K1-D3
Method	BLASTN
NCBI GI	g451543
BLAST score	58
E value	1.0e-23
Match length	252
% identity	85
NCBI Description	Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi|1598725|gb|I18370|I18370 Sequence 25 from patent US

Seq. No.	198815
Contig ID	47588_1.R1039
5'-most EST	LIB3189-049-P1-K1-A12
Method	BLASTX
NCBI GI	g1076315
BLAST score	192
E value	2.0e-14

Match length 123
% identity 34
NCBI Description cytochrome P450 - Arabidopsis thaliana >gi|853719|emb|CAA60793| (X87367) CYP90 protein [Arabidopsis thaliana] >gi|871988|emb|CAA60794| (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No. 198816
Contig ID 47594_1.R1039
5'-most EST uC-gsronu33B130g12b1
Method BLASTX
NCBI GI g4337175
BLAST score 211
E value 7.0e-17
Match length 101
% identity 47
NCBI Description (AC006416) ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 198817
Contig ID 47619_1.R1039
5'-most EST LIB3189-049-P1-K1-H8
Method BLASTX
NCBI GI g1710151
BLAST score 866
E value 2.0e-93
Match length 181
% identity 88
NCBI Description (U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No. 198818
Contig ID 47629_1.R1039
5'-most EST g5047659

Seq. No. 198819
Contig ID 47640_1.R1039
5'-most EST LIB3189-012-P1-K1-E11
Method BLASTX
NCBI GI g3643603
BLAST score 546
E value 6.0e-56
Match length 125
% identity 84
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 198820
Contig ID 47658_1.R1039
5'-most EST LIB3189-032-P1-K1-G9
Method BLASTN
NCBI GI g2647948
BLAST score 108
E value 2.0e-53
Match length 284
% identity 85
NCBI Description Olea europaea cytochrome b5 gene-1

Seq. No.	198821
Contig ID	47672_1.R1039
5'-most EST	g5045784
Method	BLASTX
NCBI GI	g2983997
BLAST score	264
E value	7.0e-23
Match length	102
% identity	50
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	198822
Contig ID	47672_2.R1039
5'-most EST	LIB3189-033-P1-K1-B2
Method	BLASTX
NCBI GI	g3861068
BLAST score	174
E value	2.0e-12
Match length	60
% identity	50
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	198823
Contig ID	47688_1.R1039
5'-most EST	LIB3189-033-P1-K1-H2
Method	BLASTX
NCBI GI	g2738982
BLAST score	217
E value	1.0e-17
Match length	69
% identity	58
NCBI Description	(AF022157) CYP71A10 [Glycine max]

Seq. No.	198824
Contig ID	47699_1.R1039
5'-most EST	LIB3189-021-P1-K1-A6
Method	BLASTX
NCBI GI	g133728
BLAST score	575
E value	2.0e-59
Match length	124
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi|81525|pir||B23525 ribosomal protein S11 - spinach chloroplast >gi|12264|emb|CAA27213| (X03496) pot. ribosomal protein S11 (aa 1-138) [Spinacia oleracea]

Seq. No.	198825
Contig ID	47710_1.R1039
5'-most EST	LIB3272-055-P1-K1-H10
Method	BLASTX
NCBI GI	g629791
BLAST score	401
E value	6.0e-39
Match length	77
% identity	99

NCBI Description	tubulin beta chain - rice >gi|460991|emb|CAA55022| (X78143) beta tubulin [Oryza sativa]

Seq. No.	198826
Contig ID	47712_1.R1039
5'-most EST	g5049657
Method	BLASTX
NCBI GI	g294668
BLAST score	687
E value	2.0e-72
Match length	191
% identity	77
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	198827
Contig ID	47719_1.R1039
5'-most EST	LIB3189-021-P1-K1-D1
Method	BLASTX
NCBI GI	g4218120
BLAST score	1109
E value	1.0e-121
Match length	314
% identity	68
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	198828
Contig ID	47727_1.R1039
5'-most EST	LIB3189-025-P1-K1-D8

Seq. No.	198829
Contig ID	47760_1.R1039
5'-most EST	LIB3189-050-P1-K1-G10
Method	BLASTX
NCBI GI	g4102839
BLAST score	677
E value	5.0e-71
Match length	313
% identity	46
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	198830
Contig ID	47769_1.R1039
5'-most EST	LIB3189-050-P1-K1-H10
Method	BLASTN
NCBI GI	g170293
BLAST score	51
E value	2.0e-19
Match length	303
% identity	82
NCBI Description	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) mRNA, complete cds

Seq. No.	198831
Contig ID	47783_1.R1039
5'-most EST	g5050077
Method	BLASTX

NCBI GI	g4567283
BLAST score	437
E value	4.0e-43
Match length	194
% identity	49
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	198832
Contig ID	47784_1.R1039
5'-most EST	LIB3189-011-P1-K1-C5
Method	BLASTX
NCBI GI	g1351408
BLAST score	450
E value	1.0e-44
Match length	136
% identity	67
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi|1076563|pir||S51117 cystein proteinase - sweet orange >gi|633185|emb|CAA87720| (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease [Citrus sinensis]

Seq. No.	198833
Contig ID	47810_1.R1039
5'-most EST	LIB3189-001-P1-K1-D12
Method	BLASTX
NCBI GI	g1352970
BLAST score	180
E value	6.0e-13
Match length	127
% identity	35
NCBI Description	HYPOTHETICAL 28.3 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION >gi|1077806|pir||S56807 hypothetical protein YJL035c - yeast (Saccharomyces cerevisiae) >gi|1008159|emb|CAA89326| (Z49310) ORF YJL035c [Saccharomyces cerevisiae]

Seq. No.	198834
Contig ID	47832_1.R1039
5'-most EST	LIB3189-001-P1-K1-D7
Method	BLASTX
NCBI GI	g4469015
BLAST score	601
E value	1.0e-62
Match length	131
% identity	91
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	198835
Contig ID	47835_1.R1039
5'-most EST	LIB3189-001-P1-K1-F7
Method	BLASTX
NCBI GI	g4490316
BLAST score	298
E value	4.0e-27
Match length	58
% identity	81
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	198836
Contig ID	47839_1.R1039
5'-most EST	LIB3189-002-P1-K1-C12
Method	BLASTX
NCBI GI	g2501555
BLAST score	684
E value	6.0e-72
Match length	165
% identity	74
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi|549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	198837
Contig ID	47862_1.R1039
5'-most EST	LIB3189-002-P1-K1-F6

Seq. No.	198838
Contig ID	47870_1.R1039
5'-most EST	LIB3189-002-P1-K1-G7
Method	BLASTX
NCBI GI	g2335101
BLAST score	688
E value	2.0e-72
Match length	196
% identity	65
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	198839
Contig ID	47893_1.R1039
5'-most EST	LIB3197-040-Q1-M1-E7
Method	BLASTX
NCBI GI	g2832625
BLAST score	608
E value	3.0e-63
Match length	165
% identity	70
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	198840
Contig ID	47905_1.R1039
5'-most EST	g5049477
Method	BLASTX
NCBI GI	g3004565
BLAST score	212
E value	1.0e-16
Match length	69
% identity	77
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	198841
Contig ID	47910_1.R1039
5'-most EST	LIB3197-023-Q1-M1-H10
Method	BLASTX
NCBI GI	g3122572
BLAST score	500
E value	8.0e-51

Match length	125
% identity	76
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi|1084434|pir||S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi|758340|emb|CAA59818| (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	198842
Contig ID	47916_1.R1039
5'-most EST	LIB3189-003-P1-K1-E8

Seq. No.	198843
Contig ID	47975_1.R1039
5'-most EST	LIB3197-055-Q1-M1-H2
Method	BLASTX
NCBI GI	g4580394
BLAST score	1248
E value	1.0e-138
Match length	407
% identity	52
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	198844
Contig ID	47991_1.R1039
5'-most EST	LIB3189-004-P1-K1-G1
Method	BLASTX
NCBI GI	g3193298
BLAST score	193
E value	2.0e-14
Match length	128
% identity	34
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	198845
Contig ID	47992_1.R1039
5'-most EST	LIB3189-004-P1-K1-G11
Method	BLASTX
NCBI GI	g1169228
BLAST score	212
E value	7.0e-17
Match length	70
% identity	60
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi|1084413|pir||S42639 helicase-like protein - Wood tobacco >gi|563986|dbj|BAA03763| (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]

Seq. No.	198846
Contig ID	47999_1.R1039
5'-most EST	LIB3189-011-P1-K1-H11

Seq. No.	198847
Contig ID	48022_1.R1039
5'-most EST	g5045834

Seq. No.	198848
Contig ID	48023_1.R1039
5'-most EST	LIB3189-005-P1-K1-H4
Method	BLASTX
NCBI GI	g3880563
BLAST score	260
E value	3.0e-22
Match length	222
% identity	33
NCBI Description	(Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	198849
Contig ID	48037_1.R1039
5'-most EST	g5047446

Seq. No.	198850
Contig ID	48040_1.R1039
5'-most EST	LIB3189-006-P1-K1-C12

Seq. No.	198851
Contig ID	48044_1.R1039
5'-most EST	LIB3272-036-P1-K1-E7
Method	BLASTX
NCBI GI	g461498
BLAST score	607
E value	3.0e-63
Match length	151
% identity	75
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi|320619|pir||S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi|296204|emb|CAA49199| (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	198852
Contig ID	48048_1.R1039
5'-most EST	uC-gsronu33B171a06b1
Method	BLASTX
NCBI GI	g1706326
BLAST score	562
E value	6.0e-58
Match length	132
% identity	84
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi|2146786|pir||S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi|1177603|emb|CAA91444| (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.	198853
Contig ID	48057_1.R1039
5'-most EST	uC-gsflmaxxa047b12b1
Method	BLASTX
NCBI GI	g431162
BLAST score	411

E value 4.0e-40
Match length 167
% identity 49
NCBI Description (D21822) ORF [Lilium longiflorum]

Seq. No. 198854
Contig ID 48062_1.R1039
5'-most EST LIB3197-034-Q1-M1-E2
Method BLASTX
NCBI GI g2894612
BLAST score 408
E value 7.0e-40
Match length 111
% identity 69
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 198855
Contig ID 48093_1.R1039
5'-most EST uC-gsflmaxxa097g04b1
Method BLASTX
NCBI GI g3122388
BLAST score 751
E value 7.0e-80
Match length 192
% identity 52
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi|2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 198856
Contig ID 48103_2.R1039
5'-most EST uC-gsflmaxxa076d01b1

Seq. No. 198857
Contig ID 48129_1.R1039
5'-most EST uC-gsronu33B106h08b2

Seq. No. 198858
Contig ID 48164_1.R1039
5'-most EST LIB3189-008-P1-K1-A3
Method BLASTX
NCBI GI g3273828
BLAST score 466
E value 2.0e-52
Match length 178
% identity 66
NCBI Description (AF068686) nodule-enhanced malate dehydrogenase [Glycine max]

Seq. No. 198859
Contig ID 48165_1.R1039
5'-most EST LIB3189-008-P1-K1-A5

Seq. No. 198860
Contig ID 48173_1.R1039
5'-most EST g5050648
Method BLASTX
NCBI GI g2191130

BLAST score 184
E value 3.0e-13
Match length 147
% identity 31
NCBI Description (AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No. 198861
Contig ID 48186_1.R1039
5'-most EST uC-gsronu33B062c09b1
Method BLASTX
NCBI GI g3004564
BLAST score 239
E value 6.0e-20
Match length 88
% identity 56
NCBI Description (AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 198862
Contig ID 48187_1.R1039
5'-most EST LIB3189-008-P1-K1-C9
Method BLASTX
NCBI GI g4467133
BLAST score 425
E value 7.0e-42
Match length 128
% identity 66
NCBI Description (AL035540) geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana]

Seq. No. 198863
Contig ID 48203_1.R1039
5'-most EST g5047155
Method BLASTX
NCBI GI g1931639
BLAST score 354
E value 2.0e-33
Match length 181
% identity 39
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 198864
Contig ID 48233_1.R1039
5'-most EST LIB3197-017-P1-M1-G12
Method BLASTX
NCBI GI g1771162
BLAST score 713
E value 2.0e-75
Match length 216
% identity 61
NCBI Description (X98930) SBT2 [Lycopersicon esculentum] >gi|3687307|emb|CAA07000| (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No. 198865
Contig ID 48245_1.R1039
5'-most EST LIB3189-010-P1-K1-C11

Seq. No.	198866
Contig ID	48261_1.R1039
5'-most EST	LIB3197-005-P1-M1-E2

Seq. No.	198867
Contig ID	48266_1.R1039
5'-most EST	uC-gsflnu33B059h05b1
Method	BLASTX
NCBI GI	g2791900
BLAST score	752
E value	4.0e-80
Match length	189
% identity	71
NCBI Description	(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No.	198868
Contig ID	48271_1.R1039
5'-most EST	LIB3197-029-Q1-M1-F12
Method	BLASTX
NCBI GI	g2464905
BLAST score	686
E value	4.0e-72
Match length	217
% identity	63
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	198869
Contig ID	48274_1.R1039
5'-most EST	uC-gsflmaxxa067a07b1
Method	BLASTX
NCBI GI	g2244792
BLAST score	246
E value	2.0e-21
Match length	83
% identity	70
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	198870
Contig ID	48278_1.R1039
5'-most EST	LIB3189-010-P1-K1-H1
Method	BLASTX
NCBI GI	g2688839
BLAST score	349
E value	7.0e-33
Match length	81
% identity	80
NCBI Description	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No.	198871
Contig ID	48308_1.R1039
5'-most EST	g5049467
Method	BLASTX
NCBI GI	g2088651
BLAST score	293
E value	3.0e-26

Match length 156
% identity 37
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 198872
Contig ID 48322_1.R1039
5'-most EST LIB3189-011-P1-K1-D5

Seq. No. 198873
Contig ID 48342_1.R1039
5'-most EST g5048233
Method BLASTX
NCBI GI g3461845
BLAST score 406
E value 2.0e-39
Match length 143
% identity 62
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198874
Contig ID 48348_1.R1039
5'-most EST uC-gsronu33B163a09b2
Method BLASTX
NCBI GI g3894099
BLAST score 579
E value 6.0e-60
Match length 127
% identity 89
NCBI Description (AJ012750) MCM3 protein [Pisum sativum]

Seq. No. 198875
Contig ID 48387_1.R1039
5'-most EST uC-gsronu33B147f01b1

Seq. No. 198876
Contig ID 48394_1.R1039
5'-most EST LIB3189-012-P1-K1-D6
Method BLASTX
NCBI GI g1706082
BLAST score 593
E value 3.0e-61
Match length 221
% identity 56
NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi|629787|pir||S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi|619350|bbs|153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi|474392|emb|CAA55478| (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No. 198877
Contig ID 48417_1.R1039
5'-most EST g5044438
Method BLASTX
NCBI GI g3980396

BLAST score	830
E value	4.0e-89
Match length	176
% identity	85
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	198878
Contig ID	48418_1.R1039
5'-most EST	LIB3189-012-P1-K1-G1
Method	BLASTX
NCBI GI	g2507455
BLAST score	569
E value	8.0e-59
Match length	138
% identity	84
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi|322401|pir||A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi|170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	198879
Contig ID	48425_1.R1039
5'-most EST	LIB3189-012-P1-K1-G5

Seq. No.	198880
Contig ID	48440_1.R1039
5'-most EST	uC-gsronu33B136d12b1

Seq. No.	198881
Contig ID	48443_1.R1039
5'-most EST	LIB3189-013-P1-K1-A4
Method	BLASTX
NCBI GI	g1280611
BLAST score	824
E value	2.0e-88
Match length	220
% identity	64
NCBI Description	(U53860) steroid reductase DET2 [Arabidopsis thaliana]

Seq. No.	198882
Contig ID	48449_1.R1039
5'-most EST	LIB3189-013-P1-K1-B10

Seq. No.	198883
Contig ID	48472_1.R1039
5'-most EST	g5046077
Method	BLASTX
NCBI GI	g2245058
BLAST score	156
E value	4.0e-10
Match length	63
% identity	51
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 198884

Contig ID	48484_1.R1039
5'-most EST	g5048309
Method	BLASTX
NCBI GI	g114171
BLAST score	276
E value	1.0e-27
Match length	154
% identity	55
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi|99781|pir||S12744 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape >gi|17815|emb|CAA35839| (X51475) 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]

Seq. No.	198885
Contig ID	48524_1.R1039
5'-most EST	LIB3189-014-P1-K1-D5
Method	BLASTX
NCBI GI	g2815493
BLAST score	365
E value	7.0e-35
Match length	113
% identity	61
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) (CP-MI) >gi|1731988|emb|CAA70816| (Y09603) serine carboxypeptidase I, CP-MI [Hordeum vulgare]

Seq. No.	198886
Contig ID	48529_1.R1039
5'-most EST	LIB3189-014-P1-K1-E12
Method	BLASTX
NCBI GI	g1888357
BLAST score	1236
E value	1.0e-136
Match length	420
% identity	57
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi|1890154|emb|CAA72432| (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	198887
Contig ID	48546_1.R1039
5'-most EST	g5044582
Method	BLASTX
NCBI GI	g2494162
BLAST score	394
E value	4.0e-38
Match length	197
% identity	39
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi|3879803|emb|CAA87414| (Z47356) similar to DNAJ [Caenorhabditis elegans]

Seq. No.	198888
Contig ID	48548_1.R1039

5'-most EST	uC-gsflnu33B091d10b1
Method	BLASTX
NCBI GI	g4455223
BLAST score	393
E value	6.0e-38
Match length	98
% identity	43
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	198889
Contig ID	48549_1.R1039
5'-most EST	LIB3189-014-P1-K1-G4
Method	BLASTX
NCBI GI	g416758
BLAST score	126
E value	2.0e-13
Match length	67
% identity	60
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi|166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi|445120|prf||1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	198890
Contig ID	48574_1.R1039
5'-most EST	uC-gsflnu33B088h05b1
Method	BLASTX
NCBI GI	g2462748
BLAST score	583
E value	3.0e-60
Match length	122
% identity	93
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	198891
Contig ID	48576_1.R1039
5'-most EST	LIB3189-015-P1-K1-B4

Seq. No.	198892
Contig ID	48588_1.R1039
5'-most EST	g3326574
Method	BLASTN
NCBI GI	g3510345
BLAST score	49
E value	3.0e-18
Match length	185
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	198893
Contig ID	48588_2.R1039
5'-most EST	uC-gsflmaxxa097c05b1
Method	BLASTN
NCBI GI	g3510345

BLAST score 63
E value 1.0e-26
Match length 268
% identity 83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No. 198894
Contig ID 48599_1.R1039
5'-most EST g5045063

Seq. No. 198895
Contig ID 48602_1.R1039
5'-most EST LIB3189-016-P1-K1-C3
Method BLASTX
NCBI GI g3386598
BLAST score 1245
E value 1.0e-137
Match length 319
% identity 74
NCBI Description (AC004665) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 198896
Contig ID 48622_1.R1039
5'-most EST LIB3189-048-P1-K1-B5

Seq. No. 198897
Contig ID 48626_1.R1039
5'-most EST LIB3189-041-P1-K1-D1

Seq. No. 198898
Contig ID 48635_1.R1039
5'-most EST LIB3189-016-P1-K1-F8
Method BLASTX
NCBI GI g2804278
BLAST score 465
E value 3.0e-73
Match length 203
% identity 69
NCBI Description (AB003516) squalene epoxidase [Panax ginseng]

Seq. No. 198899
Contig ID 48642_1.R1039
5'-most EST LIB3189-016-P1-K1-G4

Seq. No. 198900
Contig ID 48655_1.R1039
5'-most EST LIB3197-030-Q1-M1-A8
Method BLASTX
NCBI GI g4138722
BLAST score 333
E value 5.0e-31
Match length 127
% identity 55
NCBI Description (Y09590) hexose transporter [Vitis vinifera]

Seq. No. 198901

Contig ID	48696_1.R1039
5'-most EST	LIB3189-018-P1-K1-A12
Method	BLASTX
NCBI GI	g3785971
BLAST score	405
E value	2.0e-39
Match length	141
% identity	60
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi|4262248|gb|AAD14541| (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198902
Contig ID	48710_1.R1039
5'-most EST	uC-gsronu33B144g06b1

Seq. No.	198903
Contig ID	48718_1.R1039
5'-most EST	LIB3189-018-P1-K1-C9
Method	BLASTX
NCBI GI	g3738304
BLAST score	183
E value	3.0e-13
Match length	182
% identity	27
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	198904
Contig ID	48725_1.R1039
5'-most EST	LIB3189-022-P1-K1-C4

Seq. No.	198905
Contig ID	48730_1.R1039
5'-most EST	uC-gsflmaxxa097a01b1
Method	BLASTX
NCBI GI	g729480
BLAST score	455
E value	3.0e-45
Match length	126
% identity	73
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR) >gi|435647|dbj|BAA04232| (D17410) ferredoxin-NADP+ reductase [Oryza sativa] >gi|902936|dbj|BAA07479| (D38445) root ferredoxin-NADP+ reductase [Oryza sativa] >gi|1096932|prf||2113196A ferredoxin-NADP oxidoreductase [Oryza sativa]

Seq. No.	198906
Contig ID	48731_1.R1039
5'-most EST	LIB3189-018-P1-K1-E3
Method	BLASTX
NCBI GI	g1653702
BLAST score	276
E value	3.0e-24
Match length	82
% identity	70
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2)

of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	198907
Contig ID	48755_1.R1039
5'-most EST	LIB3197-041-Q1-M1-H8
Method	BLASTX
NCBI GI	g3650037
BLAST score	482
E value	1.0e-48
Match length	116
% identity	82
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	198908
Contig ID	48774_1.R1039
5'-most EST	LIB3189-022-P1-K1-C3
Method	BLASTX
NCBI GI	g2244931
BLAST score	157
E value	2.0e-10
Match length	114
% identity	35
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana] >gi|3426058|emb|CAA07572| (AJ007585) IB1P8-4 protein [Arabidopsis thaliana]

Seq. No.	198909
Contig ID	48794_1.R1039
5'-most EST	uC-gsflnu33B127g06b1
Method	BLASTX
NCBI GI	g1617036
BLAST score	375
E value	6.0e-36
Match length	89
% identity	76
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	198910
Contig ID	48817_1.R1039
5'-most EST	uC-gsflnu33B115g04b1
Method	BLASTX
NCBI GI	g2570338
BLAST score	212
E value	8.0e-17
Match length	69
% identity	61
NCBI Description	(U90927) glyoxalase II isozyme [Arabidopsis thaliana]

Seq. No.	198911
Contig ID	48823_1.R1039
5'-most EST	LIB3189-023-P1-K1-B11
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	37

% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	198912
Contig ID	48824_1.R1039
5'-most EST	LIB3272-036-P1-K1-C7
Method	BLASTX
NCBI GI	g4455225
BLAST score	486
E value	8.0e-49
Match length	152
% identity	56
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	198913
Contig ID	48838_1.R1039
5'-most EST	LIB3197-008-P1-M1-A6
Method	BLASTX
NCBI GI	g3641836
BLAST score	216
E value	1.0e-30
Match length	177
% identity	44
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	198914
Contig ID	48851_1.R1039
5'-most EST	LIB3189-023-P1-K1-D8

Seq. No.	198915
Contig ID	48862_1.R1039
5'-most EST	LIB3197-001-P1-M1-G1

Seq. No.	198916
Contig ID	48867_1.R1039
5'-most EST	LIB3197-051-Q1-M1-D4
Method	BLASTX
NCBI GI	g3687237
BLAST score	433
E value	2.0e-42
Match length	245
% identity	60
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	198917
Contig ID	48870_1.R1039
5'-most EST	uC-gsflmaxxa028e10b1
Method	BLASTX
NCBI GI	g3319355
BLAST score	537
E value	7.0e-55
Match length	115
% identity	94
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	198918
Contig ID	48875_1.R1039
5'-most EST	uC-gsronu33B107f12b1
Method	BLASTN
NCBI GI	g3319339
BLAST score	46
E value	1.0e-16
Match length	270
% identity	87
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	198919
Contig ID	48879_1.R1039
5'-most EST	LIB3189-023-P1-K1-G9

Seq. No.	198920
Contig ID	48883_1.R1039
5'-most EST	g3325850
Method	BLASTX
NCBI GI	g129960
BLAST score	281
E value	1.0e-24
Match length	119
% identity	49
NCBI Description	4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No.	198921
Contig ID	48902_1.R1039
5'-most EST	LIB3189-024-P1-K1-B7

Seq. No.	198922
Contig ID	48903_1.R1039
5'-most EST	LIB3189-024-P1-K1-C1

Seq. No.	198923
Contig ID	48911_1.R1039
5'-most EST	LIB3189-024-P1-K1-D4

Seq. No.	198924
Contig ID	48922_1.R1039
5'-most EST	LIB3189-046-P1-K1-G10

Seq. No.	198925
Contig ID	48931_1.R1039
5'-most EST	g5049049
Method	BLASTX
NCBI GI	g1172558
BLAST score	287
E value	1.0e-25
Match length	114
% identity	48
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi|480122|pir||S36454 porin por1 - garden pea >gi|396819|emb|CAA80988| (Z25540) Porin [Pisum sativum]

Seq. No.	198926
Contig ID	48938_1.R1039
5'-most EST	uC-gsflmaxxa049a07b1
Method	BLASTX
NCBI GI	g3885334
BLAST score	264
E value	6.0e-23
Match length	70
% identity	64
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	198927
Contig ID	48947_1.R1039
5'-most EST	LIB3189-025-P1-K1-A9
Method	BLASTX
NCBI GI	g444327
BLAST score	302
E value	2.0e-27
Match length	129
% identity	48
NCBI Description	O-methyltransferase [Populus trichocarpa x Populus deltoides]

Seq. No.	198928
Contig ID	48979_1.R1039
5'-most EST	LIB3189-050-P1-K1-E9
Method	BLASTX
NCBI GI	g3420008
BLAST score	842
E value	3.0e-90
Match length	297
% identity	54
NCBI Description	(AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No.	198929
Contig ID	49029_1.R1039
5'-most EST	uC-gsflmaxxa040a06b1
Method	BLASTX
NCBI GI	g3668089
BLAST score	371
E value	5.0e-55
Match length	189
% identity	53
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	198930
Contig ID	49043_1.R1039
5'-most EST	LIB3272-055-P1-K1-H6

Seq. No.	198931
Contig ID	49052_1.R1039
5'-most EST	LIB3197-027-Q1-M1-F1
Method	BLASTX
NCBI GI	g2252840
BLAST score	600
E value	7.0e-62

Match length	264
% identity	44
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	198932
Contig ID	49053_1.R1039
5'-most EST	LIB3189-028-P1-K1-H10

Seq. No.	198933
Contig ID	49059_1.R1039
5'-most EST	uC-gsronu33B082h01b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	248
E value	2.0e-21
Match length	73
% identity	67
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	198934
Contig ID	49075_1.R1039
5'-most EST	uC-gsronu33B047c04b1

Seq. No.	198935
Contig ID	49080_1.R1039
5'-most EST	LIB3189-030-P1-K1-D6
Method	BLASTX
NCBI GI	g4249402
BLAST score	373
E value	8.0e-36
Match length	116
% identity	65
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	198936
Contig ID	49091_1.R1039
5'-most EST	LIB3189-030-P1-K1-F2
Method	BLASTX
NCBI GI	g1703574
BLAST score	481
E value	3.0e-48
Match length	185
% identity	50
NCBI Description	(U80437) C43E11.9 [Caenorhabditis elegans]

Seq. No.	198937
Contig ID	49103_1.R1039
5'-most EST	LIB3189-044-P1-K1-G12

Seq. No.	198938
Contig ID	49125_1.R1039
5'-most EST	uC-gsflmaxxa048e06b1

Seq. No.	198939
Contig ID	49152_1.R1039
5'-most EST	LIB3272-038-P1-K1-H3

Method	BLASTX
NCBI GI	g1699370
BLAST score	467
E value	1.0e-46
Match length	198
% identity	49
NCBI Description	(S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9} [mice, liver, Peptide, 493 aa] [Mus sp.]

Seq. No.	198940
Contig ID	49155_1.R1039
5'-most EST	LIB3196-029-P1-M1-B4
Method	BLASTX
NCBI GI	g2894378
BLAST score	426
E value	5.0e-42
Match length	146
% identity	61
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	198941
Contig ID	49173_1.R1039
5'-most EST	LIB3189-005-P1-K1-B5
Method	BLASTX
NCBI GI	g3096947
BLAST score	208
E value	2.0e-16
Match length	115
% identity	57
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	198942
Contig ID	49197_1.R1039
5'-most EST	LIB3189-034-P1-K1-F12
Method	BLASTX
NCBI GI	g1872521
BLAST score	600
E value	3.0e-62
Match length	160
% identity	72
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi|1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	198943
Contig ID	49216_1.R1039
5'-most EST	g5048566
Method	BLASTX
NCBI GI	g3036807
BLAST score	845
E value	9.0e-91
Match length	258
% identity	66
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	198944

Contig ID	49220_1.R1039
5'-most EST	LIB3196-003-P1-M1-C7
Method	BLASTX
NCBI GI	g1785488
BLAST score	215
E value	3.0e-17
Match length	120
% identity	37
NCBI Description	(D14590) flavonoid 3',5'-hydroxylase [Campanula medium]

Seq. No.	198945
Contig ID	49238_1.R1039
5'-most EST	LIB3189-035-P1-K1-C4
Method	BLASTX
NCBI GI	g4263791
BLAST score	175
E value	2.0e-12
Match length	56
% identity	54
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	198946
Contig ID	49250_1.R1039
5'-most EST	LIB3196-030-P1-M1-B6

Seq. No.	198947
Contig ID	49262_1.R1039
5'-most EST	LIB3197-028-Q1-M1-G2
Method	BLASTX
NCBI GI	g1449179
BLAST score	203
E value	6.0e-16
Match length	63
% identity	57
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	198948
Contig ID	49303_1.R1039
5'-most EST	LIB3189-036-P1-K1-C8
Method	BLASTX
NCBI GI	g3688170
BLAST score	185
E value	9.0e-14
Match length	100
% identity	46
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	198949
Contig ID	49325_1.R1039
5'-most EST	g5047471
Method	BLASTX
NCBI GI	g2191130
BLAST score	239
E value	8.0e-20
Match length	177

% identity	38
NCBI Description	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No.	198950
Contig ID	49333_1.R1039
5'-most EST	LIB3197-054-Q1-M1-G4
Method	BLASTX
NCBI GI	g2894378
BLAST score	458
E value	2.0e-45
Match length	181
% identity	52
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	198951
Contig ID	49343_1.R1039
5'-most EST	LIB3189-036-P1-K1-H2

Seq. No.	198952
Contig ID	49364_1.R1039
5'-most EST	LIB3189-037-P1-K1-B3
Method	BLASTX
NCBI GI	g99898
BLAST score	1017
E value	1.0e-111
Match length	230
% identity	85
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) largest chain (isoform B1) - soybean (fragment)

Seq. No.	198953
Contig ID	49403_1.R1039
5'-most EST	LIB3189-041-P1-K1-A11

Seq. No.	198954
Contig ID	49406_1.R1039
5'-most EST	LIB3189-041-P1-K1-G1
Method	BLASTX
NCBI GI	g2760839
BLAST score	279
E value	1.0e-24
Match length	82
% identity	61
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	198955
Contig ID	49470_1.R1039
5'-most EST	LIB3189-041-P1-K1-H11
Method	BLASTX
NCBI GI	g2498885
BLAST score	182
E value	2.0e-25
Match length	143
% identity	48
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A >gi|1296664|emb|CAA65774| (X97064) Sec23 protein [Homo sapiens]

Seq. No.	198956
Contig ID	49473_1.R1039
5'-most EST	uC-gsronu33B055a12b1
Method	BLASTX
NCBI GI	g1246403
BLAST score	284
E value	4.0e-25
Match length	86
% identity	66
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi|3406035 (AC005405) TINY [Arabidopsis thaliana]

Seq. No.	198957
Contig ID	49476_1.R1039
5'-most EST	uC-gsflmaxxa090c12b1
Method	BLASTX
NCBI GI	g3075398
BLAST score	238
E value	8.0e-20
Match length	89
% identity	51
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	198958
Contig ID	49480_1.R1039
5'-most EST	uC-gsflmaxxa089f03b1
Method	BLASTX
NCBI GI	g3954807
BLAST score	706
E value	1.0e-74
Match length	178
% identity	75
NCBI Description	(AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus roseus]

Seq. No.	198959
Contig ID	49491_1.R1039
5'-most EST	LIB3189-043-P1-K1-A8
Method	BLASTX
NCBI GI	g3334661
BLAST score	356
E value	9.0e-34
Match length	117
% identity	56
NCBI Description	(Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	198960
Contig ID	49492_1.R1039
5'-most EST	g5048358
Method	BLASTX
NCBI GI	g4455800
BLAST score	321
E value	2.0e-29
Match length	104
% identity	59
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	198961
Contig ID	49521_1.R1039
5'-most EST	uC-gsronu33B017h09b1
Method	BLASTX
NCBI GI	g2623199
BLAST score	529
E value	6.0e-54
Match length	112
% identity	90
NCBI Description	(AF030290) protein phosphatase X isoform 2 [Arabidopsis thaliana]

Seq. No.	198962
Contig ID	49524_1.R1039
5'-most EST	LIB3189-043-P1-K1-E10
Method	BLASTX
NCBI GI	g2982465
BLAST score	215
E value	3.0e-17
Match length	123
% identity	42
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	198963
Contig ID	49541_1.R1039
5'-most EST	g5047179
Method	BLASTX
NCBI GI	g2072986
BLAST score	1125
E value	1.0e-123
Match length	239
% identity	85
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi|2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]

Seq. No.	198964
Contig ID	49544_1.R1039
5'-most EST	LIB3197-054-Q1-M1-E2
Method	BLASTX
NCBI GI	g498038
BLAST score	542
E value	2.0e-62
Match length	160
% identity	78
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	198965
Contig ID	49552_1.R1039
5'-most EST	g5049898
Method	BLASTX
NCBI GI	g113363
BLAST score	385
E value	5.0e-76
Match length	260
% identity	55

NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi|279445|pir||DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia >gi|20506|emb|CAA38039| (X54106) alcohol dehydrogenase [Petunia x hybrida]

Seq. No.	198966
Contig ID	49561_1.R1039
5'-most EST	uC-gsflmaxxa097c08b1
Method	BLASTX
NCBI GI	g1944518
BLAST score	609
E value	2.0e-63
Match length	158
% identity	72
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi|3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	198967
Contig ID	49580_1.R1039
5'-most EST	uC-gsflnu33B090e11b1
Method	BLASTX
NCBI GI	g2811031
BLAST score	474
E value	1.0e-47
Match length	143
% identity	66
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi|2109299|gb|AAB58165.1| (AF000132) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	198968
Contig ID	49596_1.R1039
5'-most EST	uC-gsronu33B103f05b1
Method	BLASTX
NCBI GI	g2511590
BLAST score	920
E value	1.0e-99
Match length	198
% identity	88
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi|3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	198969
Contig ID	49601_1.R1039
5'-most EST	g5050178
Method	BLASTX
NCBI GI	g2245017
BLAST score	388
E value	2.0e-37
Match length	170
% identity	46
NCBI Description	(Z97341) membrane protein homolog [Arabidopsis thaliana]

Seq. No. 198970

Contig ID	49666_1.R1039
5'-most EST	LIB3189-046-P1-K1-B5
Method	BLASTX
NCBI GI	g115610
BLAST score	636
E value	3.0e-66
Match length	135
% identity	95
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) >gi|68030|pir||QYNT phosphoenolpyruvate carboxylase (EC 4.1.1.31) - common tobacco >gi|22589|emb|CAA41758| (X59016) phosphoenolpyruvate carboxylase [Nicotiana tabacum]

Seq. No.	198971
Contig ID	49671_1.R1039
5'-most EST	LIB3197-053-Q1-M1-G12
Method	BLASTN
NCBI GI	g399628
BLAST score	42
E value	4.0e-14
Match length	78
% identity	90
NCBI Description	Lycopersicon esculentum (DB207) meloidogyne-induced giant cell protein mRNA, 3' end

Seq. No.	198972
Contig ID	49673_1.R1039
5'-most EST	LIB3189-046-P1-K1-C12
Method	BLASTN
NCBI GI	g3449327
BLAST score	39
E value	2.0e-12
Match length	67
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	198973
Contig ID	49691_1.R1039
5'-most EST	LIB3189-046-P1-K1-E7
Method	BLASTX
NCBI GI	g2911050
BLAST score	182
E value	2.0e-13
Match length	106
% identity	43
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	198974
Contig ID	49703_1.R1039
5'-most EST	uC-gsflnu33B036e05b1
Method	BLASTN
NCBI GI	g4079614
BLAST score	43
E value	8.0e-15
Match length	119
% identity	84

NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	198975
Contig ID	49704_1.R1039
5'-most EST	LIB3197-060-Q1-M1-B12

Seq. No.	198976
Contig ID	49724_1.R1039
5'-most EST	LIB3189-046-P1-K1-H7
Method	BLASTX
NCBI GI	g3395436
BLAST score	261
E value	1.0e-22
Match length	128
% identity	39
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	198977
Contig ID	49726_1.R1039
5'-most EST	LIB3189-046-P1-K1-H9

Seq. No.	198978
Contig ID	49748_1.R1039
5'-most EST	LIB3189-047-P1-K1-E5
Method	BLASTX
NCBI GI	g3805845
BLAST score	352
E value	7.0e-39
Match length	147
% identity	61
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	198979
Contig ID	49762_1.R1039
5'-most EST	uC-gsronu33B038f06b1
Method	BLASTX
NCBI GI	g1176658
BLAST score	256
E value	4.0e-44
Match length	204
% identity	44
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi|726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	198980
Contig ID	49804_1.R1039
5'-most EST	LIB3189-048-P1-K1-E1

Seq. No.	198981
Contig ID	49812_1.R1039
5'-most EST	uC-gsflnu33B056a02b1
Method	BLASTX
NCBI GI	g1575327
BLAST score	227
E value	8.0e-19

Match length	88
% identity	61
NCBI Description	(U59738) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	198982
Contig ID	49816_1.R1039
5'-most EST	LIB3189-048-P1-K1-F10
Method	BLASTX
NCBI GI	g3600054
BLAST score	192
E value	2.0e-14
Match length	106
% identity	40
NCBI Description	(AF080120) No definition line found [Arabidopsis thaliana]

Seq. No.	198983
Contig ID	49835_1.R1039
5'-most EST	LIB3189-048-P1-K1-H5

Seq. No.	198984
Contig ID	49835_2.R1039
5'-most EST	LIB3196-058-P1-M1-F8

Seq. No.	198985
Contig ID	49841_1.R1039
5'-most EST	LIB3189-049-P1-K1-A7
Method	BLASTX
NCBI GI	g549061
BLAST score	650
E value	4.0e-71
Match length	243
% identity	58
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (CCT-ZETA-1) >gi|631655|pir||S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi|468554|emb|CAA83432| (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus]

Seq. No.	198986
Contig ID	49860_1.R1039
5'-most EST	g5044958
Method	BLASTN
NCBI GI	g2264309
BLAST score	46
E value	2.0e-16
Match length	121
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	198987
Contig ID	49875_1.R1039
5'-most EST	LIB3189-050-P1-K1-C8
Method	BLASTX
NCBI GI	g3759184
BLAST score	722
E value	2.0e-76

Match length	245
% identity	61
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	198988
Contig ID	49916_1.R1039
5'-most EST	uC-gsflmaxxa040g04b1
Method	BLASTX
NCBI GI	g3451075
BLAST score	540
E value	3.0e-55
Match length	148
% identity	68
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	198989
Contig ID	49931_1.R1039
5'-most EST	uC-gsflmaxxa040c08b1
Method	BLASTX
NCBI GI	g4106061
BLAST score	199
E value	8.0e-16
Match length	75
% identity	60
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	198990
Contig ID	49950_1.R1039
5'-most EST	uC-gsflnu33B036b06b1
Method	BLASTX
NCBI GI	g4574320
BLAST score	228
E value	1.0e-18
Match length	78
% identity	65
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No.	198991
Contig ID	49961_1.R1039
5'-most EST	LIB3189-052-P1-K1-G8
Method	BLASTX
NCBI GI	g2191168
BLAST score	479
E value	5.0e-48
Match length	179
% identity	55
NCBI Description	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]

Seq. No.	198992
Contig ID	49967_1.R1039
5'-most EST	LIB3189-053-P1-K1-F10
Method	BLASTX
NCBI GI	g3281868
BLAST score	401
E value	5.0e-56

Match length	214
% identity	56
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	198993
Contig ID	49987_1.R1039
5'-most EST	LIB3189-034-P1-K1-B3
Method	BLASTX
NCBI GI	g1170745
BLAST score	769
E value	5.0e-82
Match length	151
% identity	100
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi|167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	198994
Contig ID	50022_1.R1039
5'-most EST	LIB3189-037-P1-K1-F12

Seq. No.	198995
Contig ID	50035_1.R1039
5'-most EST	g3325747
Method	BLASTX
NCBI GI	g4102600
BLAST score	321
E value	2.0e-29
Match length	156
% identity	54
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	198996
Contig ID	50052_1.R1039
5'-most EST	LIB3189-005-P1-K1-A5
Method	BLASTX
NCBI GI	g4579913
BLAST score	751
E value	6.0e-80
Match length	167
% identity	84
NCBI Description	(AB023423) sulfate transporter [Arabidopsis thaliana]

Seq. No.	198997
Contig ID	50102_1.R1039
5'-most EST	g5046627
Method	BLASTX
NCBI GI	g4240305
BLAST score	170
E value	9.0e-12
Match length	160
% identity	29
NCBI Description	(AB020715) KIAA0908 protein [Homo sapiens]

Seq. No.	198998
Contig ID	50103_1.R1039

5'-most EST	LIB3189-052-P1-K1-A11
Method	BLASTX
NCBI GI	g4406775
BLAST score	181
E value	7.0e-13
Match length	144
% identity	37
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	198999
Contig ID	50116_1.R1039
5'-most EST	LIB3197-045-Q1-M1-H8
Method	BLASTX
NCBI GI	g2947063
BLAST score	287
E value	3.0e-25
Match length	234
% identity	37
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	199000
Contig ID	50120_1.R1039
5'-most EST	LIB3189-052-P1-K1-C6
Method	BLASTX
NCBI GI	g3928150
BLAST score	432
E value	1.0e-42
Match length	123
% identity	61
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	199001
Contig ID	50123_1.R1039
5'-most EST	uC-gsflmaxxa028a01b1
Method	BLASTN
NCBI GI	g2264316
BLAST score	34
E value	2.0e-09
Match length	171
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	199002
Contig ID	50147_1.R1039
5'-most EST	uC-gsronu33B132g02b1
Method	BLASTX
NCBI GI	g4567226
BLAST score	183
E value	2.0e-13
Match length	73
% identity	55
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	199003
Contig ID	50157_1.R1039

5'-most EST	g3326091
Seq. No.	199004
Contig ID	50160_1.R1039
5'-most EST	LIB3189-039-P1-K1-D4
Method	BLASTX
NCBI GI	g2129559
BLAST score	312
E value	1.0e-28
Match length	144
% identity	47
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi|1022807 (U37702) cellulase [Arabidopsis thaliana] >gi|3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi|3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi|3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]
Seq. No.	199005
Contig ID	50170_1.R1039
5'-most EST	LIB3189-039-P1-K1-E4
Method	BLASTX
NCBI GI	g1168735
BLAST score	250
E value	2.0e-21
Match length	152
% identity	36
NCBI Description	CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi|1073970|pir||F64118 cytoplasmic axial filament protein (cafA) homolog - Haemophilus influenzae (strain Rd KW20) >gi|1574815 (U32814) cytoplasmic axial filament protein (cafA) [Haemophilus influenzae Rd]
Seq. No.	199006
Contig ID	50220_1.R1039
5'-most EST	LIB3197-059-Q1-M1-B3
Method	BLASTX
NCBI GI	g2088651
BLAST score	188
E value	8.0e-14
Match length	207
% identity	26
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	199007
Contig ID	50221_1.R1039
5'-most EST	LIB3189-001-P1-K1-E1
Method	BLASTX
NCBI GI	g1076660
BLAST score	380
E value	2.0e-36
Match length	104
% identity	74
NCBI Description	D13F(MYBST1) protein - potato >gi|786426|bbs|159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	199008
Contig ID	50231_1.R1039
5'-most EST	LIB3189-052-P1-K1-G4

Seq. No.	199009
Contig ID	50245_1.R1039
5'-most EST	LIB3189-053-P1-K1-A5

Seq. No.	199010
Contig ID	50287_1.R1039
5'-most EST	LIB3189-053-P1-K1-E9
Method	BLASTX
NCBI GI	g4455209
BLAST score	570
E value	9.0e-59
Match length	145
% identity	76
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]

Seq. No.	199011
Contig ID	50289_1.R1039
5'-most EST	LIB3189-053-P1-K1-F3
Method	BLASTX
NCBI GI	g3776084
BLAST score	270
E value	1.0e-23
Match length	85
% identity	59
NCBI Description	(Y18251) NtN2 [Medicago truncatula]

Seq. No.	199012
Contig ID	50318_1.R1039
5'-most EST	g5048907
Method	BLASTX
NCBI GI	g3738320
BLAST score	585
E value	2.0e-60
Match length	238
% identity	50
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	199013
Contig ID	50321_1.R1039
5'-most EST	g3326255
Method	BLASTX
NCBI GI	g3025205
BLAST score	177
E value	2.0e-12
Match length	73
% identity	51
NCBI Description	HYPOTHETICAL 65.1 KD PROTEIN SLR1919 >gi|1652223|dbj|BAA17147| (D90903) ABC1-like [Synechocystis sp.]

Seq. No.	199014
Contig ID	50326_1.R1039
5'-most EST	uC-gsronu33B031e10b1
Method	BLASTX
NCBI GI	g3258637
BLAST score	607
E value	4.0e-63
Match length	173
% identity	72
NCBI Description	(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No.	199015
Contig ID	50327_1.R1039
5'-most EST	uC-gsronu33B078b12b1
Method	BLASTX
NCBI GI	g1518113
BLAST score	739
E value	2.0e-78
Match length	205
% identity	68
NCBI Description	(U66193) SLL2 [Brassica napus]

Seq. No.	199016
Contig ID	50334_1.R1039
5'-most EST	uC-gsflmaxxa048c07b1
Method	BLASTX
NCBI GI	g2129559
BLAST score	665
E value	8.0e-70
Match length	164
% identity	78
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi|1022807 (U37702) cellulase [Arabidopsis thaliana] >gi|3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi|3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi|3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	199017
Contig ID	50363_1.R1039
5'-most EST	g5045584
Method	BLASTX
NCBI GI	g3980396
BLAST score	462
E value	4.0e-92
Match length	204
% identity	79
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	199018
Contig ID	50382_1.R1039
5'-most EST	LIB3197-005-P1-M1-B1
Method	BLASTX
NCBI GI	g3341681
BLAST score	687

E value	2.0e-72
Match length	148
% identity	91
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	199019
Contig ID	50394_1.R1039
5'-most EST	g5047335
Method	BLASTX
NCBI GI	g4432859
BLAST score	172
E value	5.0e-12
Match length	159
% identity	33
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	199020
Contig ID	50403_1.R1039
5'-most EST	LIB3189-002-P1-K1-H6
Method	BLASTX
NCBI GI	g1055368
BLAST score	811
E value	4.0e-87
Match length	151
% identity	99
NCBI Description	(U39567) ribulose-1,5-bisphosphate carboxylase small subunit [Glycine max]

Seq. No.	199021
Contig ID	50415_1.R1039
5'-most EST	LIB3189-015-P1-K1-C10

Seq. No.	199022
Contig ID	50487_1.R1039
5'-most EST	LIB3189-042-P1-K1-A4

Seq. No.	199023
Contig ID	50492_1.R1039
5'-most EST	LIB3197-047-Q1-M1-A2
Method	BLASTX
NCBI GI	g1107526
BLAST score	175
E value	4.0e-12
Match length	94
% identity	43
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	199024
Contig ID	50498_1.R1039
5'-most EST	LIB3189-042-P1-K1-B4
Method	BLASTX
NCBI GI	g3395426
BLAST score	506
E value	5.0e-51
Match length	169

% identity	59
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	199025
Contig ID	50501_1.R1039
5'-most EST	uC-gsronu33B129e03b1

Seq. No.	199026
Contig ID	50503_1.R1039
5'-most EST	LIB3189-042-P1-K1-C2
Method	BLASTX
NCBI GI	g4539404
BLAST score	210
E value	1.0e-16
Match length	107
% identity	45
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	199027
Contig ID	50516_1.R1039
5'-most EST	LIB3189-042-P1-K1-D5
Method	BLASTX
NCBI GI	g3482967
BLAST score	410
E value	4.0e-40
Match length	96
% identity	79
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|4559345|gb|AAD23006.1|AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	199028
Contig ID	50518_1.R1039
5'-most EST	LIB3189-042-P1-K1-D8
Method	BLASTX
NCBI GI	g3643611
BLAST score	496
E value	3.0e-50
Match length	137
% identity	64
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	199029
Contig ID	50549_1.R1039
5'-most EST	LIB3189-047-P1-K1-D2
Method	BLASTX
NCBI GI	g3894191
BLAST score	277
E value	2.0e-24
Match length	122
% identity	45
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	199030
Contig ID	50564_1.R1039
5'-most EST	LIB3189-048-P1-K1-C10
Method	BLASTX

NCBI GI g3876865
BLAST score 218
E value 2.0e-17
Match length 188
% identity 30
NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 199031
Contig ID 50565_1.R1039
5'-most EST LIB3189-048-P1-K1-C4
Method BLASTX
NCBI GI g1561774
BLAST score 361
E value 4.0e-34
Match length 147
% identity 52
NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]

Seq. No. 199032
Contig ID 50581_1.R1039
5'-most EST LIB3197-045-Q1-M1-A5

Seq. No. 199033
Contig ID 50601_1.R1039
5'-most EST LIB3189-031-P1-K1-A5
Method BLASTX
NCBI GI g2342723
BLAST score 245
E value 2.0e-20
Match length 155
% identity 37
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 199034
Contig ID 50626_1.R1039
5'-most EST LIB3189-042-P1-K1-E12

Seq. No. 199035
Contig ID 50628_1.R1039
5'-most EST LIB3272-003-P1-K1-A5
Method BLASTX
NCBI GI g401213
BLAST score 215
E value 4.0e-17
Match length 77
% identity 62
NCBI Description ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi|166792 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi|445600|prf||1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 199036
Contig ID 50636_1.R1039

5'-most EST	LIB3197-030-Q1-M1-A3
Seq. No.	199037
Contig ID	50675_1.R1039
5'-most EST	LIB3197-048-Q1-M1-C10
Method	BLASTX
NCBI GI	g120649
BLAST score	669
E value	2.0e-70
Match length	140
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi|625203|pir||DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi|182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi|182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi|182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi|182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi|224880|prf||1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]
Seq. No.	199038
Contig ID	50680_1.R1039
5'-most EST	LIB3196-052-P1-M1-A11
Method	BLASTX
NCBI GI	g2605714
BLAST score	800
E value	2.0e-85
Match length	201
% identity	77
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]
Seq. No.	199039
Contig ID	50683_1.R1039
5'-most EST	LIB3196-002-P1-M1-F6
Method	BLASTX
NCBI GI	g1346344
BLAST score	1772
E value	0.0e+00
Match length	358
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi|2119221|pir||A57398 keratin type II - human >gi|908779 (L42583) keratin type II [Homo sapiens]
Seq. No.	199040
Contig ID	50683_2.R1039
5'-most EST	LIB3196-008-P1-M1-B3
Method	BLASTX
NCBI GI	g547753
BLAST score	1339
E value	1.0e-148
Match length	364
% identity	77

NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	199041
Contig ID	50683_3.R1039
5'-most EST	LIB3197-021-Q1-M1-E7
Method	BLASTX
NCBI GI	g88044
BLAST score	1011
E value	1.0e-110
Match length	278
% identity	77
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi|34073|emb|CAA30534| (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	199042
Contig ID	50683_4.R1039
5'-most EST	LIB3196-027-P1-M1-E4
Method	BLASTX
NCBI GI	g125105
BLAST score	1033
E value	1.0e-112
Match length	340
% identity	67
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi|88051|pir||A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi|307082 (M21389) keratin type II [Homo sapiens] >gi|4557890|ref|NP_000415.1|pKRT5| keratin

Seq. No.	199043
Contig ID	50695_1.R1039
5'-most EST	LIB3196-043-P1-M1-A1
Method	BLASTX
NCBI GI	g2496887
BLAST score	288
E value	1.0e-25
Match length	119
% identity	54
NCBI Description	HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III >gi|732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]

Seq. No.	199044
Contig ID	50718_1.R1039
5'-most EST	LIB3197-023-Q1-M1-H2
Method	BLASTX
NCBI GI	g2493416
BLAST score	170
E value	5.0e-12
Match length	88
% identity	38
NCBI Description	S100 CALCIUM-BINDING PROTEIN A13 >gi|2134853|pir||JC5064 calcium-binding protein S100 A13 - human >gi|1694828|emb|CAA68188| (X99920) S100 calcium-binding protein A13 (S100A13) [Homo sapiens]

Seq. No.	199045
Contig ID	50719_1.R1039
5'-most EST	LIB3196-002-P1-M1-B7
Method	BLASTX
NCBI GI	g3335226
BLAST score	447
E value	2.0e-44
Match length	102
% identity	24
NCBI Description	(AF077374) small proline-rich protein [Homo sapiens]

Seq. No.	199046
Contig ID	50720_1.R1039
5'-most EST	LIB3196-024-P1-M1-G5
Method	BLASTX
NCBI GI	g1351173
BLAST score	664
E value	6.0e-70
Match length	134
% identity	98
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi|1050527|emb|CAA62635| (X91257) seryl-tRNA synthetase [Homo sapiens]

Seq. No.	199047
Contig ID	50722_1.R1039
5'-most EST	LIB3197-052-Q1-M1-E10
Method	BLASTX
NCBI GI	g113944
BLAST score	1258
E value	1.0e-139
Match length	260
% identity	53
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi|71756|pir||LUHU annexin I - human >gi|34388|emb|CAA29338| (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi|224956|prf||1204261A lipocortin [Homo sapiens] >gi|4502101|ref|NP_000691.1|pANX1| annexin I (lipocortin I)

Seq. No.	199048
Contig ID	50729_1.R1039
5'-most EST	LIB3196-014-P1-M1-A2
Method	BLASTX
NCBI GI	g121116
BLAST score	591
E value	4.0e-61
Match length	122
% identity	34
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi|71649|pir||FAHUP gelsolin precursor, plasma - human >gi|736249|emb|CAA28000| (X04412) plasma gelsolin [Homo sapiens] >gi|225304|prf||1211330A gelsolin [Homo sapiens] >gi|4504165|ref|NP_000168.1|pGSN| gelsolin (amyloidosis, Finnish type)

Seq. No.	199049
Contig ID	50729_2.R1039
5'-most EST	LIB3196-030-P1-M1-D4
Method	BLASTX
NCBI GI	g121116
BLAST score	592
E value	2.0e-83
Match length	165
% identity	55
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi|71649|pir||FAHUP gelsolin precursor, plasma - human >gi|736249|emb|CAA28000| (X04412) plasma gelsolin [Homo sapiens] >gi|225304|prf||1211330A gelsolin [Homo sapiens] >gi|4504165|ref|NP_000168.1|pGSN| gelsolin (amyloidosis, Finnish type)

Seq. No.	199050
Contig ID	50751_1.R1039
5'-most EST	LIB3196-058-P1-M1-D3
Method	BLASTX
NCBI GI	g2118403
BLAST score	368
E value	3.0e-35
Match length	145
% identity	50
NCBI Description	alpha-2-macroglobulin - human (fragment) >gi|177872 (M36501) alpha-2-macroglobulin [Homo sapiens]

Seq. No.	199051
Contig ID	50754_1.R1039
5'-most EST	LIB3196-045-P1-M1-C10
Method	BLASTX
NCBI GI	g137479
BLAST score	415
E value	8.0e-41
Match length	89
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi|107394|pir||A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human >gi|189676 (M62762) vacuolar H+ ATPase proton channel subunit [Homo sapiens] >gi|4502313|ref|NP_001685.1|pATP6C| ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD

Seq. No.	199052
Contig ID	50756_1.R1039
5'-most EST	LIB3196-018-P1-M1-D7
Method	BLASTX
NCBI GI	g126719
BLAST score	468
E value	5.0e-47
Match length	107
% identity	85
NCBI Description	T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN >gi|88813|pir||A29472 T-cell surface glycoprotein MAL, splice form a - human >gi|307157 (M15800) MAL protein [Homo sapiens] >gi|435478|emb|CAA54100| (X76678) MAL-a [Homo

sapiens] >gi|2654296|emb|CAA53809| (X76220) MAL [Homo sapiens] >gi|4505091|ref|NP_002362.1|pMAL| mal, T-cell differentiation protein

Seq. No.	199053
Contig ID	50790_1.R1039
5'-most EST	LIB3196-039-P1-M1-B12
Method	BLASTN
NCBI GI	g3201999
BLAST score	226
E value	1.0e-124
Match length	363
% identity	96
NCBI Description	Homo sapiens scaffold attachment factor A (SAF-A) mRNA, complete cds

Seq. No.	199054
Contig ID	50794_1.R1039
5'-most EST	LIB3196-002-P1-M1-E2
Method	BLASTX
NCBI GI	g2635765
BLAST score	239
E value	4.0e-20
Match length	79
% identity	61
NCBI Description	(Z99120) similar to NifS protein homolog [Bacillus subtilis]

Seq. No.	199055
Contig ID	50799_1.R1039
5'-most EST	uC-gsronu33B109h09b1
Method	BLASTX
NCBI GI	g1351222
BLAST score	620
E value	1.0e-64
Match length	129
% identity	93
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi|945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	199056
Contig ID	50800_1.R1039
5'-most EST	LIB3196-002-P1-M1-F10
Method	BLASTX
NCBI GI	g2118384
BLAST score	599
E value	2.0e-62
Match length	133
% identity	89
NCBI Description	squamous cell carcinoma antigen 2 - human

Seq. No.	199057
Contig ID	50807_1.R1039
5'-most EST	LIB3196-005-P1-M1-F9
Method	BLASTX
NCBI GI	g113950
BLAST score	731

E value	1.0e-77
Match length	147
% identity	57
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi|71761|pir||LUHU36 annexin II - human >gi|219910|dbj|BAA00013| (D00017) lipocortin II [Homo sapiens]

Seq. No.	199058
Contig ID	50809_1.R1039
5'-most EST	LIB3196-002-P1-M1-G10
Method	BLASTX
NCBI GI	g2137308
BLAST score	400
E value	1.0e-52
Match length	135
% identity	44
NCBI Description	G protein beta subuit like - mouse >gi|475012|dbj|BAA06185| (D29802) G protein beta subuit like [Mus musculus]

Seq. No.	199059
Contig ID	50818_1.R1039
5'-most EST	LIB3196-050-P1-M1-E11
Method	BLASTX
NCBI GI	g1754538
BLAST score	470
E value	3.0e-47
Match length	96
% identity	94
NCBI Description	(U66894) ESX [Homo sapiens] >gi|1841523 (U73843) ESE-1b [Homo sapiens] >gi|2338756 (AF017307) Ets-related transcription factor [Homo sapiens] >gi|2384740 (AF016295) Ets transcription factor [Homo sapiens] >gi|2459797 (U97156) epthelial-specific ets protein [Homo sapiens]

Seq. No.	199060
Contig ID	50824_1.R1039
5'-most EST	LIB3196-059-P1-M1-G1
Method	BLASTX
NCBI GI	g477138
BLAST score	501
E value	9.0e-51
Match length	99
% identity	91
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi|31591|emb|CAA31781| (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]

Seq. No.	199061
Contig ID	50832_1.R1039
5'-most EST	LIB3196-008-P1-M1-F2
Method	BLASTX
NCBI GI	g539663
BLAST score	443
E value	6.0e-44
Match length	98

% identity	87
NCBI Description	PR264/SC35 protein - human >gi|35597|emb|CAA44307| (X62447) PR 264 [Homo sapiens] >gi|455419|emb|CAA53383| (X75755) PR264/SC35 [Homo sapiens] >gi|3335676 (AF077858) splicing factor SC35 [Mus musculus] >gi|228504|prf||1805195B RNA-binding protein PR264 [Homo sapiens]

Seq. No.	199062
Contig ID	50861_1.R1039
5'-most EST	LIB3196-007-P1-M1-C7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	199063
Contig ID	50867_1.R1039
5'-most EST	LIB3196-017-P1-M1-F11
Method	BLASTX
NCBI GI	g1504040
BLAST score	155
E value	4.0e-10
Match length	159
% identity	18
NCBI Description	(D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]

Seq. No.	199064
Contig ID	50870_1.R1039
5'-most EST	LIB3196-005-P1-M1-E6
Method	BLASTX
NCBI GI	g3746127
BLAST score	539
E value	4.0e-55
Match length	153
% identity	71
NCBI Description	(U76253) E25B protein [Mus musculus]

Seq. No.	199065
Contig ID	50872_1.R1039
5'-most EST	LIB3196-054-P1-M1-D1
Method	BLASTX
NCBI GI	g478818
BLAST score	325
E value	6.0e-30
Match length	182
% identity	36
NCBI Description	strictosidine synthase - Rauvolfia mannii (fragment) >gi|21097|emb|CAA45025| (X63431) strictosidine synthase [Rauvolfia mannii]

Seq. No.	199066
Contig ID	50874_1.R1039
5'-most EST	LIB3196-018-P1-M1-E4

Method	BLASTX
NCBI GI	g115502
BLAST score	726
E value	5.0e-77
Match length	147
% identity	64
NCBI Description	CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) >gi|71690|pir||MCHUNB calmodulin-related protein NB-1 - human >gi|29650|emb|CAA31809| (X13461) hGH6 calmodulin-like protein [Homo sapiens] >gi|189081 (M58026) NB-1 [Homo sapiens]

Seq. No.	199067
Contig ID	50883_1.R1039
5'-most EST	LIB3196-003-P1-M1-F12
Method	BLASTX
NCBI GI	g586120
BLAST score	242
E value	4.0e-20
Match length	207
% identity	34
NCBI Description	TRICHOHYALIN >gi|539701|pir||A45973 trichohyalin - human >gi|292836 (L09190) trichohyalin [Homo sapiens]

Seq. No.	199068
Contig ID	50894_1.R1039
5'-most EST	LIB3196-038-P1-M1-F9
Method	BLASTX
NCBI GI	g4467804
BLAST score	785
E value	4.0e-84
Match length	151
% identity	95
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	199069
Contig ID	50936_1.R1039
5'-most EST	LIB3196-004-P1-M1-C6
Method	BLASTX
NCBI GI	g398953
BLAST score	807
E value	2.0e-86
Match length	162
% identity	99
NCBI Description	14-3-3 PROTEIN SIGMA (STRATIFIN) (EPITHELIAL CELL MARKER PROTEIN 1) >gi|486666|pir||S34753 stratifin - human >gi|23940|emb|CAA40623| (X57348) 9112 [Homo sapiens] >gi|2702353 (AF029081) 14-3-3 sigma protein [Homo sapiens] >gi|2702355 (AF029082) 14-3-3 sigma protein [Homo sapiens]

Seq. No.	199070
Contig ID	50939_1.R1039
5'-most EST	LIB3196-004-P1-M1-D1

Seq. No.	199071

Contig ID	51013_1.R1039
5'-most EST	LIB3196-005-P1-M1-C9
Method	BLASTN
NCBI GI	g3451362
BLAST score	238
E value	1.0e-131
Match length	362
% identity	74
NCBI Description	Homo sapiens clone UWGC:370m23.013 from 6p21, complete sequence [Homo sapiens]

Seq. No.	199072
Contig ID	51014_1.R1039
5'-most EST	uC-gsflmaxxa055a06b1
Method	BLASTX
NCBI GI	g4008441
BLAST score	214
E value	3.0e-17
Match length	62
% identity	63
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	199073
Contig ID	51021_1.R1039
5'-most EST	LIB3196-009-P1-M1-F12
Method	BLASTN
NCBI GI	g183749
BLAST score	204
E value	1.0e-111
Match length	519
% identity	95
NCBI Description	Human H19 RNA gene, complete cds

Seq. No.	199074
Contig ID	51029_1.R1039
5'-most EST	LIB3196-005-P1-M1-E7
Method	BLASTX
NCBI GI	g399365
BLAST score	771
E value	3.0e-82
Match length	171
% identity	90
NCBI Description	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3) >gi|178402 (M74542) aldehyde dehydrogenase type III [Homo sapiens] >gi|4502035|ref|NP_000682.1|pALDH3| aldehyde dehydrogenase

Seq. No.	199075
Contig ID	51051_1.R1039
5'-most EST	LIB3196-005-P1-M1-G7

Seq. No.	199076
Contig ID	51057_1.R1039
5'-most EST	LIB3196-005-P1-M1-H12

Method	BLASTX
NCBI GI	g1076398
BLAST score	143
E value	6.0e-09
Match length	38
% identity	68
NCBI Description	ribosomal protein L2 - Arabidopsis thaliana >gi|572523|emb|CAA57902| (X82556) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	199077
Contig ID	51072_1.R1039
5'-most EST	LIB3196-040-P1-M1-G8

Seq. No.	199078
Contig ID	51072_2.R1039
5'-most EST	uC-gsflnu33B018d07b1

Seq. No.	199079
Contig ID	51084_1.R1039
5'-most EST	LIB3197-008-P1-M1-E8
Method	BLASTX
NCBI GI	g4240253
BLAST score	321
E value	2.0e-29
Match length	188
% identity	39
NCBI Description	(AB020689) KIAA0882 protein [Homo sapiens]

Seq. No.	199080
Contig ID	51088_1.R1039
5'-most EST	LIB3196-006-P1-M1-C1
Method	BLASTX
NCBI GI	g125077
BLAST score	556
E value	6.0e-57
Match length	153
% identity	76
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi|71526|pir||KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi|34033|emb|CAA32786| (X14640) keratin 13 [Homo sapiens]

Seq. No.	199081
Contig ID	51098_1.R1039
5'-most EST	LIB3196-024-P1-M1-E10
Method	BLASTN
NCBI GI	g3108279
BLAST score	66
E value	1.0e-28
Match length	180
% identity	85
NCBI Description	Gossypium barbadense clone pXP104 repetitive DNA sequence

Seq. No.	199082
Contig ID	51112_1.R1039
5'-most EST	LIB3196-054-P1-M1-G3

Method	BLASTX
NCBI GI	g100001
BLAST score	758
E value	1.0e-80
Match length	205
% identity	71
NCBI Description	endopeptidase C1 - kidney bean >gi|1345573|emb|CAA40073| (X56753) endopeptidase (EP-C1) [Phaseolus vulgaris]

Seq. No.	199083
Contig ID	51117_1.R1039
5'-most EST	LIB3196-036-P1-M1-G8
Method	BLASTX
NCBI GI	g479532
BLAST score	469
E value	4.0e-47
Match length	96
% identity	99
NCBI Description	GTP-binding regulatory protein Gs alpha chain - human >gi|1335091|emb|CAA39484| (X56009) alpha subunit of GsGTP binding protein [Homo sapiens]

Seq. No.	199084
Contig ID	51126_1.R1039
5'-most EST	LIB3196-047-P1-M1-F5
Method	BLASTX
NCBI GI	g113339
BLAST score	779
E value	2.0e-83
Match length	155
% identity	95
NCBI Description	ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE) >gi|67782|pir||DUHUA adenosine deaminase (EC 3.5.4.4) - human >gi|28380|emb|CAA26734| (X02994) adenosine deaminase [Homo sapiens] >gi|178077 (M13792) adenosine deaminase [Homo sapiens]

Seq. No.	199085
Contig ID	51128_1.R1039
5'-most EST	LIB3196-006-P1-M1-F9
Method	BLASTN
NCBI GI	g2924257
BLAST score	72
E value	3.0e-32
Match length	138
% identity	92
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	199086
Contig ID	51141_1.R1039
5'-most EST	LIB3196-006-P1-M1-H6

Seq. No.	199087
Contig ID	51162_1.R1039
5'-most EST	LIB3272-011-P1-K1-H9

Seq. No. 199088

Contig ID	51163_1.R1039
5'-most EST	g5049474
Method	BLASTX
NCBI GI	g1653702
BLAST score	523
E value	3.0e-53
Match length	162
% identity	63
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	199089
Contig ID	51173_1.R1039
5'-most EST	LIB3196-030-P1-M1-G5
Method	BLASTX
NCBI GI	g136479
BLAST score	502
E value	5.0e-51
Match length	99
% identity	99
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23) >gi|88948|pir||S06590 IgE-dependent histamine-releasing factor - human >gi|37496|emb|CAA34200| (X16064) tumor protein (AA 1 - 172) [Homo sapiens] >gi|4507669|ref|NP_003286.1|pTPT1| tumor protein, translationally-controlled

Seq. No.	199090
Contig ID	51185_1.R1039
5'-most EST	uC-gsflnu33B008h08b1
Method	BLASTX
NCBI GI	g3688598
BLAST score	619
E value	1.0e-64
Match length	141
% identity	78
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	199091
Contig ID	51188_1.R1039
5'-most EST	LIB3196-059-P1-M1-H4
Method	BLASTX
NCBI GI	g133041
BLAST score	763
E value	2.0e-81
Match length	153
% identity	97
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi|71137|pir||R5HUP0 acidic ribosomal protein P0 - human >gi|190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi|2935618|gb|AAC05176| (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi|4506667|ref|NP_000993.1|pRPLP0| ribosomal protein, large, P0

Seq. No.	199092
Contig ID	51193_1.R1039

5'-most EST	LIB3196-064-P1-M1-B8
Method	BLASTX
NCBI GI	g224877
BLAST score	502
E value	5.0e-51
Match length	99
% identity	96
NCBI Description	deaminase a,adenosine [Homo sapiens]

Seq. No.	199093
Contig ID	51199_1.R1039
5'-most EST	LIB3196-007-P1-M1-E7
Method	BLASTN
NCBI GI	g3603252
BLAST score	234
E value	1.0e-129
Match length	377
% identity	90
NCBI Description	Homo sapiens keratin 13 gene, complete cds

Seq. No.	199094
Contig ID	51202_1.R1039
5'-most EST	LIB3196-007-P1-M1-F1
Method	BLASTX
NCBI GI	g2736151
BLAST score	215
E value	3.0e-17
Match length	82
% identity	50
NCBI Description	(AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]

Seq. No.	199095
Contig ID	51212_1.R1039
5'-most EST	LIB3196-054-P1-M1-B8
Method	BLASTX
NCBI GI	g1170097
BLAST score	579
E value	1.0e-59
Match length	120
% identity	89
NCBI Description	GLUTATHIONE S-TRANSFERASE MU 5 (GSTM5-5) (CLASS-MU) >gi|423000|pir||A46048 glutathione transferase (EC 2.5.1.18) class mu, GSTM5 - human >gi|468260 (L02321) glutathione S-transferase GSTM5-5 [Homo sapiens] >gi|4504181|ref|NP_000842.1|pGSTM5| glutathione S-transferase M5

Seq. No.	199096
Contig ID	51218_1.R1039
5'-most EST	LIB3196-007-P1-M1-G6
Method	BLASTX
NCBI GI	g461776
BLAST score	309
E value	3.0e-28
Match length	53
% identity	98

NCBI Description	CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) >gi|251369|bbs|108679 (S40060) spr1=small proline rich squamous cell marker [Rhesus monkeys, tracheobronchial epithelium, Peptide, 89 aa] [Rhesus monkeys] >gi|342297 (M83999) small proline-rich protein [Macaca mulatta]

Seq. No.	199097
Contig ID	51222_1.R1039
5'-most EST	LIB3196-007-P1-M1-H11
Method	BLASTN
NCBI GI	g4406655
BLAST score	365
E value	0.0e+00
Match length	409
% identity	97
NCBI Description	Homo sapiens clone 25077 mRNA sequence, complete cds

Seq. No.	199098
Contig ID	51225_1.R1039
5'-most EST	uC-gsronu33B104e04b1
Method	BLASTX
NCBI GI	g2160694
BLAST score	537
E value	8.0e-55
Match length	138
% identity	72
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	199099
Contig ID	51243_1.R1039
5'-most EST	LIB3196-028-P1-M1-D3
Method	BLASTX
NCBI GI	g1944407
BLAST score	205
E value	3.0e-16
Match length	45
% identity	82
NCBI Description	(D86988) KIAA0221 [Homo sapiens]

Seq. No.	199100
Contig ID	51247_1.R1039
5'-most EST	LIB3196-008-P1-M1-B8
Method	BLASTX
NCBI GI	g4539005
BLAST score	237
E value	6.0e-20
Match length	122
% identity	41
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	199101
Contig ID	51252_1.R1039
5'-most EST	LIB3196-049-P1-M1-E2
Method	BLASTX
NCBI GI	g484102

BLAST score	226
E value	2.0e-18
Match length	82
% identity	55
NCBI Description	(U02082) guanine nucleotide regulatory protein [Homo sapiens] >gi|3041860 (AC004534) guanine nucleotide regulatory protein [Homo sapiens]

Seq. No.	199102
Contig ID	51257_1.R1039
5'-most EST	LIB3196-025-P1-M1-C12

Seq. No.	199103
Contig ID	51258_1.R1039
5'-most EST	uC-gsronu33B011f09b1

Seq. No.	199104
Contig ID	51301_1.R1039
5'-most EST	LIB3196-008-P1-M1-H10
Method	BLASTX
NCBI GI	g3292827
BLAST score	297
E value	1.0e-26
Match length	102
% identity	65
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	199105
Contig ID	51324_1.R1039
5'-most EST	LIB3196-059-P1-M1-F3
Method	BLASTX
NCBI GI	g2829461
BLAST score	304
E value	2.0e-27
Match length	80
% identity	74
NCBI Description	METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS) >gi|2135628|pir||JC5224 methionine--tRNA ligase (EC 6.1.1.10) - human >gi|1702932|emb|CAA64381| (X94754) yeast methionyl-tRNA synthetase homolog [Homo sapiens]

Seq. No.	199106
Contig ID	51328_1.R1039
5'-most EST	LIB3197-022-Q1-M1-B10

Seq. No.	199107
Contig ID	51336_1.R1039
5'-most EST	LIB3196-009-P1-M1-C5
Method	BLASTX
NCBI GI	g3845568
BLAST score	334
E value	5.0e-31
Match length	141
% identity	50
NCBI Description	(AB012042) keratin 6 beta [Mus musculus]

Seq. No.	199108

Contig ID	51347_1.R1039
5'-most EST	g5048959
Method	BLASTX
NCBI GI	g3334128
BLAST score	197
E value	7.0e-15
Match length	88
% identity	52
NCBI Description	BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) >gi|1066348 (U23155) acetyl-CoA carboxylase biotin-containing subunit [Arabidopsis thaliana]

Seq. No.	199109
Contig ID	51354_1.R1039
5'-most EST	LIB3196-009-P1-M1-E10
Method	BLASTX
NCBI GI	g3319958
BLAST score	575
E value	2.0e-59
Match length	115
% identity	11
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	199110
Contig ID	51363_1.R1039
5'-most EST	LIB3196-009-P1-M1-F1
Method	BLASTN
NCBI GI	g3319957
BLAST score	337
E value	0.0e+00
Match length	377
% identity	97
NCBI Description	Homo sapiens mRNA for VAKTI precursor

Seq. No.	199111
Contig ID	51393_1.R1039
5'-most EST	LIB3196-009-P1-M1-H6
Method	BLASTX
NCBI GI	g82228
BLAST score	295
E value	2.0e-26
Match length	72
% identity	85
NCBI Description	hypothetical protein 77 - common tobacco chloroplast >gi|225199|prf||1211235AD ORF 77 [Nicotiana tabacum]

Seq. No.	199112
Contig ID	51399_1.R1039
5'-most EST	LIB3196-034-P1-M1-B5
Method	BLASTX
NCBI GI	g1352450
BLAST score	561
E value	6.0e-58
Match length	112
% identity	100
NCBI Description	INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA)

(HEMATOPOIETIN-1) >gi|644806 (U19844) interleukin-1 alpha [Macaca mulatta]

Seq. No.	199113
Contig ID	51401_1.R1039
5'-most EST	LIB3197-004-P1-M1-A2
Method	BLASTX
NCBI GI	g2982303
BLAST score	1240
E value	1.0e-137
Match length	267
% identity	87
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	199114
Contig ID	51417_1.R1039
5'-most EST	LIB3196-010-P1-M1-C9

Seq. No.	199115
Contig ID	51440_1.R1039
5'-most EST	LIB3196-021-P1-M1-H5
Method	BLASTX
NCBI GI	g136452
BLAST score	538
E value	7.0e-55
Match length	149
% identity	68
NCBI Description	STEM-SPECIFIC PROTEIN TSJT1 >gi|100383|pir||S13551 stem-specific protein - common tobacco >gi|20037|emb|CAA36525| (X52283) stem specific, weakly expressed in other organs [Nicotiana tabacum]

Seq. No.	199116
Contig ID	51449_1.R1039
5'-most EST	uC-gsflmaxxa091h01b1
Method	BLASTX
NCBI GI	g2191175
BLAST score	293
E value	3.0e-26
Match length	164
% identity	55
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	199117
Contig ID	51455_1.R1039
5'-most EST	LIB3196-033-P1-M1-F1
Method	BLASTX
NCBI GI	g2739008
BLAST score	647
E value	1.0e-67
Match length	178
% identity	73
NCBI Description	(AF022463) CYP78A3p [Glycine max]

Seq. No.	199118
Contig ID	51466_1.R1039

5'-most EST	LIB3196-036-P1-M1-C10
Method	BLASTX
NCBI GI	g128378
BLAST score	274
E value	4.0e-24
Match length	91
% identity	56
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi|82031|pir||S07142 nonspecific lipid transfer protein - castor bean >gi|224909|prf||1204170A protein,nonspecific lipid transfer [Ricinus communis]

Seq. No.	199119
Contig ID	51476_1.R1039
5'-most EST	LIB3196-041-P1-M1-B2
Method	BLASTX
NCBI GI	g2459421
BLAST score	452
E value	4.0e-45
Match length	118
% identity	69
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	199120
Contig ID	51485_1.R1039
5'-most EST	LIB3196-011-P1-M1-C3
Method	BLASTX
NCBI GI	g4104060
BLAST score	300
E value	6.0e-27
Match length	167
% identity	30
NCBI Description	(AF031231) S222 [Triticum aestivum]

Seq. No.	199121
Contig ID	51496_1.R1039
5'-most EST	LIB3196-049-P1-M1-B3
Method	BLASTX
NCBI GI	g476850
BLAST score	712
E value	1.0e-75
Match length	157
% identity	90
NCBI Description	heat shock cognate protein 70 - mouse >gi|309319 (M19141) heat shock protein 70 cognate [Mus musculus] >gi|1661134|gb|AAB18391.1| (U73744) heat shock 70 protein [Mus musculus]

Seq. No.	199122
Contig ID	51504_1.R1039
5'-most EST	LIB3196-057-P1-M1-D5
Method	BLASTX
NCBI GI	g996057
BLAST score	751
E value	6.0e-80

Match length 148
% identity 97
NCBI Description (X90872) associated to Golgi apparatus [Homo sapiens]

Seq. No. 199123
Contig ID 51505_1.R1039
5'-most EST LIB3196-011-P1-M1-E7
Method BLASTN
NCBI GI g662993
BLAST score 324
E value 0.0e+00
Match length 383
% identity 97
NCBI Description H.sapiens mRNA encoding GPI-anchored protein p137

Seq. No. 199124
Contig ID 51512_1.R1039
5'-most EST LIB3196-011-P1-M1-F4
Method BLASTX
NCBI GI g3287489
BLAST score 626
E value 2.0e-65
Match length 125
% identity 99
NCBI Description (AF028832) Hsp89-alpha-delta-N [Homo sapiens]

Seq. No. 199125
Contig ID 51518_1.R1039
5'-most EST LIB3196-050-P1-M1-B3
Method BLASTX
NCBI GI g4204277
BLAST score 522
E value 3.0e-53
Match length 110
% identity 81
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 199126
Contig ID 51525_1.R1039
5'-most EST LIB3196-011-P1-M1-G7

Seq. No. 199127
Contig ID 51530_1.R1039
5'-most EST LIB3196-011-P1-M1-H11
Method BLASTX
NCBI GI g2493130
BLAST score 702
E value 2.0e-74
Match length 139
% identity 99
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi|459200 (U07053) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No. 199128
Contig ID 51591_1.R1039
5'-most EST LIB3196-012-P1-M1-H6

Method	BLASTX
NCBI GI	g477138
BLAST score	315
E value	5.0e-43
Match length	104
% identity	92
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi|31591|emb|CAA31781| (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]

Seq. No.	199129
Contig ID	51592_1.R1039
5'-most EST	LIB3196-052-P1-M1-G11
Method	BLASTX
NCBI GI	g2145023
BLAST score	244
E value	2.0e-20
Match length	139
% identity	40
NCBI Description	(U97700) 15.5 kDa oleosin [Sesamum indicum]

Seq. No.	199130
Contig ID	51642_1.R1039
5'-most EST	g3326594

Seq. No.	199131
Contig ID	51661_1.R1039
5'-most EST	LIB3196-032-P1-M1-F12

Seq. No.	199132
Contig ID	51664_1.R1039
5'-most EST	LIB3196-043-P1-M1-F3
Method	BLASTN
NCBI GI	g3108245
BLAST score	156
E value	3.0e-82
Match length	219
% identity	93
NCBI Description	Gossypium barbadense clone pXP020 repetitive DNA sequence

Seq. No.	199133
Contig ID	51694_1.R1039
5'-most EST	LIB3196-059-P1-M1-H8
Method	BLASTX
NCBI GI	g3861068
BLAST score	176
E value	1.0e-12
Match length	60
% identity	50
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	199134
Contig ID	51701_1.R1039
5'-most EST	LIB3196-014-P1-M1-C3
Method	BLASTX
NCBI GI	g1806146
BLAST score	538

E value	3.0e-55
Match length	115
% identity	93
NCBI Description	(X97317) cdc2MsF [Medicago sativa]

Seq. No.	199135
Contig ID	51711_1.R1039
5'-most EST	LIB3196-014-P1-M1-D8

Seq. No.	199136
Contig ID	51715_1.R1039
5'-most EST	LIB3196-014-P1-M1-E11
Method	BLASTX
NCBI GI	g1170508
BLAST score	209
E value	8.0e-17
Match length	43
% identity	91
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi|2119931|pir||S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi|475219|emb|CAA55639| (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi|475221|emb|CAA55640| (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No.	199137
Contig ID	51730_1.R1039
5'-most EST	LIB3196-014-P1-M1-F9
Method	BLASTX
NCBI GI	g2497938
BLAST score	661
E value	1.0e-69
Match length	131
% identity	97
NCBI Description	AQUAPORIN 3 >gi|1854374|dbj|BAA19237| (AB001325) aquaporin 3 [Homo sapiens]

Seq. No.	199138
Contig ID	51739_1.R1039
5'-most EST	LIB3196-035-P1-M1-A2
Method	BLASTN
NCBI GI	g1854373
BLAST score	339
E value	0.0e+00
Match length	391
% identity	97
NCBI Description	Human AQP3 gene for aquaporine 3 (water channel), partail cds

Seq. No.	199139
Contig ID	51750_1.R1039
5'-most EST	LIB3196-020-P1-M1-G11
Method	BLASTX
NCBI GI	g1778143
BLAST score	430
E value	2.0e-75

Match length	174
% identity	84
NCBI Description	(U66401) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum]

Seq. No.	199140
Contig ID	51762_1.R1039
5'-most EST	LIB3196-015-P1-M1-B10
Method	BLASTN
NCBI GI	g1778142
BLAST score	100
E value	8.0e-49
Match length	414
% identity	83
NCBI Description	Nicotiana tabacum plastid phosphate/phosphoenolpyruvate translocator precursor (TABPPT8) mRNA, complete cds

Seq. No.	199141
Contig ID	51768_1.R1039
5'-most EST	LIB3196-015-P1-M1-B5
Method	BLASTX
NCBI GI	g3643595
BLAST score	304
E value	9.0e-28
Match length	110
% identity	54
NCBI Description	(AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No.	199142
Contig ID	51776_1.R1039
5'-most EST	g3325795

Seq. No.	199143
Contig ID	51777_1.R1039
5'-most EST	LIB3196-057-P1-M1-B5
Method	BLASTN
NCBI GI	g3319957
BLAST score	390
E value	0.0e+00
Match length	488
% identity	81
NCBI Description	Homo sapiens mRNA for VAKTI precursor

Seq. No.	199144
Contig ID	51778_1.R1039
5'-most EST	LIB3196-029-P1-M1-E8
Method	BLASTX
NCBI GI	g1304668
BLAST score	494
E value	5.0e-50
Match length	96
% identity	96
NCBI Description	(U42376) RIG-E precursor [Homo sapiens] >gi|1465747 (U56145) thymic shared antigen-1/stem cell antigen-2 [Homo sapiens] >gi|1519440 (U66711) 9804 [Homo sapiens] >gi|4454267|emb|CAA92321| (Z68179) retinoic acid induced gene E [Homo sapiens] >gi|4505049|ref|NP_002337.1|pLY6E|

lymphocyte antigen 6 complex, locus E

Seq. No.	199145
Contig ID	51787_1.R1039
5'-most EST	uC-gsronu33B019c05b1

Seq. No.	199146
Contig ID	51788_1.R1039
5'-most EST	LIB3196-034-P1-M1-H2
Method	BLASTX
NCBI GI	g1399325
BLAST score	565
E value	2.0e-58
Match length	131
% identity	80
NCBI Description	(U41832) MHC class I antigen Mamu A*07 [Macaca mulatta]

Seq. No.	199147
Contig ID	51793_1.R1039
5'-most EST	LIB3196-015-P1-M1-E12

Seq. No.	199148
Contig ID	51805_1.R1039
5'-most EST	g5047748
Method	BLASTX
NCBI GI	g2842494
BLAST score	588
E value	8.0e-61
Match length	152
% identity	74
NCBI Description	(AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi|4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi|4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No.	199149
Contig ID	51821_1.R1039
5'-most EST	LIB3196-015-P1-M1-G9
Method	BLASTX
NCBI GI	g133841
BLAST score	364
E value	1.0e-34
Match length	82
% identity	89
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi|71016|pir||R3NT18 ribosomal protein S18 - common tobacco chloroplast >gi|11851|emb|CAA77371| (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi|225220|prf||1211235BB ribosomal protein S18 [Nicotiana tabacum]

Seq. No.	199150
Contig ID	51845_2.R1039
5'-most EST	LIB3196-016-P1-M1-B1

Seq. No.	199151
Contig ID	51854_1.R1039
5'-most EST	uC-gsronu33B061f01b1
Method	BLASTX

NCBI GI	g3355311
BLAST score	263
E value	6.0e-23
Match length	59
% identity	88
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	199152
Contig ID	51858_1.R1039
5'-most EST	LIB3196-016-P1-M1-C12
Method	BLASTX
NCBI GI	g1001355
BLAST score	297
E value	6.0e-27
Match length	106
% identity	57
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	199153
Contig ID	51864_1.R1039
5'-most EST	LIB3196-029-P1-M1-D9
Method	BLASTX
NCBI GI	g266691
BLAST score	179
E value	4.0e-13
Match length	101
% identity	42
NCBI Description	OLEOSIN 16.4 KD >gi|167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	199154
Contig ID	51871_1.R1039
5'-most EST	LIB3196-016-P1-M1-D12
Method	BLASTX
NCBI GI	g3094014
BLAST score	153
E value	7.0e-10
Match length	41
% identity	73
NCBI Description	(AF060862) unknown [Homo sapiens]

Seq. No.	199155
Contig ID	51887_1.R1039
5'-most EST	LIB3196-016-P1-M1-G5
Method	BLASTX
NCBI GI	g1350762
BLAST score	389
E value	1.0e-37
Match length	96
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN C140) >gi|2136251|pir||I51803 TAXREB107 - human >gi|433416|dbj|BAA04491| (D17554) TAXREB107 [Homo sapiens]

Seq. No. 199156

Contig ID 51896_1.R1039
5'-most EST uC-gsflnu33B018c04b1

Seq. No. 199157
Contig ID 51913_1.R1039
5'-most EST LIB3196-017-P1-M1-F12

Seq. No. 199158
Contig ID 51929_1.R1039
5'-most EST LIB3196-027-P1-M1-A4
Method BLASTX
NCBI GI g547299
BLAST score 550
E value 1.0e-56
Match length 99
% identity 100
NCBI Description beta 2-microglobulin, beta 2-M [Papio hamadryas=baboons, 26CB-1, Peptide, 99 aa]

Seq. No. 199159
Contig ID 51972_1.R1039
5'-most EST LIB3196-032-P1-M1-E9
Method BLASTX
NCBI GI g2833280
BLAST score 701
E value 3.0e-74
Match length 142
% identity 93
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (COMPLEX I-39KD) (CI-39KD)

Seq. No. 199160
Contig ID 51977_1.R1039
5'-most EST LIB3272-055-P1-K1-B7
Method BLASTX
NCBI GI g3413706
BLAST score 255
E value 4.0e-36
Match length 122
% identity 64
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199161
Contig ID 51981_1.R1039
5'-most EST LIB3196-017-P1-M1-F7

Seq. No. 199162
Contig ID 51982_1.R1039
5'-most EST LIB3196-017-P1-M1-F8

Seq. No. 199163
Contig ID 51986_1.R1039
5'-most EST uC-gsflnu33B108h10b1

Seq. No. 199164
Contig ID 51989_1.R1039
5'-most EST LIB3197-031-Q1-M1-C4

Seq. No.	199165
Contig ID	51994_1.R1039
5'-most EST	LIB3197-033-Q1-M1-G1
Method	BLASTX
NCBI GI	g117501
BLAST score	624
E value	3.0e-65
Match length	115
% identity	100
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) >gi|87015|pir||A37047 calreticulin precursor - human >gi|179882 (M84739) calreticulin [Homo sapiens] >gi|337487 (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi|1905911 (AD000092) calreticulin [Homo sapiens]

Seq. No.	199166
Contig ID	51995_1.R1039
5'-most EST	LIB3196-017-P1-M1-H1
Method	BLASTX
NCBI GI	g224293
BLAST score	375
E value	3.0e-36
Match length	76
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	199167
Contig ID	52003_1.R1039
5'-most EST	LIB3272-020-P1-K1-G4
Method	BLASTX
NCBI GI	g3096931
BLAST score	180
E value	3.0e-13
Match length	62
% identity	55
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	199168
Contig ID	52012_1.R1039
5'-most EST	LIB3196-018-P1-M1-A6
Method	BLASTX
NCBI GI	g2244754
BLAST score	505
E value	3.0e-51
Match length	111
% identity	80
NCBI Description	(Z97335) heat shock transcription factor homolog [Arabidopsis thaliana]

Seq. No.	199169
Contig ID	52019_1.R1039
5'-most EST	g3326137
Method	BLASTX

NCBI GI g2224931
BLAST score 162
E value 1.0e-16
Match length 98
% identity 63
NCBI Description (AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No. 199170
Contig ID 52060_1.R1039
5'-most EST uC-gsflnu33B061a08b1

Seq. No. 199171
Contig ID 52090_1.R1039
5'-most EST LIB3196-019-P1-M1-A5

Seq. No. 199172
Contig ID 52118_1.R1039
5'-most EST LIB3196-059-P1-M1-A4

Seq. No. 199173
Contig ID 52121_1.R1039
5'-most EST LIB3196-019-P1-M1-D6

Seq. No. 199174
Contig ID 52157_1.R1039
5'-most EST LIB3196-019-P1-M1-G6
Method BLASTX
NCBI GI g2760839
BLAST score 162
E value 3.0e-20
Match length 120
% identity 40
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 199175
Contig ID 52171_1.R1039
5'-most EST uC-gsflnu33B089b10b1

Seq. No. 199176
Contig ID 52175_1.R1039
5'-most EST g3326432
Method BLASTN
NCBI GI g3241925
BLAST score 52
E value 4.0e-20
Match length 289
% identity 87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 199177
Contig ID 52175_2.R1039
5'-most EST LIB3196-036-P1-M1-C3
Method BLASTX
NCBI GI g4176522
BLAST score 255

E value	1.0e-21
Match length	224
% identity	28
NCBI Description	(AL035263) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	199178
Contig ID	52183_1.R1039
5'-most EST	LIB3196-044-P1-M1-F12
Method	BLASTX
NCBI GI	g116850
BLAST score	719
E value	3.0e-76
Match length	154
% identity	93
NCBI Description	COFILIN, NON-MUSCLE ISOFORM >gi|89176|pir||A29240 cofilin - pig >gi|164425 (M20866) cofilin [Sus scrofa]

Seq. No.	199179
Contig ID	52189_1.R1039
5'-most EST	LIB3196-020-P1-M1-B8
Method	BLASTX
NCBI GI	g125887
BLAST score	271
E value	6.0e-24
Match length	119
% identity	50
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi|82092|pir||S04765 LAT52 protein precursor - tomato >gi|295812|emb|CAA33854| (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	199180
Contig ID	52205_1.R1039
5'-most EST	g5048914
Method	BLASTX
NCBI GI	g2911047
BLAST score	407
E value	1.0e-39
Match length	113
% identity	71
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	199181
Contig ID	52283_1.R1039
5'-most EST	LIB3197-039-Q1-M1-H9
Method	BLASTX
NCBI GI	g207374
BLAST score	286
E value	1.0e-25
Match length	87
% identity	69
NCBI Description	(M15202) tropomyosin T class Ib beta-1 [Rattus norvegicus]

Seq. No.	199182
Contig ID	52285_1.R1039
5'-most EST	LIB3196-057-P1-M1-E10

Seq. No.	199183
Contig ID	52338_1.R1039
5'-most EST	LIB3196-021-P1-M1-H7
Method	BLASTX
NCBI GI	g126041
BLAST score	418
E value	2.0e-41
Match length	87
% identity	98
NCBI Description	L-LACTATE DEHYDROGENASE H CHAIN (LDH-B) >gi|1070432|pir||DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >gi|34329|emb|CAA68701| (Y00711) lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >gi|1200083|emb|CAA32033| (X13794) lactate dehydrogenase B [Homo sapiens] >gi|4557032|ref|NP_002291.1|pLDHB| lactate dehydrogenase B

Seq. No.	199184
Contig ID	52350_1.R1039
5'-most EST	LIB3196-052-P1-M1-E11

Seq. No.	199185
Contig ID	52351_1.R1039
5'-most EST	LIB3196-022-P1-M1-A8
Method	BLASTX
NCBI GI	g4467804
BLAST score	504
E value	4.0e-51
Match length	117
% identity	85
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	199186
Contig ID	52359_1.R1039
5'-most EST	LIB3197-022-Q1-M1-A7
Method	BLASTX
NCBI GI	g4539327
BLAST score	900
E value	3.0e-97
Match length	232
% identity	76
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	199187
Contig ID	52429_1.R1039
5'-most EST	LIB3196-057-P1-M1-G12

Seq. No.	199188
Contig ID	52435_1.R1039
5'-most EST	LIB3196-058-P1-M1-F11

Seq. No.	199189
Contig ID	52445_1.R1039
5'-most EST	LIB3196-023-P1-M1-B6
Method	BLASTN

NCBI GI	g178868
BLAST score	242
E value	1.0e-134
Match length	337
% identity	93
NCBI Description	Human acute phase serum amyloid A protein (SAA2.2) gene, exons 1 through 4

Seq. No.	199190
Contig ID	52456_1.R1039
5'-most EST	LIB3196-023-P1-M1-C4
Method	BLASTX
NCBI GI	g2654435
BLAST score	553
E value	1.0e-79
Match length	165
% identity	83
NCBI Description	(U68187) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	199191
Contig ID	52469_1.R1039
5'-most EST	uC-gsronu33B129g04b1
Method	BLASTX
NCBI GI	g4006893
BLAST score	619
E value	2.0e-87
Match length	206
% identity	78
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	199192
Contig ID	52470_1.R1039
5'-most EST	LIB3196-023-P1-M1-D9
Method	BLASTX
NCBI GI	g3941720
BLAST score	231
E value	5.0e-19
Match length	71
% identity	63
NCBI Description	(AF087021) tyrosyl-tRNA synthetase; tyrosine--tRNA ligase [Bos taurus]

Seq. No.	199193
Contig ID	52476_1.R1039
5'-most EST	LIB3196-047-P1-M1-B10
Method	BLASTX
NCBI GI	g266344
BLAST score	619
E value	1.0e-64
Match length	135
% identity	90
NCBI Description	LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) >gi|284073|pir||S27383 elastase inhibitor - human >gi|2997692 (AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens]

Seq. No.	199194

Contig ID	52516_1.R1039
5'-most EST	uC-gsflmaxxa061b02b1
Method	BLASTX
NCBI GI	g4455367
BLAST score	702
E value	4.0e-74
Match length	215
% identity	64
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	199195
Contig ID	52533_1.R1039
5'-most EST	LIB3196-024-P1-M1-C2
Method	BLASTX
NCBI GI	g1362047
BLAST score	213
E value	4.0e-17
Match length	74
% identity	62
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - soybean >gi|479060|emb|CAA83673| (Z32795) cysteine proteinase [Glycine max] >gi|1096153|prf||2111244A Cys protease [Glycine max]

Seq. No.	199196
Contig ID	52534_1.R1039
5'-most EST	g5050491
Method	BLASTX
NCBI GI	g2618686
BLAST score	648
E value	1.0e-67
Match length	289
% identity	49
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199197
Contig ID	52571_1.R1039
5'-most EST	g5049031
Method	BLASTX
NCBI GI	g1082798
BLAST score	381
E value	1.0e-36
Match length	183
% identity	43
NCBI Description	spliceosome-associated protein SAP 61 - human >gi|508723 (U08815) SAP 61 [Homo sapiens]

Seq. No.	199198
Contig ID	52579_1.R1039
5'-most EST	LIB3196-034-P1-M1-B7
Method	BLASTX
NCBI GI	g231723
BLAST score	478
E value	4.0e-48
Match length	90
% identity	100
NCBI Description	CD9 ANTIGEN (27 KD DIPHTHERIA TOXIN RECEPTOR-ASSOCIATED

PROTEIN) (DRAP27) >gi|104994|pir||A42929 CD9 antigen - green monkey >gi|218566|dbj|BAA01569| (D10726) diphtheria toxin receptor associated protein [Chlorocebus aethiops]

Seq. No. 199199
Contig ID 52592_1.R1039
5'-most EST LIB3196-024-P1-M1-H6

Seq. No. 199200
Contig ID 52598_1.R1039
5'-most EST LIB3196-033-P1-M1-B7

Seq. No. 199201
Contig ID 52600_1.R1039
5'-most EST LIB3196-025-P1-M1-A3
Method BLASTX
NCBI GI g440945
BLAST score 424
E value 8.0e-42
Match length 92
% identity 86
NCBI Description (S66773) adenosine deaminase, ADA {exon 10, exon 11} [human, ADA deficient patient AlNe, peripheral blood T cells, Peptide PartialMutant, 143 aa] [Homo sapiens]

Seq. No. 199202
Contig ID 52645_1.R1039
5'-most EST LIB3196-025-P1-M1-E8
Method BLASTX
NCBI GI g3821055
BLAST score 570
E value 6.0e-59
Match length 127
% identity 86
NCBI Description (AJ223603) hypothetical protein [Homo sapiens]

Seq. No. 199203
Contig ID 52663_1.R1039
5'-most EST LIB3196-052-P1-M1-D2
Method BLASTX
NCBI GI g730565
BLAST score 886
E value 8.0e-96
Match length 169
% identity 99
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi|423069|pir||S34195 ribosomal protein L3 - human >gi|313659|emb|CAA51839| (X73460) ribosomal protein L3 [Homo sapiens] >gi|3850177|emb|CAA18450| (AL022326) dJ333H23.1.1 (60S Ribosomal Protein L3) [Homo sapiens] >gi|4506649|ref|NP_000958.1|pRPL3| ribosomal protein L3

Seq. No. 199204
Contig ID 52666_1.R1039
5'-most EST LIB3196-025-P1-M1-H10

Seq. No. 199205

Contig ID	52673_1.R1039
5'-most EST	uC-gsflnu33B146h11b1

Seq. No.	199206
Contig ID	52677_1.R1039
5'-most EST	LIB3196-027-P1-M1-A1
Method	BLASTN
NCBI GI	g2599359
BLAST score	40
E value	4.0e-13
Match length	129
% identity	90
NCBI Description	Homo sapiens RNA helicase p68 (HUMP68) gene, complete cds

Seq. No.	199207
Contig ID	52729_1.R1039
5'-most EST	uC-gsflnu33B037c02b1
Method	BLASTX
NCBI GI	g1055130
BLAST score	289
E value	1.0e-25
Match length	167
% identity	38
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	199208
Contig ID	52736_1.R1039
5'-most EST	LIB3196-027-P1-M1-G11

Seq. No.	199209
Contig ID	52737_1.R1039
5'-most EST	LIB3196-027-P1-M1-G12
Method	BLASTX
NCBI GI	g119339
BLAST score	457
E value	1.0e-45
Match length	92
% identity	99
NCBI Description	ALPHA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE) >gi|87368|pir||A29170 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human >gi|182114 (M14328) alpha enolase (EC 4.2.1.11) [Homo sapiens] >gi|1167843|emb|CAA34360| (X16288) alpha-enolase [Homo sapiens] >gi|4503571|ref|NP_001419.1|pENO1| enolase 1, (alpha)

Seq. No.	199210
Contig ID	52745_1.R1039
5'-most EST	LIB3272-053-P1-K1-H4
Method	BLASTX
NCBI GI	g2924509
BLAST score	199
E value	2.0e-15

Match length	91
% identity	46
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	199211
Contig ID	52746_1.R1039
5'-most EST	LIB3197-039-Q1-M1-F6
Method	BLASTX
NCBI GI	g627406
BLAST score	606
E value	6.0e-63
Match length	159
% identity	3
NCBI Description	collagen alpha 1(VII) chain precursor - human

Seq. No.	199212
Contig ID	52766_1.R1039
5'-most EST	uC-gsflmaxxa088e09b1
Method	BLASTX
NCBI GI	g1619602
BLAST score	358
E value	4.0e-34
Match length	88
% identity	78
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	199213
Contig ID	52808_1.R1039
5'-most EST	uC-gsronu33B019h03b1
Method	BLASTX
NCBI GI	g2274859
BLAST score	391
E value	9.0e-38
Match length	73
% identity	96
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi|4510420|gb|AAD21506.1| (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	199214
Contig ID	52815_1.R1039
5'-most EST	LIB3196-028-P1-M1-F8

Seq. No.	199215
Contig ID	52819_1.R1039
5'-most EST	LIB3196-028-P1-M1-G11
Method	BLASTX
NCBI GI	g3892059
BLAST score	214
E value	7.0e-17
Match length	130
% identity	42
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 199216
Contig ID 52886_1.R1039
5'-most EST LIB3196-029-P1-M1-E10

Seq. No. 199217
Contig ID 52888_1.R1039
5'-most EST LIB3196-037-P1-M1-E7

Seq. No. 199218
Contig ID 52902_1.R1039
5'-most EST LIB3196-029-P1-M1-F3

Seq. No. 199219
Contig ID 52933_1.R1039
5'-most EST LIB3196-030-P1-M1-C8
Method BLASTX
NCBI GI g2213558
BLAST score 195
E value 4.0e-15
Match length 96
% identity 44
NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 199220
Contig ID 53083_1.R1039
5'-most EST LIB3196-031-P1-M1-G2
Method BLASTX
NCBI GI g1336807
BLAST score 337
E value 1.0e-31
Match length 119
% identity 58
NCBI Description (S81193) CEN=GTP-binding protein homolog
[Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
>gi|1587482|prf||2206476A CEN gene [Antirrhinum sp.]

Seq. No. 199221
Contig ID 53090_1.R1039
5'-most EST LIB3196-032-P1-M1-D8

Seq. No. 199222
Contig ID 53115_1.R1039
5'-most EST LIB3196-032-P1-M1-B6
Method BLASTX
NCBI GI g4406801
BLAST score 138
E value 5.0e-11
Match length 70
% identity 59
NCBI Description (AC006304) unknown protein [Arabidopsis thaliana]

Seq. No. 199223
Contig ID 53117_1.R1039
5'-most EST g3326168

Seq. No. 199224
Contig ID 53131_1.R1039

5'-most EST	LIB3196-032-P1-M1-D12
Method	BLASTX
NCBI GI	g730922
BLAST score	218
E value	2.0e-42
Match length	121
% identity	83
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (TCP20) (HTR3) >gi|627402|pir||S48087 chaperonin TCP20 - human >gi|517065 (L27706) chaperonin-like protein [Homo sapiens] >gi|4502643|ref|NP_001753.1|pCCT6| chaperonin containing T-complex subunit

Seq. No.	199225
Contig ID	53138_1.R1039
5'-most EST	LIB3196-032-P1-M1-D7
Method	BLASTX
NCBI GI	g4220474
BLAST score	1003
E value	1.0e-109
Match length	262
% identity	77
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	199226
Contig ID	53143_1.R1039
5'-most EST	LIB3196-041-P1-M1-A2

Seq. No.	199227
Contig ID	53172_1.R1039
5'-most EST	LIB3196-032-P1-M1-G9
Method	BLASTX
NCBI GI	g662366
BLAST score	332
E value	5.0e-31
Match length	107
% identity	58
NCBI Description	(L39786) conglutin gamma [Lupinus angustifolius] >gi|666056|emb|CAA46552| (X65601) conglutin gamma [Lupinus angustifolius]

Seq. No.	199228
Contig ID	53177_1.R1039
5'-most EST	LIB3196-042-P1-M1-F7
Method	BLASTX
NCBI GI	g1304227
BLAST score	548
E value	3.0e-56
Match length	116
% identity	84
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi|2764804|emb|CAA55293| (X78547) epoxide hydrolase [Glycine max]

Seq. No.	199229
Contig ID	53181_1.R1039

5'-most EST	LIB3196-033-P1-M1-A8
Seq. No.	199230
Contig ID	53189_1.R1039
5'-most EST	LIB3197-033-Q1-M1-G5
Method	BLASTX
NCBI GI	g4539335
BLAST score	535
E value	9.0e-55
Match length	151
% identity	66
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	199231
Contig ID	53217_1.R1039
5'-most EST	LIB3196-033-P1-M1-D12
Seq. No.	199232
Contig ID	53243_1.R1039
5'-most EST	g5045294
Method	BLASTX
NCBI GI	g3128225
BLAST score	223
E value	5.0e-18
Match length	66
% identity	70
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.	199233
Contig ID	53267_1.R1039
5'-most EST	LIB3196-034-P1-M1-A11
Method	BLASTX
NCBI GI	g4467804
BLAST score	701
E value	5.0e-74
Match length	143
% identity	95
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]
Seq. No.	199234
Contig ID	53274_1.R1039
5'-most EST	LIB3196-034-P1-M1-A7
Method	BLASTX
NCBI GI	g1147813
BLAST score	555
E value	5.0e-57
Match length	163
% identity	72
NCBI Description	(M77830) desmoplakin I [Homo sapiens]
Seq. No.	199235
Contig ID	53298_1.R1039
5'-most EST	LIB3196-043-P1-M1-C2
Seq. No.	199236

Contig ID	53335_1.R1039
5'-most EST	LIB3197-016-P1-M1-C4
Method	BLASTN
NCBI GI	g2795921
BLAST score	198
E value	1.0e-107
Match length	221
% identity	97
NCBI Description	Homo sapiens clone 23954 mRNA sequence

Seq. No.	199237
Contig ID	53373_1.R1039
5'-most EST	LIB3196-044-P1-M1-D3
Method	BLASTX
NCBI GI	g2654435
BLAST score	412
E value	2.0e-40
Match length	98
% identity	82
NCBI Description	(U68187) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	199238
Contig ID	53411_1.R1039
5'-most EST	LIB3196-035-P1-M1-G3

Seq. No.	199239
Contig ID	53420_1.R1039
5'-most EST	LIB3196-035-P1-M1-H11

Seq. No.	199240
Contig ID	53448_1.R1039
5'-most EST	LIB3196-036-P1-M1-B8
Method	BLASTX
NCBI GI	g3212868
BLAST score	705
E value	1.0e-74
Match length	153
% identity	83
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	199241
Contig ID	53485_1.R1039
5'-most EST	LIB3197-041-Q1-M1-D3

Seq. No.	199242
Contig ID	53497_1.R1039
5'-most EST	LIB3196-036-P1-M1-H10

Seq. No.	199243
Contig ID	53529_1.R1039
5'-most EST	LIB3196-037-P1-M1-C2

Seq. No.	199244
Contig ID	53573_1.R1039
5'-most EST	LIB3196-037-P1-M1-G3
Method	BLASTX
NCBI GI	g399184

BLAST score	281
E value	1.0e-24
Match length	54
% identity	100
NCBI Description	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1 (CAP 1) >gi|477116|pir||A48120 adenylyl cyclase-associated CAP protein homolog - human >gi|178084 (L12168) adenylyl cyclase-associated protein [Homo sapiens] >gi|179920 (M98474) CAP protein [Homo sapiens]

Seq. No.	199245
Contig ID	53578_1.R1039
5'-most EST	LIB3196-037-P1-M1-G8
Method	BLASTX
NCBI GI	g2500587
BLAST score	599
E value	2.0e-62
Match length	117
% identity	66
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53) >gi|1082799|pir||A54964 spliceosome-associated protein SAP-49 - human >gi|556217 (L35013) spliceosomal protein [Homo sapiens]

Seq. No.	199246
Contig ID	53603_1.R1039
5'-most EST	LIB3197-054-Q1-M1-G3

Seq. No.	199247
Contig ID	53608_1.R1039
5'-most EST	LIB3196-059-P1-M1-C1
Method	BLASTN
NCBI GI	g833885
BLAST score	365
E value	0.0e+00
Match length	460
% identity	95
NCBI Description	CD24=glycosyl phosphatidylinositol (GPI)-linked glycoprotein [human, monochromosomal somatic cell hybrids, mRNA, 1659 nt]

Seq. No.	199248
Contig ID	53613_1.R1039
5'-most EST	LIB3196-038-P1-M1-C6
Method	BLASTN
NCBI GI	g188683
BLAST score	321
E value	0.0e+00
Match length	377
% identity	96
NCBI Description	Human modulator recognition factor I (MRF-1) mRNA, 3' end

Seq. No.	199249
Contig ID	53622_1.R1039
5'-most EST	LIB3196-038-P1-M1-D5
Method	BLASTX
NCBI GI	g2529678

BLAST score	185
E value	8.0e-14
Match length	75
% identity	55
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	199250
Contig ID	53634_1.R1039
5'-most EST	uC-gsflmaxxa039e02b1

Seq. No.	199251
Contig ID	53657_1.R1039
5'-most EST	LIB3196-038-P1-M1-G8
Method	BLASTX
NCBI GI	g2582665
BLAST score	433
E value	8.0e-43
Match length	95
% identity	88
NCBI Description	(Z82983) thi [Citrus sinensis]

Seq. No.	199252
Contig ID	53659_1.R1039
5'-most EST	uC-gsflmaxxa098f02b1

Seq. No.	199253
Contig ID	53665_1.R1039
5'-most EST	LIB3196-038-P1-M1-H5
Method	BLASTX
NCBI GI	g119172
BLAST score	854
E value	4.0e-92
Match length	164
% identity	99
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi|2144947|pir||EFHU2 translation elongation factor eEF-2 - human >gi|31106|emb|CAA35829| (X51466) elongation factor 2 [Homo sapiens] >gi|31108|emb|CAA77750| (Z11692) human elongation factor 2 [Homo sapiens] >gi|4503483|ref|NP_001952.1|pEEF2| eukaryotic translation elongation factor

Seq. No.	199254
Contig ID	53674_1.R1039
5'-most EST	LIB3196-039-P1-M1-A5
Method	BLASTN
NCBI GI	g31105
BLAST score	423
E value	0.0e+00
Match length	495
% identity	96
NCBI Description	Human mRNA for elongation factor 2 >gi|4503482|ref|NM_001961.1|EEF2| Homo sapiens eukaryotic translation elongation factor 2 (EEF2) mRNA

Seq. No.	199255
Contig ID	53688_1.R1039
5'-most EST	LIB3196-039-P1-M1-B9

Method	BLASTX
NCBI GI	g129697
BLAST score	470
E value	4.0e-64
Match length	157
% identity	77
NCBI Description	PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN) >gi|100698|pir||S14415 proliferating cell nuclear antigen - rice >gi|20284|emb|CAA37979| (X54046) proliferating cell nuclear antigen [Oryza sativa]

Seq. No.	199256
Contig ID	53700_1.R1039
5'-most EST	LIB3196-039-P1-M1-D1
Method	BLASTX
NCBI GI	g2134892
BLAST score	472
E value	2.0e-47
Match length	92
% identity	100
NCBI Description	cell surface glycoprotein - human >gi|188256 (M60334) cell surface glycoprotein [Homo sapiens] >gi|1834460|emb|CAB06609| (Z84814) HLA-DRA*0102 [Homo sapiens]

Seq. No.	199257
Contig ID	53701_1.R1039
5'-most EST	g5049901
Method	BLASTX
NCBI GI	g2191127
BLAST score	475
E value	1.0e-47
Match length	101
% identity	89
NCBI Description	(AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]

Seq. No.	199258
Contig ID	53715_1.R1039
5'-most EST	LIB3196-039-P1-M1-E2

Seq. No.	199259
Contig ID	53716_1.R1039
5'-most EST	LIB3196-064-P1-M1-B6

Seq. No.	199260
Contig ID	53746_1.R1039
5'-most EST	LIB3196-047-P1-M1-A4
Method	BLASTX
NCBI GI	g3121828
BLAST score	705
E value	1.0e-74
Match length	147
% identity	91
NCBI Description	BENE PROTEIN >gi|2135423|pir||I38891 hypothetical protein - human (fragment) >gi|1000712 (U17077) unknown [Homo sapiens]

Seq. No.	199261
Contig ID	53772_1.R1039
5'-most EST	LIB3196-040-P1-M1-C2
Method	BLASTX
NCBI GI	g544939
BLAST score	469
E value	4.0e-47
Match length	138
% identity	70
NCBI Description	(S68736) myosin heavy chain, MHC [rats, CCl4-cirrhotic liver fat-storing cell line, Peptide, 882 aa] [Rattus sp.]

Seq. No.	199262
Contig ID	53786_1.R1039
5'-most EST	uC-gsflnu33B113f04b1
Method	BLASTX
NCBI GI	g2911060
BLAST score	377
E value	8.0e-36
Match length	182
% identity	36
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi|3297826|emb|CAA19884.1| (AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	199263
Contig ID	53806_1.R1039
5'-most EST	LIB3196-059-P1-M1-A1
Method	BLASTN
NCBI GI	g3184183
BLAST score	382
E value	0.0e+00
Match length	454
% identity	96
NCBI Description	Homo sapiens mRNA for airway trypsin-like protease, complete cds

Seq. No.	199264
Contig ID	53820_1.R1039
5'-most EST	LIB3196-064-P1-M1-F11
Method	BLASTX
NCBI GI	g567767
BLAST score	703
E value	2.0e-74
Match length	140
% identity	46
NCBI Description	(L13783) p125 protein [Bovine viral diarrhea virus]

Seq. No.	199265
Contig ID	53842_1.R1039
5'-most EST	LIB3197-022-Q1-M1-E7

Seq. No.	199266
Contig ID	53850_1.R1039
5'-most EST	LIB3196-041-P1-M1-B7
Method	BLASTX
NCBI GI	g3127127

BLAST score	410
E value	3.0e-40
Match length	101
% identity	85
NCBI Description	(AF061016) UDP-glucose dehydrogenase [Homo sapiens] >gi|3452405|emb|CAA07609| (AJ007702) UDPglucose dehydrogenase [Homo sapiens] >gi|4507813|ref|NP_003350.1|pUGDH| UDP-glucose dehydrogenase

Seq. No.	199267
Contig ID	53853_1.R1039
5'-most EST	uC-gsflnu33B019h08b1
Method	BLASTX
NCBI GI	g2832661
BLAST score	151
E value	2.0e-17
Match length	113
% identity	43
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	199268
Contig ID	53876_1.R1039
5'-most EST	LIB3197-003-P1-M1-G10
Method	BLASTX
NCBI GI	g4467153
BLAST score	950
E value	1.0e-103
Match length	235
% identity	74
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	199269
Contig ID	53881_1.R1039
5'-most EST	LIB3196-059-P1-M1-B5

Seq. No.	199270
Contig ID	53882_1.R1039
5'-most EST	g5050720

Seq. No.	199271
Contig ID	53895_1.R1039
5'-most EST	LIB3196-046-P1-M1-F3
Method	BLASTX
NCBI GI	g2804273
BLAST score	775
E value	6.0e-83
Match length	149
% identity	38
NCBI Description	(D89980) alpha actinin 4 [Homo sapiens]

Seq. No.	199272
Contig ID	53944_1.R1039
5'-most EST	LIB3196-042-P1-M1-D3

Seq. No.	199273
Contig ID	54015_1.R1039
5'-most EST	uC-gsflmaxxa001c10b1
Method	BLASTX
NCBI GI	g2507222
BLAST score	460
E value	5.0e-46
Match length	125
% identity	66
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi|1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	199274
Contig ID	54018_1.R1039
5'-most EST	LIB3196-043-P1-M1-D1
Method	BLASTX
NCBI GI	g4490295
BLAST score	178
E value	8.0e-13
Match length	136
% identity	30
NCBI Description	(AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199275
Contig ID	54047_1.R1039
5'-most EST	LIB3196-045-P1-M1-G7
Method	BLASTX
NCBI GI	g4432855
BLAST score	752
E value	4.0e-80
Match length	166
% identity	89
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	199276
Contig ID	54053_1.R1039
5'-most EST	uC-gsronu33B050h06b1
Method	BLASTX
NCBI GI	g3249066
BLAST score	358
E value	6.0e-34
Match length	171
% identity	50
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb|984964. ESTs gb|F15433 and gb|AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No.	199277
Contig ID	54107_1.R1039
5'-most EST	LIB3196-044-P1-M1-F9
Method	BLASTX
NCBI GI	g1707017
BLAST score	336
E value	3.0e-31
Match length	80
% identity	80

NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 199278
Contig ID 54135_1.R1039
5'-most EST uC-gsflnu33B070c03b1

Seq. No. 199279
Contig ID 54162_1.R1039
5'-most EST g5049389
Method BLASTX
NCBI GI g4191793
BLAST score 479
E value 5.0e-73
Match length 243
% identity 61
NCBI Description (AC005917) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 199280
Contig ID 54206_1.R1039
5'-most EST LIB3196-046-P1-M1-A9
Method BLASTX
NCBI GI g4455335
BLAST score 409
E value 4.0e-40
Match length 118
% identity 69
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 199281
Contig ID 54274_1.R1039
5'-most EST LIB3196-047-P1-M1-A8

Seq. No. 199282
Contig ID 54281_1.R1039
5'-most EST LIB3196-047-P1-M1-B6

Seq. No. 199283
Contig ID 54295_1.R1039
5'-most EST LIB3196-049-P1-M1-E1
Method BLASTX
NCBI GI g3108075
BLAST score 210
E value 2.0e-16
Match length 113
% identity 42
NCBI Description (AF060797) putative beta-ureidopropionase [Manduca sexta]

Seq. No. 199284
Contig ID 54302_1.R1039
5'-most EST LIB3196-047-P1-M1-D8
Method BLASTX
NCBI GI g2270990
BLAST score 177
E value 6.0e-13
Match length 123
% identity 38

NCBI Description (AF004807) dehydrin [Glycine max]

Seq. No. 199285
Contig ID 54332_1.R1039
5'-most EST LIB3196-047-P1-M1-H4
Method BLASTX
NCBI GI g1688233
BLAST score 192
E value 1.0e-14
Match length 94
% identity 52
NCBI Description (U77655) DNA binding protein homolog [Solanum tuberosum]

Seq. No. 199286
Contig ID 54358_1.R1039
5'-most EST LIB3196-048-P1-M1-C12
Method BLASTX
NCBI GI g3913425
BLAST score 210
E value 1.0e-45
Match length 121
% identity 85
NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi|2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 199287
Contig ID 54362_1.R1039
5'-most EST LIB3196-048-P1-M1-C6
Method BLASTX
NCBI GI g4158219
BLAST score 643
E value 3.0e-67
Match length 176
% identity 69
NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 199288
Contig ID 54368_1.R1039
5'-most EST LIB3196-048-P1-M1-D2

Seq. No. 199289
Contig ID 54390_1.R1039
5'-most EST uC-gsronu33B103c10b1

Seq. No. 199290
Contig ID 54428_1.R1039
5'-most EST uC-gsflmaxxa027e08b1
Method BLASTX
NCBI GI g3641837
BLAST score 459
E value 6.0e-46
Match length 122
% identity 80
NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	199291
Contig ID	54430_1.R1039
5'-most EST	uC-gsronu33B080d05b1
Method	BLASTX
NCBI GI	g3860333
BLAST score	431
E value	2.0e-42
Match length	102
% identity	72
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	199292
Contig ID	54498_1.R1039
5'-most EST	uC-gsronu33B040f12b1

Seq. No.	199293
Contig ID	54501_1.R1039
5'-most EST	LIB3196-049-P1-M1-H6
Method	BLASTX
NCBI GI	g3329386
BLAST score	602
E value	1.0e-62
Match length	117
% identity	96
NCBI Description	(AF038958) synaptic glycoprotein SC2 spliced variant [Homo sapiens]

Seq. No.	199294
Contig ID	54533_1.R1039
5'-most EST	g3325926
Method	BLASTX
NCBI GI	g1086833
BLAST score	168
E value	4.0e-15
Match length	137
% identity	33
NCBI Description	(U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No.	199295
Contig ID	54549_1.R1039
5'-most EST	LIB3196-050-P1-M1-E12
Method	BLASTX
NCBI GI	g4006924
BLAST score	257
E value	4.0e-22
Match length	110
% identity	43
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	199296
Contig ID	54553_1.R1039
5'-most EST	LIB3196-050-P1-M1-E5

Seq. No.	199297

Contig ID	54563_1.R1039
5'-most EST	uC-gsflnu33B109e10b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	407
E value	1.0e-39
Match length	166
% identity	59
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	199298
Contig ID	54569_1.R1039
5'-most EST	LIB3196-050-P1-M1-G10

Seq. No.	199299
Contig ID	54663_1.R1039
5'-most EST	g5045813
Method	BLASTX
NCBI GI	g4469019
BLAST score	421
E value	2.0e-60
Match length	132
% identity	92
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	199300
Contig ID	54670_1.R1039
5'-most EST	LIB3196-057-P1-M1-G1
Method	BLASTX
NCBI GI	g3283166
BLAST score	299
E value	4.0e-27
Match length	112
% identity	54
NCBI Description	(AF057526) erythrocyte membrane protein Rh50 [Mus musculus] >gi|3329467 (AF065395) Rh50-like protein [Mus musculus] >gi|3445508|dbj|BAA32441| (AB015192) 50 kD glycoprotein (Rh50) [Mus musculus]

Seq. No.	199301
Contig ID	54671_1.R1039
5'-most EST	LIB3196-053-P1-M1-B7
Method	BLASTX
NCBI GI	g1381394
BLAST score	648
E value	4.0e-68
Match length	139
% identity	89
NCBI Description	(U40989) tat interactive protein [Homo sapiens]

Seq. No.	199302
Contig ID	54680_1.R1039
5'-most EST	LIB3196-053-P1-M1-B9
Method	BLASTN
NCBI GI	g1125005
BLAST score	386
E value	0.0e+00

Match length	418
% identity	98
NCBI Description	Human tat interactive protein mRNA, complete cds

Seq. No.	199303
Contig ID	54762_1.R1039
5'-most EST	LIB3197-054-Q1-M1-H3
Method	BLASTX
NCBI GI	g2921213
BLAST score	467
E value	1.0e-46
Match length	124
% identity	73
NCBI Description	(AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla frutescens]

Seq. No.	199304
Contig ID	54829_1.R1039
5'-most EST	uC-gsronu33B108g10b1

Seq. No.	199305
Contig ID	54848_1.R1039
5'-most EST	LIB3196-055-P1-M1-C2

Seq. No.	199306
Contig ID	54851_1.R1039
5'-most EST	LIB3196-055-P1-M1-C6

Seq. No.	199307
Contig ID	54886_1.R1039
5'-most EST	LIB3196-055-P1-M1-G10
Method	BLASTX
NCBI GI	g3643607
BLAST score	574
E value	2.0e-59
Match length	129
% identity	42
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	199308
Contig ID	54955_1.R1039
5'-most EST	LIB3196-056-P1-M1-G10
Method	BLASTX
NCBI GI	g2088662
BLAST score	211
E value	1.0e-16
Match length	102
% identity	48
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	199309
Contig ID	54957_1.R1039
5'-most EST	LIB3196-056-P1-M1-G12
Method	BLASTX
NCBI GI	g2507222
BLAST score	144
E value	4.0e-09

Match length	60
% identity	45
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi|1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	199310
Contig ID	54971_1.R1039
5'-most EST	LIB3196-057-P1-M1-A1

Seq. No.	199311
Contig ID	54983_1.R1039
5'-most EST	LIB3196-057-P1-M1-B9
Method	BLASTN
NCBI GI	g3452378
BLAST score	315
E value	1.0e-177
Match length	407
% identity	95
NCBI Description	Homo sapiens glutamate oxaloacetate transaminase (GOT1) gene, exon 9 and complete cds

Seq. No.	199312
Contig ID	55021_1.R1039
5'-most EST	LIB3196-057-P1-M1-E9
Method	BLASTX
NCBI GI	g1083762
BLAST score	305
E value	7.0e-28
Match length	98
% identity	64
NCBI Description	prolactin-induced T cell protein c15 - rat >gi|619907|emb|CAA57825| (X82445) RnudC [Rattus norvegicus]

Seq. No.	199313
Contig ID	55073_1.R1039
5'-most EST	g5045311
Method	BLASTX
NCBI GI	g2980790
BLAST score	174
E value	3.0e-12
Match length	109
% identity	48
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199314
Contig ID	55176_1.R1039
5'-most EST	g3326405
Method	BLASTX
NCBI GI	g2129727
BLAST score	151
E value	8.0e-13
Match length	121
% identity	45
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi|1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 199315
Contig ID 55267_1.R1039
5'-most EST LIB3196-064-P1-M1-E10

Seq. No. 199316
Contig ID 55339_1.R1039
5'-most EST uC-gsflnu33B027g08b1
Method BLASTX
NCBI GI g3219935
BLAST score 368
E value 4.0e-47
Match length 143
% identity 64
NCBI Description PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C57A10.03 >gi|2058370|emb|CAB08166| (Z94864) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq. No. 199317
Contig ID 55350_1.R1039
5'-most EST LIB3272-007-P1-K1-G2

Seq. No. 199318
Contig ID 55379_1.R1039
5'-most EST LIB3272-045-P1-K1-B6
Method BLASTN
NCBI GI g1163180
BLAST score 34
E value 2.0e-09
Match length 57
% identity 91
NCBI Description Glycine max arginine decarboxylase mRNA, complete cds

Seq. No. 199319
Contig ID 55402_1.R1039
5'-most EST LIB3197-001-P1-M1-E2

Seq. No. 199320
Contig ID 55406_1.R1039
5'-most EST LIB3197-022-Q1-M1-F6

Seq. No. 199321
Contig ID 55425_1.R1039
5'-most EST LIB3197-001-P1-M1-G9
Method BLASTX
NCBI GI g2191150
BLAST score 221
E value 7.0e-18
Match length 67
% identity 79
NCBI Description (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No. 199322
Contig ID 55427_1.R1039
5'-most EST LIB3197-001-P1-M1-H12

Seq. No. 199323

Contig ID	55431_1.R1039
5'-most EST	LIB3197-001-P1-M1-H9
Method	BLASTX
NCBI GI	g2231312
BLAST score	830
E value	4.0e-89
Match length	176
% identity	90
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	199324
Contig ID	55442_1.R1039
5'-most EST	LIB3272-031-P1-K1-D5
Method	BLASTX
NCBI GI	g600178
BLAST score	643
E value	2.0e-67
Match length	141
% identity	83
NCBI Description	(L27074) acetyl-CoA carboxylase [Arabidopsis thaliana] >gi|1090217|prf||2018327A Ac-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	199325
Contig ID	55461_1.R1039
5'-most EST	g5047984
Method	BLASTN
NCBI GI	g3985934
BLAST score	37
E value	3.0e-11
Match length	101
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	199326
Contig ID	55461_2.R1039
5'-most EST	LIB3197-002-P1-M1-D12
Method	BLASTN
NCBI GI	g3985934
BLAST score	50
E value	1.0e-18
Match length	464
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	199327
Contig ID	55462_1.R1039
5'-most EST	LIB3197-002-P1-M1-D2
Method	BLASTX
NCBI GI	g1688074
BLAST score	229
E value	1.0e-18
Match length	138
% identity	40
NCBI Description	(U46570) tetratricopeptide repeat protein [Homo sapiens]

>gi|4507711|ref|NP_003305.1|pTTC1| tetratricopeptide repeat domain

Seq. No.	199328
Contig ID	55533_1.R1039
5'-most EST	LIB3197-003-P1-M1-F6
Method	BLASTN
NCBI GI	g3702732
BLAST score	35
E value	8.0e-10
Match length	94
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	199329
Contig ID	55538_1.R1039
5'-most EST	LIB3197-003-P1-M1-G4
Method	BLASTX
NCBI GI	g3298555
BLAST score	253
E value	9.0e-22
Match length	54
% identity	85
NCBI Description	(AC004681) putative homeobox protein, 3' partial [Arabidopsis thaliana]

Seq. No.	199330
Contig ID	55540_1.R1039
5'-most EST	LIB3197-003-P1-M1-H10
Method	BLASTX
NCBI GI	g4510348
BLAST score	362
E value	3.0e-34
Match length	123
% identity	61
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	199331
Contig ID	55541_1.R1039
5'-most EST	g5048137
Method	BLASTX
NCBI GI	g2827139
BLAST score	1436
E value	1.0e-160
Match length	297
% identity	91
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi|4049343|emb|CAA22568| (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	199332
Contig ID	55579_1.R1039
5'-most EST	g5046738
Method	BLASTX
NCBI GI	g2982456

BLAST score 454
E value 3.0e-58
Match length 142
% identity 82
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 199333
Contig ID 55594_1.R1039
5'-most EST LIB3197-004-P1-M1-G7
Method BLASTX
NCBI GI g2642429
BLAST score 307
E value 4.0e-28
Match length 134
% identity 53
NCBI Description (AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 199334
Contig ID 55606_1.R1039
5'-most EST LIB3197-005-P1-M1-A2
Method BLASTX
NCBI GI g1351856
BLAST score 466
E value 6.0e-47
Match length 108
% identity 86
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi|868003|dbj|BAA06108| (D29629) aconitase [Cucurbita sp.]

Seq. No. 199335
Contig ID 55636_1.R1039
5'-most EST LIB3197-005-P1-M1-D12
Method BLASTX
NCBI GI g2292917
BLAST score 563
E value 2.0e-58
Match length 156
% identity 75
NCBI Description (X99851) galactokinase [Arabidopsis thaliana]

Seq. No. 199336
Contig ID 55648_1.R1039
5'-most EST LIB3197-005-P1-M1-E5
Method BLASTX
NCBI GI g2088662
BLAST score 186
E value 1.0e-27
Match length 196
% identity 42
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 199337
Contig ID 55654_1.R1039
5'-most EST uC-gsflmaxxa060h01b1

Seq. No.	199338
Contig ID	55663_1.R1039
5'-most EST	uC-gsflmaxxa041c04b1

Seq. No.	199339
Contig ID	55665_1.R1039
5'-most EST	LIB3197-005-P1-M1-G5
Method	BLASTX
NCBI GI	g4138171
BLAST score	153
E value	6.0e-10
Match length	66
% identity	52
NCBI Description	(AJ011955) allergen [Malassezia furfur]

Seq. No.	199340
Contig ID	55677_1.R1039
5'-most EST	LIB3197-005-P1-M1-H9

Seq. No.	199341
Contig ID	55678_1.R1039
5'-most EST	LIB3197-006-P1-M1-A1
Method	BLASTX
NCBI GI	g3080435
BLAST score	243
E value	1.0e-20
Match length	56
% identity	75
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	199342
Contig ID	55691_1.R1039
5'-most EST	uC-gsflmaxxa042d04b1
Method	BLASTX
NCBI GI	g480602
BLAST score	192
E value	2.0e-14
Match length	49
% identity	67
NCBI Description	polyadenylate-binding protein - fern (Anemia phyllitidis) >gi|398327|emb|CAA81127| (Z26042) poly(A)-mRNA binding protein [Anemia phyllitidis]

Seq. No.	199343
Contig ID	55698_1.R1039
5'-most EST	LIB3197-006-P1-M1-C1
Method	BLASTX
NCBI GI	g549060
BLAST score	376
E value	3.0e-36
Match length	95
% identity	78
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi|631656|pir||S43058 CCTeta protein eta chain - mouse >gi|468504|emb|CAA83274| (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	199344
Contig ID	55700_1.R1039
5'-most EST	LIB3197-006-P1-M1-C11
Method	BLASTX
NCBI GI	g3881780
BLAST score	173
E value	2.0e-12
Match length	116
% identity	38
NCBI Description	(Z48638) similar to lipid transfer protein [Caenorhabditis elegans]

Seq. No.	199345
Contig ID	55702_1.R1039
5'-most EST	LIB3197-006-P1-M1-C2
Method	BLASTX
NCBI GI	g4186184
BLAST score	248
E value	3.0e-21
Match length	120
% identity	43
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	199346
Contig ID	55712_1.R1039
5'-most EST	LIB3197-006-P1-M1-D5
Method	BLASTX
NCBI GI	g4468979
BLAST score	439
E value	2.0e-43
Match length	112
% identity	72
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	199347
Contig ID	55717_1.R1039
5'-most EST	LIB3197-006-P1-M1-E3
Method	BLASTX
NCBI GI	g3540185
BLAST score	421
E value	3.0e-41
Match length	129
% identity	61
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	199348
Contig ID	55722_1.R1039
5'-most EST	LIB3197-006-P1-M1-F7
Method	BLASTX
NCBI GI	g3892056
BLAST score	559
E value	3.0e-57
Match length	126
% identity	87
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 199349
Contig ID 55745_1.R1039
5'-most EST uC-gsronu33B058g06b1

Seq. No. 199350
Contig ID 55753_1.R1039
5'-most EST LIB3197-007-P1-M1-F4
Method BLASTX
NCBI GI g3873710
BLAST score 346
E value 2.0e-32
Match length 110
% identity 56
NCBI Description (Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No. 199351
Contig ID 55771_1.R1039
5'-most EST g5048652
Method BLASTX
NCBI GI g2244765
BLAST score 386
E value 4.0e-37
Match length 187
% identity 45
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199352
Contig ID 55781_1.R1039
5'-most EST LIB3197-008-P1-M1-B6
Method BLASTX
NCBI GI g1213460
BLAST score 143
E value 8.0e-09
Match length 110
% identity 32
NCBI Description (U03374) C subunit of V-ATPase [Amblyomma americanum]

Seq. No. 199353
Contig ID 55795_1.R1039
5'-most EST uC-gsronu33B001g05b1

Seq. No. 199354
Contig ID 55796_1.R1039
5'-most EST LIB3197-008-P1-M1-D1
Method BLASTX
NCBI GI g2344894
BLAST score 441
E value 8.0e-44
Match length 135
% identity 63
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199355

Contig ID	55799_1.R1039
5'-most EST	g5046682
Method	BLASTX
NCBI GI	g3337356
BLAST score	864
E value	3.0e-93
Match length	181
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	199356
Contig ID	55805_1.R1039
5'-most EST	LIB3197-008-P1-M1-D7
Method	BLASTX
NCBI GI	g3695388
BLAST score	209
E value	2.0e-16
Match length	62
% identity	60
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	199357
Contig ID	55825_1.R1039
5'-most EST	g5048926
Method	BLASTX
NCBI GI	g3881189
BLAST score	567
E value	2.0e-58
Match length	157
% identity	67
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	199358
Contig ID	55827_1.R1039
5'-most EST	LIB3197-008-P1-M1-G3
Method	BLASTX
NCBI GI	g1706652
BLAST score	385
E value	6.0e-37
Match length	114
% identity	63
NCBI Description	ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi|498862 (U09736) enolase [Entamoeba histolytica]

Seq. No.	199359
Contig ID	55834_1.R1039
5'-most EST	LIB3197-047-Q1-M1-D12

Seq. No.	199360
Contig ID	55837_1.R1039
5'-most EST	uC-gsflmaxxa040e08b1

Seq. No. 199361
Contig ID 55837_3.R1039
5'-most EST LIB3197-008-P1-M1-H3

Seq. No. 199362
Contig ID 55854_1.R1039
5'-most EST LIB3272-017-P1-K1-H2
Method BLASTX
NCBI GI g3800951
BLAST score 195
E value 5.0e-15
Match length 86
% identity 44
NCBI Description (AF100657) No definition line found [Caenorhabditis elegans]

Seq. No. 199363
Contig ID 55856_1.R1039
5'-most EST LIB3197-010-P1-M1-B12

Seq. No. 199364
Contig ID 55863_1.R1039
5'-most EST LIB3197-010-P1-M1-C10

Seq. No. 199365
Contig ID 55885_1.R1039
5'-most EST LIB3197-010-P1-M1-E3
Method BLASTX
NCBI GI g4098128
BLAST score 393
E value 3.0e-38
Match length 91
% identity 85
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 199366
Contig ID 55886_1.R1039
5'-most EST LIB3197-010-P1-M1-E4
Method BLASTX
NCBI GI g3273200
BLAST score 517
E value 2.0e-52
Match length 157
% identity 69
NCBI Description (AB010917) responce reactor3 [Arabidopsis thaliana] >gi|3894192 (AC005662) response regulator 3 [Arabidopsis thaliana]

Seq. No. 199367
Contig ID 55893_1.R1039
5'-most EST g5044904
Method BLASTX
NCBI GI g3395938
BLAST score 513
E value 7.0e-52
Match length 194
% identity 57

NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]
Seq. No.	199368
Contig ID	55904_1.R1039
5'-most EST	uC-gsflmaxxa067g04b1
Seq. No.	199369
Contig ID	55919_1.R1039
5'-most EST	g5050668
Method	BLASTX
NCBI GI	g2500717
BLAST score	483
E value	2.0e-48
Match length	137
% identity	62
NCBI Description	STS14 PROTEIN PRECURSOR >gi|2129995|pir||S65052 pistil-specific protein sts14 precursor - potato >gi|1236785|emb|CAA57976| (X82652) sts14 [Solanum tuberosum] >gi|1589691|prf||2211417A sts14 gene [Solanum tuberosum]
Seq. No.	199370
Contig ID	55922_1.R1039
5'-most EST	g5047025
Method	BLASTX
NCBI GI	g2252841
BLAST score	353
E value	3.0e-33
Match length	148
% identity	49
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.	199371
Contig ID	55933_1.R1039
5'-most EST	uC-gsronu33B157d04b1
Seq. No.	199372
Contig ID	55934_1.R1039
5'-most EST	LIB3272-037-P1-K1-B4
Method	BLASTX
NCBI GI	g1586940
BLAST score	433
E value	9.0e-43
Match length	122
% identity	69
NCBI Description	Ser/Thr kinase [Lycopersicon esculentum]
Seq. No.	199373
Contig ID	55935_1.R1039
5'-most EST	LIB3197-011-P1-M1-C7
Method	BLASTX
NCBI GI	g2245000
BLAST score	344
E value	2.0e-32
Match length	91
% identity	77

NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	199374
Contig ID	55941_1.R1039
5'-most EST	LIB3197-011-P1-M1-D7
Method	BLASTX
NCBI GI	g266862
BLAST score	292
E value	4.0e-26
Match length	145
% identity	27
NCBI Description	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (PYRIMIDINE-BINDING PROTEIN) (PYBP)
Seq. No.	199375
Contig ID	55996_1.R1039
5'-most EST	g5046786
Method	BLASTX
NCBI GI	g3925363
BLAST score	655
E value	1.0e-68
Match length	169
% identity	75
NCBI Description	(AF067961) homeodomain protein [Malus domestica]
Seq. No.	199376
Contig ID	56003_1.R1039
5'-most EST	LIB3197-051-Q1-M1-G10
Method	BLASTX
NCBI GI	g1495273
BLAST score	545
E value	8.0e-56
Match length	124
% identity	84
NCBI Description	(Z50752) sugar transporter [Arabidopsis thaliana]
Seq. No.	199377
Contig ID	56005_1.R1039
5'-most EST	uC-gsflnu33B133h11b1
Seq. No.	199378
Contig ID	56016_1.R1039
5'-most EST	uC-gsflmaxxa098h08b1
Method	BLASTX
NCBI GI	g629602
BLAST score	409
E value	7.0e-40
Match length	100
% identity	76
NCBI Description	probable imbibition protein - wild cabbage >gi|488787|emb|CAA55893| (X79330) putative imbibition protein [Brassica oleracea]
Seq. No.	199379
Contig ID	56047_1.R1039
5'-most EST	g3325966

Seq. No.	199380
Contig ID	56050_1.R1039
5'-most EST	LIB3197-013-P1-M1-G1
Method	BLASTX
NCBI GI	g2244866
BLAST score	410
E value	1.0e-63
Match length	193
% identity	58
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199381
Contig ID	56051_1.R1039
5'-most EST	LIB3197-013-P1-M1-G10

Seq. No.	199382
Contig ID	56057_1.R1039
5'-most EST	g5044763
Method	BLASTX
NCBI GI	g2853081
BLAST score	530
E value	7.0e-54
Match length	126
% identity	79
NCBI Description	(AL021768) ATP binding protein - like [Arabidopsis thaliana]

Seq. No.	199383
Contig ID	56059_1.R1039
5'-most EST	LIB3197-013-P1-M1-H4
Method	BLASTX
NCBI GI	g1076318
BLAST score	470
E value	8.0e-47
Match length	176
% identity	35
NCBI Description	dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - Arabidopsis thaliana (fragment) >gi|559395|emb|CAA86300| (Z46230) dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis thaliana]

Seq. No.	199384
Contig ID	56064_1.R1039
5'-most EST	LIB3197-014-P1-M1-A3
Method	BLASTX
NCBI GI	g3176874
BLAST score	402
E value	4.0e-39
Match length	130
% identity	61
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	199385
Contig ID	56074_1.R1039

5'-most EST	LIB3197-014-P1-M1-C12
Method	BLASTX
NCBI GI	g4103952
BLAST score	294
E value	2.0e-26
Match length	91
% identity	65
NCBI Description	(AF029980) A37 [Arabidopsis thaliana] >gi|4103954 (AF029981) A37 [Arabidopsis thaliana]

Seq. No.	199386
Contig ID	56100_1.R1039
5'-most EST	uC-gsflmaxxa091a08b1

Seq. No.	199387
Contig ID	56139_1.R1039
5'-most EST	LIB3197-015-P1-M1-E5

Seq. No.	199388
Contig ID	56147_1.R1039
5'-most EST	LIB3197-015-P1-M1-F5

Seq. No.	199389
Contig ID	56153_1.R1039
5'-most EST	LIB3197-024-Q1-M1-E3
Method	BLASTX
NCBI GI	g1419390
BLAST score	345
E value	4.0e-40
Match length	131
% identity	61
NCBI Description	(X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	199390
Contig ID	56159_1.R1039
5'-most EST	g5045660

Seq. No.	199391
Contig ID	56159_2.R1039
5'-most EST	LIB3197-015-P1-M1-H1
Method	BLASTX
NCBI GI	g2829911
BLAST score	239
E value	1.0e-33
Match length	119
% identity	29
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	199392
Contig ID	56217_1.R1039
5'-most EST	g5046702
Method	BLASTX
NCBI GI	g2244850
BLAST score	576
E value	3.0e-59
Match length	187

% identity	65
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	199393
Contig ID	56245_1.R1039
5'-most EST	uC-gsronu33B137g12b1
Seq. No.	199394
Contig ID	56246_1.R1039
5'-most EST	LIB3197-019-Q1-M1-A5
Seq. No.	199395
Contig ID	56265_1.R1039
5'-most EST	LIB3197-024-Q1-M1-G10
Seq. No.	199396
Contig ID	56290_1.R1039
5'-most EST	g5050731
Method	BLASTX
NCBI GI	g4314378
BLAST score	334
E value	2.0e-32
Match length	176
% identity	47
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.	199397
Contig ID	56301_1.R1039
5'-most EST	LIB3197-019-Q1-M1-F5
Method	BLASTX
NCBI GI	g4521249
BLAST score	603
E value	2.0e-62
Match length	181
% identity	67
NCBI Description	(AB013912) DNA helicase [Mus musculus]
Seq. No.	199398
Contig ID	56315_1.R1039
5'-most EST	LIB3197-057-Q1-M1-C3
Method	BLASTX
NCBI GI	g3892051
BLAST score	227
E value	3.0e-28
Match length	82
% identity	79
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]
Seq. No.	199399
Contig ID	56334_1.R1039
5'-most EST	LIB3197-020-Q1-M1-B5
Method	BLASTX
NCBI GI	g3063710
BLAST score	295
E value	2.0e-26
Match length	69

% identity	74
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	199400
Contig ID	56340_1.R1039
5'-most EST	uC-gsflmaxxa061c09b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	502
E value	2.0e-57
Match length	233
% identity	39
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	199401
Contig ID	56344_1.R1039
5'-most EST	uC-gsflmaxxa091e02b1
Method	BLASTN
NCBI GI	g4321400
BLAST score	42
E value	5.0e-14
Match length	137
% identity	86
NCBI Description	Helianthus annuus LIM domain protein PLIM-2 mRNA, complete cds

Seq. No.	199402
Contig ID	56354_1.R1039
5'-most EST	LIB3197-020-Q1-M1-F5
Method	BLASTX
NCBI GI	g3695059
BLAST score	496
E value	3.0e-50
Match length	151
% identity	66
NCBI Description	(AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No.	199403
Contig ID	56356_1.R1039
5'-most EST	LIB3197-020-Q1-M1-G11

Seq. No.	199404
Contig ID	56392_1.R1039
5'-most EST	LIB3197-021-Q1-M1-B8

Seq. No.	199405
Contig ID	56412_1.R1039
5'-most EST	uC-gsronu33B139a03b1
Method	BLASTX
NCBI GI	g4469005
BLAST score	252
E value	1.0e-22
Match length	127
% identity	46
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199406
Contig ID	56440_1.R1039
5'-most EST	g5044545
Method	BLASTX
NCBI GI	g3122638
BLAST score	274
E value	2.0e-27
Match length	154
% identity	47
NCBI Description	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 >gi|1076381|pir||S49820 PRL1 protein - Arabidopsis thaliana >gi|577733|emb|CAA58031| (X82824) PRL1 [Arabidopsis thaliana] >gi|577735|emb|CAA58032| (X82825) PRL1 [Arabidopsis thaliana] >gi|2244947|emb|CAB10369.1| (Z97339) PRL1 protein - Arabidopsis thaliana

Seq. No.	199407
Contig ID	56447_1.R1039
5'-most EST	uC-gsronu33B166b09b2
Method	BLASTX
NCBI GI	g2979559
BLAST score	232
E value	6.0e-19
Match length	63
% identity	68
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	199408
Contig ID	56452_1.R1039
5'-most EST	uC-gsflmaxxa029c10b1
Method	BLASTX
NCBI GI	g309557
BLAST score	550
E value	2.0e-56
Match length	119
% identity	91
NCBI Description	(L21007) chaperonin 60 [Zea mays]

Seq. No.	199409
Contig ID	56460_1.R1039
5'-most EST	LIB3197-022-Q1-M1-A1

Seq. No.	199410
Contig ID	56472_1.R1039
5'-most EST	LIB3272-008-P1-K1-G5

Seq. No.	199411
Contig ID	56495_1.R1039
5'-most EST	uC-gsronu33B076g05b1
Method	BLASTX
NCBI GI	g2257756
BLAST score	145
E value	5.0e-09
Match length	91
% identity	46

NCBI Description	(U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi|3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No.	199412
Contig ID	56497_1.R1039
5'-most EST	LIB3197-022-Q1-M1-D9
Method	BLASTX
NCBI GI	g3482979
BLAST score	411
E value	5.0e-40
Match length	119
% identity	62
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi|4567258|gb|AAD23672.1|AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199413
Contig ID	56499_1.R1039
5'-most EST	LIB3197-022-Q1-M1-E12
Method	BLASTX
NCBI GI	g1351856
BLAST score	1046
E value	1.0e-114
Match length	216
% identity	91
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi|868003|dbj|BAA06108| (D29629) aconitase [Cucurbita sp.]

Seq. No.	199414
Contig ID	56501_1.R1039
5'-most EST	LIB3197-022-Q1-M1-E3
Method	BLASTX
NCBI GI	g2924509
BLAST score	340
E value	8.0e-32
Match length	131
% identity	52
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	199415
Contig ID	56513_1.R1039
5'-most EST	LIB3197-022-Q1-M1-F5

Seq. No.	199416
Contig ID	56517_1.R1039
5'-most EST	g5049421
Method	BLASTX
NCBI GI	g2827552
BLAST score	618
E value	2.0e-64
Match length	159
% identity	47
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	199417
Contig ID	56518_1.R1039
5'-most EST	g5050252
Method	BLASTX
NCBI GI	g2706455
BLAST score	397
E value	2.0e-38
Match length	148
% identity	48
NCBI Description	(AL021046) probable involvement in transcription initiation [Schizosaccharomyces pombe]

Seq. No.	199418
Contig ID	56523_1.R1039
5'-most EST	LIB3197-022-Q1-M1-G5
Method	BLASTX
NCBI GI	g3249098
BLAST score	360
E value	7.0e-34
Match length	176
% identity	52
NCBI Description	(AC003114) ESTs gb|T04610, gb|N38459, gb|T45174, gb|R30481 and gb|N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	199419
Contig ID	56549_1.R1039
5'-most EST	g3326641
Method	BLASTX
NCBI GI	g4220537
BLAST score	402
E value	6.0e-39
Match length	158
% identity	50
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	199420
Contig ID	56559_1.R1039
5'-most EST	g5044339
Method	BLASTX
NCBI GI	g3420801
BLAST score	828
E value	8.0e-89
Match length	247
% identity	66
NCBI Description	(AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]

Seq. No.	199421
Contig ID	56566_1.R1039
5'-most EST	LIB3197-035-Q1-M1-E4

Seq. No.	199422
Contig ID	56588_1.R1039
5'-most EST	LIB3197-024-Q1-M1-A4
Method	BLASTX
NCBI GI	g4454479
BLAST score	176

E value	1.0e-12
Match length	40
% identity	82
NCBI Description	(AC006234) putative riboflavin synthase alpha chain [Arabidopsis thaliana]

Seq. No.	199423
Contig ID	56593_1.R1039
5'-most EST	g5045597

Seq. No.	199424
Contig ID	56607_1.R1039
5'-most EST	g5049789
Method	BLASTX
NCBI GI	g4512686
BLAST score	292
E value	7.0e-26
Match length	69
% identity	77
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi|4559326|gb|AAD22988.1|AC007087_7 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199425
Contig ID	56619_1.R1039
5'-most EST	g5048033
Method	BLASTX
NCBI GI	g4455309
BLAST score	487
E value	6.0e-49
Match length	139
% identity	69
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199426
Contig ID	56636_1.R1039
5'-most EST	LIB3272-021-P1-K1-G8
Method	BLASTX
NCBI GI	g3953471
BLAST score	346
E value	1.0e-32
Match length	115
% identity	62
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	199427
Contig ID	56641_1.R1039
5'-most EST	g5050231
Method	BLASTX
NCBI GI	g3122152
BLAST score	217
E value	3.0e-17
Match length	124
% identity	37
NCBI Description	GLUCOSE INHIBITED DIVISION PROTEIN B >gi|629285|pir||S48581 hypothetical protein - Mycoplasma capricolum (SGC3) (fragment) >gi|950065|emb|CAA83698| (Z33013)

methyltransferases [Mycoplasma capricolum]

Seq. No.	199428
Contig ID	56643_1.R1039
5'-most EST	LIB3197-024-Q1-M1-H11
Method	BLASTX
NCBI GI	g1708191
BLAST score	341
E value	5.0e-32
Match length	108
% identity	61
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi|467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	199429
Contig ID	56646_1.R1039
5'-most EST	uC-gsflmaxxa067g09b1
Method	BLASTX
NCBI GI	g2388710
BLAST score	521
E value	5.0e-53
Match length	144
% identity	69
NCBI Description	(AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	199430
Contig ID	56693_1.R1039
5'-most EST	LIB3197-026-Q1-M1-B10
Method	BLASTX
NCBI GI	g2290528
BLAST score	557
E value	4.0e-57
Match length	182
% identity	54
NCBI Description	(U94746) ATAN11 [Arabidopsis thaliana]

Seq. No.	199431
Contig ID	56721_1.R1039
5'-most EST	uC-gsronu33B004f05b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	291
E value	7.0e-26
Match length	152
% identity	44
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	199432
Contig ID	56734_1.R1039
5'-most EST	LIB3272-008-P1-K1-C7

Seq. No.	199433
Contig ID	56734_2.R1039
5'-most EST	LIB3272-028-P1-K1-H8

Seq. No.	199434

Contig ID 56744_1.R1039
5'-most EST uC-gsflnu33B137a02b1

Seq. No. 199435
Contig ID 56770_1.R1039
5'-most EST LIB3197-027-Q1-M1-A4

Seq. No. 199436
Contig ID 56772_1.R1039
5'-most EST LIB3197-027-Q1-M1-A6
Method BLASTX
NCBI GI g1174470
BLAST score 316
E value 4.0e-29
Match length 88
% identity 61
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi|508543 (L34260) integral membrane protein 1 [Mus musculus] >gi|1588285|prf||2208301A integral membrane protein [Mus musculus]

Seq. No. 199437
Contig ID 56778_1.R1039
5'-most EST LIB3197-027-Q1-M1-B12
Method BLASTX
NCBI GI g2558655
BLAST score 516
E value 3.0e-52
Match length 241
% identity 48
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 199438
Contig ID 56784_1.R1039
5'-most EST LIB3272-019-P1-K1-B2

Seq. No. 199439
Contig ID 56796_1.R1039
5'-most EST LIB3197-027-Q1-M1-D10
Method BLASTX
NCBI GI g3608137
BLAST score 285
E value 2.0e-25
Match length 145
% identity 43
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 199440
Contig ID 56801_1.R1039
5'-most EST LIB3197-027-Q1-M1-D4
Method BLASTX
NCBI GI g3660467
BLAST score 394
E value 3.0e-38
Match length 115
% identity 69
NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis

thaliana]

Seq. No.	199441
Contig ID	56804_1.R1039
5'-most EST	uC-gsflnu33B082c02b1
Method	BLASTX
NCBI GI	g1399273
BLAST score	337
E value	2.0e-31
Match length	138
% identity	53
NCBI Description	(U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi|3080419|emb|CAA18738| (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No.	199442
Contig ID	56807_1.R1039
5'-most EST	LIB3197-027-Q1-M1-E10
Method	BLASTX
NCBI GI	g3738324
BLAST score	325
E value	5.0e-30
Match length	124
% identity	50
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	199443
Contig ID	56814_1.R1039
5'-most EST	LIB3197-027-Q1-M1-E6
Method	BLASTX
NCBI GI	g3337356
BLAST score	587
E value	7.0e-61
Match length	119
% identity	97
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	199444
Contig ID	56840_1.R1039
5'-most EST	g5049654
Method	BLASTX
NCBI GI	g1477468
BLAST score	392
E value	1.0e-37
Match length	186
% identity	45
NCBI Description	(U35244) vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]

Seq. No.	199445
Contig ID	56848_1.R1039
5'-most EST	uC-gsflmaxxa040e04b1
Method	BLASTX
NCBI GI	g3157943
BLAST score	381

E value	9.0e-37
Match length	117
% identity	60
NCBI Description	(AC002131) Contains similarity to BAP31 protein gb|X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	199446
Contig ID	56909_1.R1039
5'-most EST	LIB3197-028-Q1-M1-G3
Method	BLASTX
NCBI GI	g1041706
BLAST score	844
E value	8.0e-91
Match length	172
% identity	86
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	199447
Contig ID	56943_1.R1039
5'-most EST	LIB3197-029-Q1-M1-B8
Method	BLASTX
NCBI GI	g4309681
BLAST score	380
E value	2.0e-36
Match length	142
% identity	52
NCBI Description	(AC006930) R33423_1 [Homo sapiens]

Seq. No.	199448
Contig ID	56953_1.R1039
5'-most EST	LIB3197-029-Q1-M1-C7
Method	BLASTX
NCBI GI	g3337350
BLAST score	1146
E value	1.0e-126
Match length	243
% identity	89
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	199449
Contig ID	56957_1.R1039
5'-most EST	LIB3197-029-Q1-M1-D11
Method	BLASTX
NCBI GI	g3860263
BLAST score	330
E value	9.0e-31
Match length	85
% identity	68
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	199450
Contig ID	56959_1.R1039
5'-most EST	g5048312
Method	BLASTX
NCBI GI	g2497543
BLAST score	446

E value	4.0e-44
Match length	99
% identity	81
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|542061|pir||S41379 pyruvate kinase - common tobacco >gi|444023|emb|CAA82628| (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	199451
Contig ID	56964_1.R1039
5'-most EST	LIB3197-029-Q1-M1-D9
Method	BLASTN
NCBI GI	g2244901
BLAST score	37
E value	3.0e-11
Match length	152
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	199452
Contig ID	56965_1.R1039
5'-most EST	LIB3197-029-Q1-M1-E3

Seq. No.	199453
Contig ID	56998_1.R1039
5'-most EST	LIB3197-029-Q1-M1-H1
Method	BLASTX
NCBI GI	g4406789
BLAST score	453
E value	4.0e-45
Match length	111
% identity	79
NCBI Description	(AC006532) putative glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	199454
Contig ID	57000_1.R1039
5'-most EST	g5045076

Seq. No.	199455
Contig ID	57034_1.R1039
5'-most EST	LIB3197-030-Q1-M1-C3

Seq. No.	199456
Contig ID	57043_1.R1039
5'-most EST	LIB3197-030-Q1-M1-D4
Method	BLASTN
NCBI GI	g2656032
BLAST score	36
E value	1.0e-10
Match length	165
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	199457
Contig ID	57061_1.R1039

5'-most EST	LIB3197-030-Q1-M1-G4
Method	BLASTX
NCBI GI	g1174470
BLAST score	261
E value	5.0e-31
Match length	121
% identity	59
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi|508543 (L34260) integral membrane protein 1 [Mus musculus] >gi|1588285|prf||2208301A integral membrane protein [Mus musculus]

Seq. No.	199458
Contig ID	57100_1.R1039
5'-most EST	LIB3272-029-P1-K1-D10
Method	BLASTX
NCBI GI	g3377813
BLAST score	413
E value	3.0e-40
Match length	157
% identity	54
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.	199459
Contig ID	57100_2.R1039
5'-most EST	LIB3272-029-P1-K1-D12
Method	BLASTX
NCBI GI	g3377813
BLAST score	499
E value	5.0e-54
Match length	222
% identity	55
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.	199460
Contig ID	57107_1.R1039
5'-most EST	uC-gsronu33B162c12b2
Method	BLASTX
NCBI GI	g3885343
BLAST score	244
E value	3.0e-20
Match length	192
% identity	44
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199461
Contig ID	57128_1.R1039
5'-most EST	LIB3197-031-Q1-M1-H1
Method	BLASTX
NCBI GI	g2462744
BLAST score	434
E value	1.0e-42
Match length	184
% identity	49
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 199462

Contig ID 57154_1.R1039
5'-most EST uC-gsflnu33B026c08b1
Method BLASTX
NCBI GI g4544399
BLAST score 675
E value 4.0e-71
Match length 156
% identity 85
NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 199463
Contig ID 57158_1.R1039
5'-most EST uC-gsflnu33B062b01b1
Method BLASTX
NCBI GI g2499535
BLAST score 356
E value 2.0e-37
Match length 107
% identity 66
NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi|595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]

Seq. No. 199464
Contig ID 57174_1.R1039
5'-most EST g5045814
Method BLASTX
NCBI GI g3873837
BLAST score 174
E value 3.0e-12
Match length 102
% identity 35
NCBI Description (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com

Seq. No. 199465
Contig ID 57179_1.R1039
5'-most EST LIB3197-033-Q1-M1-E5

Seq. No. 199466
Contig ID 57182_1.R1039
5'-most EST LIB3197-060-Q1-M1-B7
Method BLASTX
NCBI GI g1245343
BLAST score 261
E value 2.0e-22
Match length 92
% identity 54
NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 199467
Contig ID 57223_1.R1039
5'-most EST LIB3197-034-Q1-M1-B11
Method BLASTX

NCBI GI g3395432
BLAST score 172
E value 3.0e-12
Match length 74
% identity 53
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 199468
Contig ID 57230_1.R1039
5'-most EST LIB3197-034-Q1-M1-B8
Method BLASTX
NCBI GI g3047111
BLAST score 362
E value 3.0e-34
Match length 93
% identity 60
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 199469
Contig ID 57275_1.R1039
5'-most EST g5048296
Method BLASTX
NCBI GI g4467116
BLAST score 279
E value 2.0e-24
Match length 143
% identity 46
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199470
Contig ID 57295_1.R1039
5'-most EST LIB3197-035-Q1-M1-A2
Method BLASTX
NCBI GI g4567312
BLAST score 167
E value 1.0e-11
Match length 72
% identity 44
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199471
Contig ID 57297_1.R1039
5'-most EST uC-gsflmaxxa069e07b1
Method BLASTX
NCBI GI g2129753
BLAST score 381
E value 1.0e-36
Match length 95
% identity 67
NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi|1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No. 199472
Contig ID 57304_1.R1039
5'-most EST g5046178
Method BLASTX

NCBI GI	g113742
BLAST score	463
E value	4.0e-46
Match length	205
% identity	46
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi|147142 (M15273) peptidase N [Escherichia coli] >gi|147144 (M15676) aminopeptidase N [Escherichia coli] >gi|1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi|4062498|dbj|BAA35684| (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	199473
Contig ID	57338_2.R1039
5'-most EST	LIB3197-041-Q1-M1-C3

Seq. No.	199474
Contig ID	57339_1.R1039
5'-most EST	LIB3197-035-Q1-M1-E2

Seq. No.	199475
Contig ID	57342_1.R1039
5'-most EST	LIB3197-035-Q1-M1-E5

Seq. No.	199476
Contig ID	57381_1.R1039
5'-most EST	uC-gsflmaxxa088d09b1
Method	BLASTX
NCBI GI	g479413
BLAST score	219
E value	4.0e-18
Match length	94
% identity	50
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	199477
Contig ID	57386_1.R1039
5'-most EST	LIB3197-044-Q1-M1-E9
Method	BLASTX
NCBI GI	g1174718
BLAST score	144
E value	7.0e-11
Match length	130
% identity	39
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi|322579|pir||JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi|166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	199478
Contig ID	57397_1.R1039
5'-most EST	g5049281
Method	BLASTX
NCBI GI	g2789660
BLAST score	738
E value	2.0e-78

Match length	194
% identity	74
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	199479
Contig ID	57407_1.R1039
5'-most EST	LIB3272-024-P1-K1-E4

Seq. No.	199480
Contig ID	57421_1.R1039
5'-most EST	LIB3272-041-P1-K1-E4
Method	BLASTX
NCBI GI	g3880602
BLAST score	228
E value	3.0e-18
Match length	236
% identity	24
NCBI Description	(Z82080) cDNA EST EMBL:D66071 comes from this gene; cDNA EST yk274a10.3 comes from this gene; cDNA EST yk289f12.3 comes from this gene; cDNA EST yk289f12.5 comes from this gene; cDNA EST yk274a10.5 comes from this gene; cDNA ES

Seq. No.	199481
Contig ID	57434_1.R1039
5'-most EST	LIB3197-039-Q1-M1-C12
Method	BLASTX
NCBI GI	g4490308
BLAST score	622
E value	1.0e-64
Match length	159
% identity	79
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	199482
Contig ID	57436_2.R1039
5'-most EST	LIB3197-039-Q1-M1-C3
Method	BLASTX
NCBI GI	g2827537
BLAST score	421
E value	2.0e-41
Match length	120
% identity	68
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	199483
Contig ID	57462_1.R1039
5'-most EST	LIB3197-039-Q1-M1-G11
Method	BLASTX
NCBI GI	g3914996
BLAST score	206
E value	3.0e-16
Match length	45
% identity	87
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi|1665831|dbj|BAA13640| (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]

	>gi|2804260|dbj|BAA24441| (AB010408) phosphoserine aminotransferase [Arabidopsis thaliana] >gi|3367581|emb|CAA20033| (AL031135) phosphoserine aminotransferase [Arabidopsis thaliana]
Seq. No.	199484
Contig ID	57483_1.R1039
5'-most EST	LIB3197-040-Q1-M1-B5
Method	BLASTX
NCBI GI	g4204695
BLAST score	423
E value	1.0e-41
Match length	152
% identity	59
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]
Seq. No.	199485
Contig ID	57484_1.R1039
5'-most EST	uC-gsronu33B047c12b1
Seq. No.	199486
Contig ID	57498_1.R1039
5'-most EST	LIB3272-014-P1-K1-D5
Method	BLASTX
NCBI GI	g4103324
BLAST score	589
E value	5.0e-61
Match length	129
% identity	89
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]
Seq. No.	199487
Contig ID	57505_1.R1039
5'-most EST	g5048135
Seq. No.	199488
Contig ID	57532_1.R1039
5'-most EST	g3326268
Method	BLASTX
NCBI GI	g2827529
BLAST score	258
E value	5.0e-22
Match length	122
% identity	45
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]
Seq. No.	199489
Contig ID	57548_1.R1039
5'-most EST	uC-gsronu33B019f10b1
Seq. No.	199490
Contig ID	57550_1.R1039
5'-most EST	LIB3197-040-Q1-M1-H6
Method	BLASTX
NCBI GI	g3451075

BLAST score 370
E value 2.0e-35
Match length 103
% identity 64
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 199491
Contig ID 57551_1.R1039
5'-most EST uC-gsflmaxxa040h05b1
Method BLASTX
NCBI GI g4309726
BLAST score 117
E value 3.0e-11
Match length 92
% identity 52
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199492
Contig ID 57551_2.R1039
5'-most EST uC-gsflnu33B093g06b1
Method BLASTX
NCBI GI g2347198
BLAST score 368
E value 4.0e-35
Match length 86
% identity 80
NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199493
Contig ID 57589_1.R1039
5'-most EST LIB3197-041-Q1-M1-D4
Method BLASTX
NCBI GI g1785622
BLAST score 349
E value 1.0e-32
Match length 101
% identity 68
NCBI Description (Z84202) ORFc [Arabidopsis thaliana]

Seq. No. 199494
Contig ID 57593_1.R1039
5'-most EST LIB3197-041-Q1-M1-D8
Method BLASTX
NCBI GI g3122386
BLAST score 512
E value 3.0e-52
Match length 113
% identity 83
NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi|2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]

Seq. No. 199495
Contig ID 57604_1.R1039
5'-most EST LIB3197-041-Q1-M1-E7

Seq. No. 199496
Contig ID 57613_1.R1039

5'-most EST	LIB3197-053-Q1-M1-F8
Seq. No.	199497
Contig ID	57615_1.R1039
5'-most EST	LIB3197-041-Q1-M1-F8
Method	BLASTX
NCBI GI	g2275210
BLAST score	188
E value	4.0e-14
Match length	97
% identity	44
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
Seq. No.	199498
Contig ID	57624_1.R1039
5'-most EST	LIB3272-001-P1-K1-F7
Method	BLASTX
NCBI GI	g1652434
BLAST score	177
E value	8.0e-13
Match length	51
% identity	65
NCBI Description	(D90905) N-acetylglutamate kinase [Synechocystis sp.]
Seq. No.	199499
Contig ID	57632_1.R1039
5'-most EST	LIB3197-041-Q1-M1-H2
Method	BLASTX
NCBI GI	g2749939
BLAST score	525
E value	3.0e-53
Match length	204
% identity	56
NCBI Description	(U70999) CCS1 [Chlamydomonas reinhardtii] >gi|2749941 (U71000) CCS1 [Chlamydomonas reinhardtii]
Seq. No.	199500
Contig ID	57655_1.R1039
5'-most EST	g5048368
Seq. No.	199501
Contig ID	57666_1.R1039
5'-most EST	g5044312
Method	BLASTX
NCBI GI	g2623300
BLAST score	419
E value	1.0e-40
Match length	302
% identity	50
NCBI Description	(AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	199502
Contig ID	57671_1.R1039
5'-most EST	LIB3197-043-Q1-M1-A4

Seq. No.	199503
Contig ID	57685_1.R1039
5'-most EST	g3325848
Method	BLASTX
NCBI GI	g2335098
BLAST score	309
E value	5.0e-42
Match length	139
% identity	65
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	199504
Contig ID	57701_1.R1039
5'-most EST	g5045013
Method	BLASTX
NCBI GI	g4519417
BLAST score	316
E value	7.0e-29
Match length	88
% identity	65
NCBI Description	(AB024327) WD-40 repeat protein [Homo sapiens]

Seq. No.	199505
Contig ID	57704_1.R1039
5'-most EST	uC-gsflmaxxa038d10b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	523
E value	4.0e-53
Match length	224
% identity	52
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	199506
Contig ID	57722_1.R1039
5'-most EST	g5048345
Method	BLASTX
NCBI GI	g266463
BLAST score	951
E value	1.0e-111
Match length	241
% identity	87
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi|82259|pir||S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - potato >gi|22643|emb|CAA47720| (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi|445064|prf||1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No.	199507
Contig ID	57740_1.R1039
5'-most EST	LIB3197-044-Q1-M1-E7

Seq. No.	199508
Contig ID	57747_1.R1039
5'-most EST	LIB3197-044-Q1-M1-F2

Seq. No.	199509
Contig ID	57788_1.R1039
5'-most EST	g5050568
Method	BLASTX
NCBI GI	g4508079
BLAST score	598
E value	6.0e-62
Match length	177
% identity	66
NCBI Description	(AC005882) 66284 [Arabidopsis thaliana]

Seq. No.	199510
Contig ID	57847_1.R1039
5'-most EST	LIB3197-045-Q1-M1-G3
Method	BLASTX
NCBI GI	g1946355
BLAST score	352
E value	2.0e-33
Match length	124
% identity	56
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi|2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	199511
Contig ID	57850_1.R1039
5'-most EST	LIB3197-060-Q1-M1-E6
Method	BLASTX
NCBI GI	g2129578
BLAST score	229
E value	4.0e-34
Match length	141
% identity	62
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi|928932|emb|CAA89205| (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi|1585435|prf||2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	199512
Contig ID	57901_1.R1039
5'-most EST	LIB3197-046-Q1-M1-D7
Method	BLASTX
NCBI GI	g4406780
BLAST score	680
E value	2.0e-71
Match length	153
% identity	80
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	199513
Contig ID	57912_1.R1039
5'-most EST	LIB3197-046-Q1-M1-E8
Method	BLASTX
NCBI GI	g3763932
BLAST score	219

E value	9.0e-18
Match length	68
% identity	62
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	199514
Contig ID	57918_1.R1039
5'-most EST	g5047345
Method	BLASTX
NCBI GI	g4138912
BLAST score	589
E value	7.0e-61
Match length	129
% identity	78
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	199515
Contig ID	57932_1.R1039
5'-most EST	uC-gsflmaxxa046b02b1
Method	BLASTX
NCBI GI	g2213425
BLAST score	439
E value	2.0e-43
Match length	88
% identity	48
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]

Seq. No.	199516
Contig ID	57932_2.R1039
5'-most EST	uC-gsflnu33B022f10b1
Method	BLASTX
NCBI GI	g3738331
BLAST score	254
E value	8.0e-22
Match length	53
% identity	81
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	199517
Contig ID	57932_3.R1039
5'-most EST	LIB3197-046-Q1-M1-G8
Method	BLASTX
NCBI GI	g2213425
BLAST score	379
E value	1.0e-36
Match length	110
% identity	42
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]

Seq. No.	199518
Contig ID	57939_1.R1039
5'-most EST	LIB3197-046-Q1-M1-H4
Method	BLASTX
NCBI GI	g1764100
BLAST score	422
E value	1.0e-41
Match length	111

% identity	75
NCBI Description	(U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana]

Seq. No.	199519
Contig ID	57940_1.R1039
5'-most EST	uC-gsflmaxxa006b10b1

Seq. No.	199520
Contig ID	57945_1.R1039
5'-most EST	g5045288
Method	BLASTX
NCBI GI	g3420751
BLAST score	493
E value	1.0e-49
Match length	173
% identity	55
NCBI Description	(AF079448) cytochrome c oxidase assembly protein [Dictyostelium discoideum]

Seq. No.	199521
Contig ID	57980_1.R1039
5'-most EST	LIB3197-047-Q1-M1-D3
Method	BLASTX
NCBI GI	g135535
BLAST score	757
E value	1.0e-80
Match length	169
% identity	89
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi|322602|pir||JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi|217871|dbj|BAA01955| (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi|2326265|dbj|BAA21772| (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	199522
Contig ID	57989_1.R1039
5'-most EST	LIB3197-047-Q1-M1-E12
Method	BLASTX
NCBI GI	g4539351
BLAST score	744
E value	4.0e-79
Match length	204
% identity	70
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	199523
Contig ID	58012_1.R1039
5'-most EST	LIB3197-047-Q1-M1-G5
Method	BLASTX
NCBI GI	g3775987
BLAST score	500
E value	7.0e-51
Match length	118
% identity	86
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	199524
Contig ID	58017_1.R1039
5'-most EST	LIB3197-047-Q1-M1-H11
Method	BLASTX
NCBI GI	g3769671
BLAST score	212
E value	1.0e-16
Match length	94
% identity	48
NCBI Description	(AF095284) Tic22 [Pisum sativum]

Seq. No.	199525
Contig ID	58044_1.R1039
5'-most EST	g5050781
Method	BLASTX
NCBI GI	g2388564
BLAST score	154
E value	7.0e-10
Match length	123
% identity	38
NCBI Description	(AC000098) ESTs gb|AA042402,gb|ATTS1380 come from this gene. [Arabidopsis thaliana]

Seq. No.	199526
Contig ID	58050_1.R1039
5'-most EST	LIB3197-048-Q1-M1-H8

Seq. No.	199527
Contig ID	58056_1.R1039
5'-most EST	uC-gsronu33B108a09b1

Seq. No.	199528
Contig ID	58057_1.R1039
5'-most EST	g3325862

Seq. No.	199529
Contig ID	58110_1.R1039
5'-most EST	uC-gsflmaxxa038b07b1
Method	BLASTX
NCBI GI	g2842490
BLAST score	411
E value	5.0e-40
Match length	146
% identity	58
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	199530
Contig ID	58111_1.R1039
5'-most EST	g5047942
Method	BLASTX
NCBI GI	g4510406
BLAST score	784
E value	9.0e-84
Match length	202
% identity	72
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	199531
Contig ID	58139_1.R1039
5'-most EST	g5044807
Method	BLASTX
NCBI GI	g2586127
BLAST score	396
E value	1.0e-40
Match length	195
% identity	45
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	199532
Contig ID	58177_1.R1039
5'-most EST	uC-gsronu33B002b04b1

Seq. No.	199533
Contig ID	58201_1.R1039
5'-most EST	LIB3197-050-Q1-M1-H8
Method	BLASTX
NCBI GI	g1168750
BLAST score	169
E value	6.0e-12
Match length	77
% identity	47
NCBI Description	CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi|458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No.	199534
Contig ID	58203_1.R1039
5'-most EST	LIB3197-051-Q1-M1-A7

Seq. No.	199535
Contig ID	58215_1.R1039
5'-most EST	uC-gsflmaxxa043b11b1
Method	BLASTX
NCBI GI	g2384673
BLAST score	250
E value	2.0e-21
Match length	72
% identity	62
NCBI Description	(AF012658) putative potassium transporter AtKT3p [Arabidopsis thaliana]

Seq. No.	199536
Contig ID	58309_1.R1039
5'-most EST	LIB3197-052-Q1-M1-D3
Method	BLASTX
NCBI GI	g1722933
BLAST score	248
E value	1.0e-20
Match length	208
% identity	35
NCBI Description	HYPOTHETICAL 39.2 KD PROTEIN CY427.09C >gi|1261930|emb|CAA94651| (Z70692) hypothetical protein Rv2228c [Mycobacterium tuberculosis]

Seq. No.	199537
Contig ID	58332_1.R1039
5'-most EST	uC-gsflmaxxa088c12b1

Seq. No.	199538
Contig ID	58336_1.R1039
5'-most EST	g5050799
Method	BLASTX
NCBI GI	g2827621
BLAST score	624
E value	5.0e-65
Match length	156
% identity	74
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	199539
Contig ID	58362_1.R1039
5'-most EST	uC-gsflmaxxa043d10b1
Method	BLASTX
NCBI GI	g1749546
BLAST score	223
E value	5.0e-18
Match length	98
% identity	52
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	199540
Contig ID	58368_1.R1039
5'-most EST	LIB3272-007-P1-K1-A4
Method	BLASTX
NCBI GI	g2494905
BLAST score	220
E value	9.0e-18
Match length	127
% identity	41
NCBI Description	MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi|2132107|pir||S67174 hypothetical protein YOR272w - yeast (Saccharomyces cerevisiae) >gi|1279699|emb|CAA61778| (X89633) hypothetical protein [Saccharomyces cerevisiae] >gi|1420610|emb|CAA99497| (Z75180) ORF YOR272w [Saccharomyces cerevisiae] >gi|1928989 (U92821) microtubule-associated protein [Saccharomyces cerevisiae]

Seq. No.	199541
Contig ID	58382_1.R1039
5'-most EST	LIB3197-053-Q1-M1-C5
Method	BLASTX
NCBI GI	g3914467
BLAST score	373
E value	6.0e-43
Match length	145
% identity	61
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi|1864003|dbj|BAA19252| (AB001422) 21D7 [Nicotiana

tabacum]

Seq. No. 199542
Contig ID 58407_1.R1039
5'-most EST LIB3197-053-Q1-M1-F10

Seq. No. 199543
Contig ID 58418_1.R1039
5'-most EST LIB3197-053-Q1-M1-G1

Seq. No. 199544
Contig ID 58446_1.R1039
5'-most EST g5049543
Method BLASTX
NCBI GI g3281868
BLAST score 1107
E value 1.0e-121
Match length 264
% identity 81
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 199545
Contig ID 58480_1.R1039
5'-most EST uC-gsronu33B156h07b1
Method BLASTX
NCBI GI g2842704
BLAST score 507
E value 4.0e-53
Match length 246
% identity 20
NCBI Description HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I >gi|1644326|emb|CAB03616| (Z81317) serine rich pumilio family rna binding domain protein [Schizosaccharomyces pombe]

Seq. No. 199546
Contig ID 58512_1.R1039
5'-most EST LIB3197-054-Q1-M1-H10

Seq. No. 199547
Contig ID 58521_1.R1039
5'-most EST LIB3197-054-Q1-M1-H9
Method BLASTX
NCBI GI g1213460
BLAST score 532
E value 4.0e-54
Match length 230
% identity 47
NCBI Description (U03374) C subunit of V-ATPase [Amblyomma americanum]

Seq. No. 199548
Contig ID 58539_1.R1039
5'-most EST g5050275

Seq. No. 199549
Contig ID 58541_1.R1039
5'-most EST g3326448

Method	BLASTX
NCBI GI	g3694872
BLAST score	496
E value	3.0e-50
Match length	116
% identity	80
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	199550
Contig ID	58562_1.R1039
5'-most EST	LIB3197-055-Q1-M1-G5
Method	BLASTX
NCBI GI	g4490316
BLAST score	402
E value	7.0e-39
Match length	240
% identity	40
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	199551
Contig ID	58659_1.R1039
5'-most EST	LIB3272-027-P1-K1-C3
Method	BLASTX
NCBI GI	g3881978
BLAST score	682
E value	3.0e-87
Match length	245
% identity	48
NCBI Description	(Y11348) annexin-like protein [Medicago sativa]

Seq. No.	199552
Contig ID	58689_1.R1039
5'-most EST	uC-gsflmaxxa097e01b1
Method	BLASTX
NCBI GI	g4455221
BLAST score	350
E value	5.0e-33
Match length	89
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	199553
Contig ID	58692_1.R1039
5'-most EST	LIB3197-057-Q1-M1-D11
Method	BLASTX
NCBI GI	g3047085
BLAST score	1246
E value	1.0e-137
Match length	320
% identity	75
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]

Seq. No.	199554
Contig ID	58716_1.R1039
5'-most EST	LIB3197-058-Q1-M1-C3
Method	BLASTX
NCBI GI	g3025299

BLAST score	152
E value	7.0e-10
Match length	125
% identity	31
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi|2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No.	199555
Contig ID	58718_1.R1039
5'-most EST	uC-gsflmaxxa097a12b1

Seq. No.	199556
Contig ID	58737_1.R1039
5'-most EST	LIB3197-057-Q1-M1-H12

Seq. No.	199557
Contig ID	58758_1.R1039
5'-most EST	LIB3197-058-Q1-M1-D1
Method	BLASTX
NCBI GI	g3193284
BLAST score	604
E value	2.0e-62
Match length	291
% identity	44
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	199558
Contig ID	58759_1.R1039
5'-most EST	LIB3272-029-P1-K1-B6
Method	BLASTN
NCBI GI	g4220643
BLAST score	51
E value	2.0e-19
Match length	316
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	199559
Contig ID	58760_1.R1039
5'-most EST	LIB3197-058-Q1-M1-D3
Method	BLASTX
NCBI GI	g3702962
BLAST score	633
E value	5.0e-66
Match length	131
% identity	92
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]

Seq. No.	199560
Contig ID	58788_1.R1039
5'-most EST	uC-gsflmaxxa015e05b1
Method	BLASTX
NCBI GI	g4539459
BLAST score	174
E value	2.0e-12

Match length	88
% identity	45
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	199561
Contig ID	58799_1.R1039
5'-most EST	LIB3197-059-Q1-M1-B10

Seq. No.	199562
Contig ID	58819_1.R1039
5'-most EST	g5048404
Method	BLASTX
NCBI GI	g2245094
BLAST score	171
E value	2.0e-13
Match length	90
% identity	53
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199563
Contig ID	58843_1.R1039
5'-most EST	LIB3197-059-Q1-M1-H2
Method	BLASTX
NCBI GI	g3413511
BLAST score	353
E value	2.0e-33
Match length	105
% identity	70
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	199564
Contig ID	58845_1.R1039
5'-most EST	uC-gsflmaxxa070f06b1
Method	BLASTX
NCBI GI	g3522929
BLAST score	279
E value	2.0e-24
Match length	167
% identity	41
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi|3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	199565
Contig ID	58858_1.R1039
5'-most EST	LIB3197-060-Q1-M1-A7

Seq. No.	199566
Contig ID	58866_1.R1039
5'-most EST	uC-gsflmaxxa054e06b1

Seq. No.	199567
Contig ID	58874_1.R1039
5'-most EST	g5048556
Method	BLASTX
NCBI GI	g1841502

BLAST score	1209
E value	1.0e-133
Match length	240
% identity	93
NCBI Description	(Y11029) glutothione-dependent formaldehyde dehydrogenase [Zea mays]

Seq. No.	199568
Contig ID	58879_1.R1039
5'-most EST	g5047765
Method	BLASTX
NCBI GI	g3269293
BLAST score	455
E value	2.0e-46
Match length	195
% identity	54
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	199569
Contig ID	58899_1.R1039
5'-most EST	LIB3272-043-P1-K1-A9
Method	BLASTX
NCBI GI	g3023815
BLAST score	193
E value	3.0e-27
Match length	108
% identity	63
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi|1362053|pir||S57785 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi|603219 (U18238) glucose-6-phosphate dehydrogenase [Medicago sativa subsp. sativa]

Seq. No.	199570
Contig ID	58900_1.R1039
5'-most EST	LIB3197-060-Q1-M1-E3
Method	BLASTX
NCBI GI	g2497492
BLAST score	281
E value	8.0e-51
Match length	174
% identity	65
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi|1653646|dbj|BAA18558| (D90915) uridine monophosphate kinase [Synechocystis sp.]

Seq. No.	199571
Contig ID	58922_1.R1039
5'-most EST	LIB3197-060-Q1-M1-G4
Method	BLASTX
NCBI GI	g4101626
BLAST score	536
E value	7.0e-55
Match length	122
% identity	80
NCBI Description	(AF005096) desaturase/cytochrome b5 protein [Ricinus communis]

Seq. No.	199572
Contig ID	58945_1.R1039
5'-most EST	uC-gsronu33B078b06b1
Method	BLASTX
NCBI GI	g3063449
BLAST score	363
E value	1.0e-34
Match length	95
% identity	73
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	199573
Contig ID	58974_1.R1039
5'-most EST	LIB3272-001-P1-K1-C6
Method	BLASTX
NCBI GI	g3603401
BLAST score	376
E value	5.0e-36
Match length	132
% identity	55
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	199574
Contig ID	58975_1.R1039
5'-most EST	uC-gsflnu33B055e11b1
Method	BLASTX
NCBI GI	g2245087
BLAST score	459
E value	1.0e-45
Match length	213
% identity	46
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199575
Contig ID	58977_1.R1039
5'-most EST	uC-gsflmaxxa045g04b1

Seq. No.	199576
Contig ID	59002_1.R1039
5'-most EST	uC-gsflmaxxa009f04b1
Method	BLASTX
NCBI GI	g4455323
BLAST score	386
E value	4.0e-37
Match length	134
% identity	62
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	199577
Contig ID	59017_1.R1039
5'-most EST	LIB3272-001-P1-K1-G4
Method	BLASTX
NCBI GI	g322598
BLAST score	473
E value	3.0e-47

Match length	206
% identity	49
NCBI Description	St12p protein - Arabidopsis thaliana
Seq. No.	199578
Contig ID	59041_1.R1039
5'-most EST	LIB3272-002-P1-K1-A6
Method	BLASTX
NCBI GI	g2459417
BLAST score	651
E value	3.0e-68
Match length	156
% identity	81
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]
Seq. No.	199579
Contig ID	59074_1.R1039
5'-most EST	uC-gsflmaxxa010b11b1
Seq. No.	199580
Contig ID	59077_1.R1039
5'-most EST	LIB3272-002-P1-K1-D9
Method	BLASTX
NCBI GI	g2739004
BLAST score	512
E value	5.0e-57
Match length	253
% identity	49
NCBI Description	(AF022461) CYP82C1p [Glycine max]
Seq. No.	199581
Contig ID	59079_1.R1039
5'-most EST	LIB3272-002-P1-K1-E10
Method	BLASTX
NCBI GI	g2117355
BLAST score	734
E value	6.0e-78
Match length	192
% identity	77
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain precursor - potato >gi|587562|emb|CAA56520| (X80236) mitochondrial processing peptidase [Solanum tuberosum]
Seq. No.	199582
Contig ID	59086_1.R1039
5'-most EST	LIB3272-002-P1-K1-E6
Method	BLASTX
NCBI GI	g2344897
BLAST score	619
E value	3.0e-64
Match length	196
% identity	61
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.	199583
Contig ID	59119_1.R1039

5'-most EST	g3325575
Method	BLASTX
NCBI GI	g3834312
BLAST score	733
E value	9.0e-78
Match length	195
% identity	67
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb|L16983 Daucus carota and a member of S locus glycoprotein family PF|00954. ESTs gb|AA067487, gb|Z35737, gb|Z30815, gb|Z35350, gb|AA713171, gb|AI100553, gb|Z34248, gb|AA728536, gb|Z30816 an

Seq. No.	199584
Contig ID	59124_1.R1039
5'-most EST	g5047680

Seq. No.	199585
Contig ID	59141_1.R1039
5'-most EST	LIB3272-003-P1-K1-C1

Seq. No.	199586
Contig ID	59142_1.R1039
5'-most EST	g5044885
Method	BLASTX
NCBI GI	g2352492
BLAST score	376
E value	7.0e-36
Match length	95
% identity	67
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi|2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	199587
Contig ID	59147_1.R1039
5'-most EST	g3326388
Method	BLASTX
NCBI GI	g3850584
BLAST score	272
E value	9.0e-24
Match length	111
% identity	56
NCBI Description	(AC005278) ESTs gb|H37641 and gb|AA651422 come from this gene. [Arabidopsis thaliana]

Seq. No.	199588
Contig ID	59150_1.R1039
5'-most EST	uC-gsronu33B159g02b1
Method	BLASTN
NCBI GI	g4457220
BLAST score	45
E value	7.0e-16
Match length	203
% identity	89
NCBI Description	Capsicum chinense putative bZIP DNA-binding protein mRNA, complete cds

Seq. No. 199589
Contig ID 59163_1.R1039
5'-most EST LIB3272-003-P1-K1-E11

Seq. No. 199590
Contig ID 59181_1.R1039
5'-most EST uC-gsronu33B114b12b1
Method BLASTX
NCBI GI g3894159
BLAST score 386
E value 2.0e-37
Match length 126
% identity 56
NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 199591
Contig ID 59182_1.R1039
5'-most EST LIB3272-003-P1-K1-G1

Seq. No. 199592
Contig ID 59201_1.R1039
5'-most EST uC-gsronu33B076e07b1
Method BLASTX
NCBI GI g2388575
BLAST score 404
E value 3.0e-39
Match length 144
% identity 53
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 199593
Contig ID 59204_1.R1039
5'-most EST uC-gsflmaxxa041e03b1

Seq. No. 199594
Contig ID 59231_1.R1039
5'-most EST LIB3272-004-P1-K1-C4
Method BLASTX
NCBI GI g2129630
BLAST score 235
E value 1.0e-19
Match length 86
% identity 45
NCBI Description lamin - Arabidopsis thaliana >gi|1262754|emb|CAA65750|
(X97023) lamin [Arabidopsis thaliana] >gi|3395760 (U77721)
unknown [Arabidopsis thaliana]

Seq. No. 199595
Contig ID 59247_1.R1039
5'-most EST LIB3272-004-P1-K1-E12

Seq. No. 199596
Contig ID 59274_1.R1039
5'-most EST g5044296
Method BLASTX
NCBI GI g2245089

BLAST score	307
E value	8.0e-28
Match length	175
% identity	41
NCBI Description	(Z97343) asparagine--tRNA ligase homolog [Arabidopsis thaliana]

Seq. No.	199597
Contig ID	59278_1.R1039
5'-most EST	g5047503
Method	BLASTX
NCBI GI	g4105269
BLAST score	252
E value	2.0e-21
Match length	132
% identity	42
NCBI Description	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]

Seq. No.	199598
Contig ID	59282_1.R1039
5'-most EST	uC-gsf1nu33B085d10b1
Method	BLASTX
NCBI GI	g4522004
BLAST score	518
E value	1.0e-52
Match length	160
% identity	67
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No.	199599
Contig ID	59298_1.R1039
5'-most EST	LIB3272-005-P1-K1-B6

Seq. No.	199600
Contig ID	59298_2.R1039
5'-most EST	LIB3272-028-P1-K1-G4

Seq. No.	199601
Contig ID	59310_1.R1039
5'-most EST	uC-gsronu33B008a02b1

Seq. No.	199602
Contig ID	59315_1.R1039
5'-most EST	LIB3272-005-P1-K1-D4
Method	BLASTX
NCBI GI	g2832623
BLAST score	512
E value	5.0e-52
Match length	138
% identity	72
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	199603
Contig ID	59392_1.R1039

5'-most EST	LIB3272-006-P1-K1-D11
Method	BLASTX
NCBI GI	g1397319
BLAST score	168
E value	2.0e-11
Match length	114
% identity	36
NCBI Description	(U61953) No definition line found [Caenorhabditis elegans]

Seq. No.	199604
Contig ID	59402_1.R1039
5'-most EST	LIB3272-006-P1-K1-E10

Seq. No.	199605
Contig ID	59408_1.R1039
5'-most EST	uC-gsronu33B015h10b1
Method	BLASTX
NCBI GI	g419963
BLAST score	280
E value	2.0e-24
Match length	86
% identity	60
NCBI Description	snRNP protein B - fruit fly (Drosophila melanogaster) >gi|290272 (L02919) ribonucleoprotein [Drosophila melanogaster]

Seq. No.	199606
Contig ID	59420_1.R1039
5'-most EST	g5045016
Method	BLASTX
NCBI GI	g585454
BLAST score	1031
E value	1.0e-157
Match length	353
% identity	79
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG D5 >gi|479389|pir||S33635 mitogen-activated protein kinase homolog (clone D5) - garden pea >gi|20808|emb|CAA50036| (X70703) MAP kinase homologue [Pisum sativum]

Seq. No.	199607
Contig ID	59436_1.R1039
5'-most EST	LIB3272-023-P1-K1-A5
Method	BLASTX
NCBI GI	g3242079
BLAST score	218
E value	1.0e-17
Match length	67
% identity	64
NCBI Description	(AJ006984) proline-rich protein [Capsicum annuum]

Seq. No.	199608
Contig ID	59488_1.R1039
5'-most EST	LIB3272-007-P1-K1-E11

Seq. No.	199609
Contig ID	59499_1.R1039

5'-most EST	LIB3272-019-P1-K1-E2
Method	BLASTX
NCBI GI	g4210948
BLAST score	601
E value	2.0e-62
Match length	115
% identity	97
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	199610
Contig ID	59517_1.R1039
5'-most EST	LIB3272-007-P1-K1-H3
Method	BLASTX
NCBI GI	g3928543
BLAST score	265
E value	7.0e-23
Match length	123
% identity	43
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	199611
Contig ID	59520_1.R1039
5'-most EST	LIB3272-007-P1-K1-H6

Seq. No.	199612
Contig ID	59524_1.R1039
5'-most EST	LIB3272-008-P1-K1-A11

Seq. No.	199613
Contig ID	59526_1.R1039
5'-most EST	LIB3272-008-P1-K1-A3
Method	BLASTX
NCBI GI	g4115559
BLAST score	318
E value	5.0e-29
Match length	153
% identity	44
NCBI Description	(AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase [Perilla frutescens]

Seq. No.	199614
Contig ID	59542_1.R1039
5'-most EST	LIB3272-008-P1-K1-B9
Method	BLASTX
NCBI GI	g3395673
BLAST score	446
E value	2.0e-44
Match length	116
% identity	74
NCBI Description	(AB016623) RWC-3 [Oryza sativa]

Seq. No.	199615
Contig ID	59546_1.R1039
5'-most EST	LIB3272-008-P1-K1-C12
Method	BLASTN
NCBI GI	g2114049

BLAST score	56
E value	1.0e-22
Match length	176
% identity	87
NCBI Description	Nicotiana excelsior mRNA for water channel protein, complete cds

Seq. No.	199616
Contig ID	59568_1.R1039
5'-most EST	LIB3272-008-P1-K1-E4
Method	BLASTX
NCBI GI	g1381676
BLAST score	1029
E value	1.0e-112
Match length	221
% identity	89
NCBI Description	(U58853) small GTP-binding protein [Glycine max]

Seq. No.	199617
Contig ID	59600_1.R1039
5'-most EST	LIB3272-008-P1-K1-H9
Method	BLASTX
NCBI GI	g4572676
BLAST score	331
E value	7.0e-31
Match length	99
% identity	63
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	199618
Contig ID	59653_1.R1039
5'-most EST	uC-gsronu33B058d06b1

Seq. No.	199619
Contig ID	59712_1.R1039
5'-most EST	LIB3272-010-P1-K1-D11
Method	BLASTX
NCBI GI	g2497953
BLAST score	269
E value	3.0e-23
Match length	131
% identity	69
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi|1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi|4469123|emb|CAB38312| (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	199620
Contig ID	59721_1.R1039
5'-most EST	g5047854
Method	BLASTX
NCBI GI	g3980380
BLAST score	991
E value	1.0e-108
Match length	243
% identity	74

NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	199621
Contig ID	59724_1.R1039
5'-most EST	LIB3272-010-P1-K1-E11

Seq. No.	199622
Contig ID	59725_1.R1039
5'-most EST	uC-gsronu33B114c06b1
Method	BLASTX
NCBI GI	g3928150
BLAST score	720
E value	2.0e-76
Match length	171
% identity	82
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	199623
Contig ID	59736_1.R1039
5'-most EST	uC-gsflnu33B027d10b1

Seq. No.	199624
Contig ID	59739_1.R1039
5'-most EST	LIB3272-010-P1-K1-F3

Seq. No.	199625
Contig ID	59740_1.R1039
5'-most EST	LIB3272-010-P1-K1-F4

Seq. No.	199626
Contig ID	59758_1.R1039
5'-most EST	uC-gsflmaxxa061g04b1

Seq. No.	199627
Contig ID	59808_1.R1039
5'-most EST	LIB3272-011-P1-K1-F1
Method	BLASTX
NCBI GI	g3522943
BLAST score	550
E value	2.0e-56
Match length	163
% identity	34
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	199628
Contig ID	59822_1.R1039
5'-most EST	LIB3272-011-P1-K1-G3

Seq. No.	199629
Contig ID	59838_1.R1039
5'-most EST	LIB3272-012-P1-K1-A3

Seq. No.	199630
Contig ID	59855_1.R1039
5'-most EST	uC-gsflmaxxa096b11b1
Method	BLASTX
NCBI GI	g2104949

BLAST score	233
E value	3.0e-19
Match length	52
% identity	83
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	199631
Contig ID	59868_1.R1039
5'-most EST	LIB3272-012-P1-K1-D6
Method	BLASTX
NCBI GI	g4056494
BLAST score	260
E value	2.0e-22
Match length	131
% identity	50
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No.	199632
Contig ID	59875_1.R1039
5'-most EST	LIB3272-012-P1-K1-E3

Seq. No.	199633
Contig ID	59885_1.R1039
5'-most EST	LIB3272-012-P1-K1-F5
Method	BLASTX
NCBI GI	g3688123
BLAST score	416
E value	9.0e-41
Match length	141
% identity	61
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	199634
Contig ID	59900_1.R1039
5'-most EST	uC-gsflnu33B008a11b1

Seq. No.	199635
Contig ID	59905_1.R1039
5'-most EST	uC-gsflnu33B050f11b1
Method	BLASTX
NCBI GI	g3337367
BLAST score	204
E value	8.0e-16
Match length	95
% identity	45
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199636
Contig ID	59914_1.R1039
5'-most EST	LIB3272-013-P1-K1-A7
Method	BLASTX
NCBI GI	g2462753
BLAST score	168
E value	7.0e-12
Match length	43

% identity	72
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	199637
Contig ID	59940_1.R1039
5'-most EST	LIB3272-013-P1-K1-D11
Method	BLASTX
NCBI GI	g4323298
BLAST score	451
E value	9.0e-45
Match length	172
% identity	41
NCBI Description	(AF099096) pulvinus outward-rectifying channel for potassium SPOCK1 [Samanea saman]

Seq. No.	199638
Contig ID	59951_1.R1039
5'-most EST	LIB3272-013-P1-K1-E11
Method	BLASTX
NCBI GI	g2708484
BLAST score	542
E value	2.0e-55
Match length	225
% identity	58
NCBI Description	(U79557) IAA24 [Arabidopsis thaliana]

Seq. No.	199639
Contig ID	60035_1.R1039
5'-most EST	LIB3272-014-P1-K1-E6

Seq. No.	199640
Contig ID	60047_2.R1039
5'-most EST	LIB3272-014-P1-K1-F3
Method	BLASTX
NCBI GI	g4406815
BLAST score	421
E value	2.0e-41
Match length	112
% identity	71
NCBI Description	(AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No.	199641
Contig ID	60141_1.R1039
5'-most EST	LIB3272-015-P1-K1-H10
Method	BLASTX
NCBI GI	g2194120
BLAST score	144
E value	1.0e-08
Match length	125
% identity	37
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	199642
Contig ID	60152_1.R1039
5'-most EST	LIB3272-016-P1-K1-A10

Seq. No.	199643
Contig ID	60165_1.R1039
5'-most EST	uC-gsflnu33B013h11b1
Method	BLASTX
NCBI GI	g602292
BLAST score	649
E value	8.0e-68
Match length	254
% identity	54
NCBI Description	(U17987) RCH2 protein [Brassica napus]

Seq. No.	199644
Contig ID	60180_1.R1039
5'-most EST	uC-gsronu33B060h11b1
Method	BLASTX
NCBI GI	g2209384
BLAST score	421
E value	2.0e-41
Match length	96
% identity	88
NCBI Description	(AF008441) glutathione reductase [Brassica rapa]

Seq. No.	199645
Contig ID	60193_1.R1039
5'-most EST	uC-gsflnu33B072f01b1
Method	BLASTX
NCBI GI	g1449179
BLAST score	763
E value	2.0e-81
Match length	162
% identity	94
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	199646
Contig ID	60208_1.R1039
5'-most EST	LIB3272-016-P1-K1-F4

Seq. No.	199647
Contig ID	60209_1.R1039
5'-most EST	LIB3272-023-P1-K1-F9

Seq. No.	199648
Contig ID	60221_1.R1039
5'-most EST	LIB3272-016-P1-K1-G7
Method	BLASTX
NCBI GI	g3413717
BLAST score	450
E value	7.0e-45
Match length	99
% identity	82
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi|3643590 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 199649

Contig ID	60226_1.R1039
5'-most EST	LIB3272-016-P1-K1-H11
Method	BLASTX
NCBI GI	g1495259
BLAST score	577
E value	2.0e-59
Match length	175
% identity	65
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	199650
Contig ID	60233_1.R1039
5'-most EST	LIB3272-016-P1-K1-H7
Method	BLASTX
NCBI GI	g1245182
BLAST score	387
E value	4.0e-37
Match length	186
% identity	47
NCBI Description	(U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.	199651
Contig ID	60235_1.R1039
5'-most EST	uC-gsronu33B109d08b1
Method	BLASTX
NCBI GI	g4263776
BLAST score	519
E value	1.0e-52
Match length	196
% identity	57
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana] >gi|4510390|gb|AAD21478.1| (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	199652
Contig ID	60241_1.R1039
5'-most EST	LIB3272-017-P1-K1-A9
Method	BLASTX
NCBI GI	g2739168
BLAST score	312
E value	2.0e-43
Match length	133
% identity	66
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	199653
Contig ID	60245_1.R1039
5'-most EST	LIB3272-017-P1-K1-B3

Seq. No.	199654
Contig ID	60252_1.R1039
5'-most EST	LIB3272-041-P1-K1-E12

Seq. No.	199655
Contig ID	60268_1.R1039
5'-most EST	LIB3272-033-P1-K1-C9

Method	BLASTX
NCBI GI	g4039014
BLAST score	409
E value	7.0e-40
Match length	180
% identity	47
NCBI Description	(AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi|4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi|4502897|ref|NP_001285.1|pCLPTM1| cleft lip and palate associated transmembrane protein

Seq. No.	199656
Contig ID	60271_1.R1039
5'-most EST	LIB3272-017-P1-K1-E1
Method	BLASTX
NCBI GI	g4572674
BLAST score	260
E value	1.0e-22
Match length	75
% identity	67
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	199657
Contig ID	60299_1.R1039
5'-most EST	LIB3272-017-P1-K1-G8

Seq. No.	199658
Contig ID	60301_1.R1039
5'-most EST	LIB3272-017-P1-K1-H10

Seq. No.	199659
Contig ID	60302_1.R1039
5'-most EST	LIB3272-017-P1-K1-H11
Method	BLASTX
NCBI GI	g4567269
BLAST score	243
E value	3.0e-20
Match length	58
% identity	78
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	199660
Contig ID	60326_1.R1039
5'-most EST	uC-gsflmaxxa014b09b1
Method	BLASTX
NCBI GI	g3176691
BLAST score	395
E value	3.0e-38
Match length	121
% identity	36
NCBI Description	(AC003671) Contains homology to serine/threonine protein kinase gb|X99618 from Mycobacterium tuberculosis. ESTs gb|F14403, gb|F14404, and gb|N96730 come from this gene. [Arabidopsis thaliana]

Seq. No. 199661

Contig ID	60337_1.R1039
5'-most EST	LIB3272-018-P1-K1-C5
Method	BLASTX
NCBI GI	g1361983
BLAST score	397
E value	1.0e-38
Match length	124
% identity	62
NCBI Description	ARP protein - Arabidopsis thaliana >gi|886434|emb|CAA89858| (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	199662
Contig ID	60363_1.R1039
5'-most EST	LIB3272-047-P1-K1-C6

Seq. No.	199663
Contig ID	60371_1.R1039
5'-most EST	LIB3272-018-P1-K1-G2

Seq. No.	199664
Contig ID	60391_1.R1039
5'-most EST	LIB3272-019-P1-K1-A12
Method	BLASTX
NCBI GI	g1142619
BLAST score	481
E value	2.0e-48
Match length	179
% identity	56
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	199665
Contig ID	60413_1.R1039
5'-most EST	LIB3272-019-P1-K1-C12
Method	BLASTX
NCBI GI	g3810848
BLAST score	329
E value	1.0e-30
Match length	110
% identity	52
NCBI Description	(AL032684) putative autophagy protein [Schizosaccharomyces pombe]

Seq. No.	199666
Contig ID	60420_1.R1039
5'-most EST	LIB3272-019-P1-K1-D12
Method	BLASTX
NCBI GI	g4406775
BLAST score	222
E value	6.0e-18
Match length	165
% identity	43
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	199667
Contig ID	60461_1.R1039
5'-most EST	uC-gsflmaxxa026h10b1

Method	BLASTN
NCBI GI	g2924729
BLAST score	47
E value	3.0e-17
Match length	197
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	199668
Contig ID	60491_1.R1039
5'-most EST	LIB3272-020-P1-K1-C11
Method	BLASTX
NCBI GI	g3789799
BLAST score	210
E value	9.0e-17
Match length	127
% identity	9
NCBI Description	(AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >gi|4557445|ref|NP_001259.1|pCHC1L| RCC1-like G exchanging factor RLG

Seq. No.	199669
Contig ID	60511_1.R1039
5'-most EST	LIB3272-020-P1-K1-E5

Seq. No.	199670
Contig ID	60566_1.R1039
5'-most EST	LIB3272-021-P1-K1-B5

Seq. No.	199671
Contig ID	60636_1.R1039
5'-most EST	uC-gsflmaxxa049c12b1

Seq. No.	199672
Contig ID	60637_1.R1039
5'-most EST	LIB3272-036-P1-K1-D7
Method	BLASTN
NCBI GI	g2564044
BLAST score	39
E value	2.0e-12
Match length	202
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	199673
Contig ID	60667_1.R1039
5'-most EST	LIB3272-022-P1-K1-D7
Method	BLASTN
NCBI GI	g2191181
BLAST score	41
E value	2.0e-13
Match length	65
% identity	91
NCBI Description	Arabidopsis thaliana BAC TM021B04

Seq. No.	199674
Contig ID	60672_1.R1039
5'-most EST	uC-gsflmaxxa006b08b1
Method	BLASTX
NCBI GI	g3329368
BLAST score	135
E value	8.0e-12
Match length	100
% identity	42
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	199675
Contig ID	60678_1.R1039
5'-most EST	g3326482
Method	BLASTX
NCBI GI	g3608139
BLAST score	139
E value	2.0e-17
Match length	210
% identity	39
NCBI Description	(AC005314) putative fibrillin [Arabidopsis thaliana]

Seq. No.	199676
Contig ID	60728_1.R1039
5'-most EST	LIB3272-023-P1-K1-B5
Method	BLASTX
NCBI GI	g2688830
BLAST score	554
E value	1.0e-56
Match length	152
% identity	72
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	199677
Contig ID	60750_1.R1039
5'-most EST	LIB3272-023-P1-K1-D5
Method	BLASTX
NCBI GI	g1234900
BLAST score	312
E value	2.0e-28
Match length	153
% identity	50
NCBI Description	(X92489) homeobox-leucine zipper protein [Glycine max]

Seq. No.	199678
Contig ID	60758_1.R1039
5'-most EST	g5044854
Method	BLASTX
NCBI GI	g2462931
BLAST score	210
E value	3.0e-16
Match length	105
% identity	52
NCBI Description	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]

Seq. No.	199679

Contig ID	60761_1.R1039
5'-most EST	uC-gsflmaxxa026c11b1

Seq. No.	199680
Contig ID	60789_1.R1039
5'-most EST	LIB3272-033-P1-K1-F11
Method	BLASTX
NCBI GI	g3695023
BLAST score	389
E value	1.0e-37
Match length	143
% identity	54
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	199681
Contig ID	60796_1.R1039
5'-most EST	uC-gsronu33B058g12b1

Seq. No.	199682
Contig ID	60819_1.R1039
5'-most EST	LIB3272-030-P1-K1-E6

Seq. No.	199683
Contig ID	60826_1.R1039
5'-most EST	LIB3272-058-P1-K1-E10

Seq. No.	199684
Contig ID	60860_1.R1039
5'-most EST	LIB3272-024-P1-K1-G3
Method	BLASTX
NCBI GI	g1922938
BLAST score	222
E value	5.0e-18
Match length	129
% identity	36
NCBI Description	(AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb|Z29094). [Arabidopsis thaliana]

Seq. No.	199685
Contig ID	60861_1.R1039
5'-most EST	LIB3272-024-P1-K1-G4

Seq. No.	199686
Contig ID	60866_1.R1039
5'-most EST	LIB3272-024-P1-K1-G9
Method	BLASTX
NCBI GI	g2832708
BLAST score	279
E value	8.0e-25
Match length	107
% identity	50
NCBI Description	(AL021713) beta-1, 3-glucanase-like protein [Arabidopsis thaliana]

Seq. No.	199687
Contig ID	60868_1.R1039
5'-most EST	LIB3272-030-P1-K1-B6

Method	BLASTX
NCBI GI	g1706326
BLAST score	631
E value	4.0e-66
Match length	135
% identity	86
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi|2146786|pir||S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi|1177603|emb|CAA91444| (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.	199688
Contig ID	60899_1.R1039
5'-most EST	LIB3272-026-P1-K1-C12

Seq. No.	199689
Contig ID	60913_1.R1039
5'-most EST	g5047357
Method	BLASTX
NCBI GI	g3309084
BLAST score	466
E value	1.0e-46
Match length	106
% identity	88
NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]

Seq. No.	199690
Contig ID	60913_2.R1039
5'-most EST	LIB3272-026-P1-K1-E1
Method	BLASTX
NCBI GI	g3309084
BLAST score	378
E value	2.0e-36
Match length	88
% identity	88
NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]

Seq. No.	199691
Contig ID	60916_1.R1039
5'-most EST	LIB3272-026-P1-K1-E12
Method	BLASTX
NCBI GI	g1351303
BLAST score	473
E value	3.0e-47
Match length	161
% identity	63
NCBI Description	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi|619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana]

Seq. No.	199692
Contig ID	60933_1.R1039
5'-most EST	uC-gsflmaxxa098h03b1
Method	BLASTX
NCBI GI	g4432864

BLAST score	890
E value	5.0e-96
Match length	253
% identity	68
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199693
Contig ID	60942_1.R1039
5'-most EST	g3326852

Seq. No.	199694
Contig ID	60960_1.R1039
5'-most EST	LIB3272-046-P1-K1-A3
Method	BLASTX
NCBI GI	g2274915
BLAST score	410
E value	4.0e-40
Match length	113
% identity	69
NCBI Description	(AJ000081) beta-1,3-glucanase [Citrus sinensis]

Seq. No.	199695
Contig ID	60978_1.R1039
5'-most EST	uC-gsflmaxxa028h06b1

Seq. No.	199696
Contig ID	60996_1.R1039
5'-most EST	uC-gsronu33B110a11b1

Seq. No.	199697
Contig ID	61055_1.R1039
5'-most EST	LIB3272-028-P1-K1-D12

Seq. No.	199698
Contig ID	61072_1.R1039
5'-most EST	uC-gsflnu33B082d09b1

Seq. No.	199699
Contig ID	61130_1.R1039
5'-most EST	uC-gsronu33B018f03b1
Method	BLASTX
NCBI GI	g4467153
BLAST score	483
E value	2.0e-48
Match length	104
% identity	82
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	199700
Contig ID	61143_1.R1039
5'-most EST	g5047330
Method	BLASTX
NCBI GI	g2827702
BLAST score	883
E value	3.0e-95
Match length	230

% identity	71
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	199701
Contig ID	61162_1.R1039
5'-most EST	g5048008
Method	BLASTX
NCBI GI	g4455227
BLAST score	583
E value	3.0e-60
Match length	135
% identity	83
NCBI Description	(AL035440) SNF8 like protein [Arabidopsis thaliana]

Seq. No.	199702
Contig ID	61172_1.R1039
5'-most EST	LIB3272-029-P1-K1-H4
Method	BLASTX
NCBI GI	g3600039
BLAST score	620
E value	1.0e-64
Match length	167
% identity	69
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	199703
Contig ID	61178_1.R1039
5'-most EST	uC-gsflnu33B055d01b1
Method	BLASTX
NCBI GI	g2347098
BLAST score	748
E value	1.0e-79
Match length	152
% identity	95
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi|4490742|emb|CAB38904.1| (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	199704
Contig ID	61192_1.R1039
5'-most EST	LIB3272-030-P1-K1-B2
Method	BLASTX
NCBI GI	g584861
BLAST score	255
E value	6.0e-22
Match length	94
% identity	49
NCBI Description	CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4) >gi|480396|pir||S36806 cytochrome P450 71A2 - eggplant >gi|408140|emb|CAA50645| (X71654) P450 hydroxylase [Solanum melongena] >gi|441185|dbj|BAA03635| (D14990) Cytochrome P-450EG4 [Solanum melongena]

Seq. No.	199705
Contig ID	61228_1.R1039
5'-most EST	g5050429

Method	BLASTX
NCBI GI	g3757523
BLAST score	447
E value	5.0e-44
Match length	147
% identity	60
NCBI Description	(AC005167) putative transportin [Arabidopsis thaliana]

Seq. No.	199706
Contig ID	61233_1.R1039
5'-most EST	uC-gsflmaxxa091b04b1
Method	BLASTX
NCBI GI	g115506
BLAST score	151
E value	1.0e-09
Match length	88
% identity	22
NCBI Description	CALMODULIN >gi|71688|pir||MCKM calmodulin - Chlamydomonas reinhardtii >gi|167411 (M20729) calmodulin [Chlamydomonas reinhardtii]

Seq. No.	199707
Contig ID	61254_1.R1039
5'-most EST	uC-gsflnu33B001d04b1
Method	BLASTX
NCBI GI	g1653767
BLAST score	623
E value	6.0e-65
Match length	185
% identity	61
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	199708
Contig ID	61312_1.R1039
5'-most EST	LIB3272-039-P1-K1-A6

Seq. No.	199709
Contig ID	61320_1.R1039
5'-most EST	LIB3272-055-P1-K1-F8
Method	BLASTX
NCBI GI	g3142698
BLAST score	673
E value	9.0e-71
Match length	181
% identity	66
NCBI Description	(AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]

Seq. No.	199710
Contig ID	61328_1.R1039
5'-most EST	LIB3272-031-P1-K1-H5

Seq. No.	199711
Contig ID	61421_1.R1039
5'-most EST	LIB3272-033-P1-K1-E5
Method	BLASTX
NCBI GI	g2244999

BLAST score	179
E value	6.0e-13
Match length	75
% identity	51
NCBI Description	(Z97341) similarity to phaseolin G-box binding protein PG2 [Arabidopsis thaliana]

Seq. No.	199712
Contig ID	61426_1.R1039
5'-most EST	LIB3272-033-P1-K1-A7
Method	BLASTX
NCBI GI	g2739279
BLAST score	148
E value	3.0e-13
Match length	181
% identity	36
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi|2791348|emb|CAA11154| (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	199713
Contig ID	61433_1.R1039
5'-most EST	LIB3272-033-P1-K1-B5
Method	BLASTX
NCBI GI	g4105698
BLAST score	196
E value	8.0e-15
Match length	69
% identity	55
NCBI Description	(AF049870) small hydrophobic protein [Arabidopsis thaliana]

Seq. No.	199714
Contig ID	61435_1.R1039
5'-most EST	g3325655

Seq. No.	199715
Contig ID	61466_1.R1039
5'-most EST	uC-gsflmaxxa097h08b1
Method	BLASTX
NCBI GI	g4455293
BLAST score	366
E value	5.0e-35
Match length	89
% identity	88
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	199716
Contig ID	61484_1.R1039
5'-most EST	uC-gsronu33B113h10b1
Method	BLASTX
NCBI GI	g3080435
BLAST score	560
E value	1.0e-57
Match length	160
% identity	71
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	199717
Contig ID	61513_1.R1039
5'-most EST	uC-gsflnu33B031h07b1
Method	BLASTX
NCBI GI	g4406780
BLAST score	400
E value	6.0e-39
Match length	101
% identity	74
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	199718
Contig ID	61559_1.R1039
5'-most EST	LIB3272-034-P1-K1-G5
Method	BLASTN
NCBI GI	g2773049
BLAST score	59
E value	2.0e-24
Match length	179
% identity	83
NCBI Description	Spinacia oleracea heat shock 70 protein (HSC70-9) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	199719
Contig ID	61579_1.R1039
5'-most EST	LIB3272-052-P1-K1-D7
Method	BLASTX
NCBI GI	g133249
BLAST score	304
E value	2.0e-27
Match length	78
% identity	44
NCBI Description	CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR >gi|100390|pir||S12111 ribonucleoprotein, 33K, precursor - common tobacco >gi|20005|emb|CAA37879| (X53932) 33 kDa ribonucleoprotein precursor [Nicotiana tabacum]

Seq. No.	199720
Contig ID	61646_1.R1039
5'-most EST	g3326686
Method	BLASTN
NCBI GI	g3241927
BLAST score	35
E value	6.0e-10
Match length	181
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	199721
Contig ID	61666_1.R1039
5'-most EST	LIB3272-036-P1-K1-B12
Method	BLASTX
NCBI GI	g2146740
BLAST score	531
E value	4.0e-54

Match length	141
% identity	72
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi|603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	199722
Contig ID	61764_1.R1039
5'-most EST	uC-gsronu33B154e01b2
Method	BLASTX
NCBI GI	g729842
BLAST score	248
E value	5.0e-21
Match length	117
% identity	55
NCBI Description	CHLOROPLAST MEMBRANE-ASSOCIATED 30 KD PROTEIN PRECURSOR (M30) >gi|1076532|pir||S47966 probable lipid transfer protein M30 precursor - garden pea >gi|169107 (M73744) IM30 [Pisum sativum]

Seq. No.	199723
Contig ID	61817_1.R1039
5'-most EST	LIB3272-038-P1-K1-A7
Method	BLASTX
NCBI GI	g1420887
BLAST score	161
E value	5.0e-11
Match length	101
% identity	35
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	199724
Contig ID	61824_1.R1039
5'-most EST	LIB3272-038-P1-K1-B10

Seq. No.	199725
Contig ID	61844_1.R1039
5'-most EST	LIB3272-042-P1-K1-G7
Method	BLASTX
NCBI GI	g3337366
BLAST score	366
E value	6.0e-35
Match length	148
% identity	29
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	199726
Contig ID	61919_1.R1039
5'-most EST	LIB3272-042-P1-K1-F11
Method	BLASTX
NCBI GI	g2262159
BLAST score	531
E value	2.0e-54
Match length	131
% identity	76
NCBI Description	(AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No.	199727
Contig ID	61984_1.R1039
5'-most EST	uC-gsflnu33B016f09b1
Method	BLASTX
NCBI GI	g3033391
BLAST score	175
E value	1.0e-12
Match length	72
% identity	49
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	199728
Contig ID	61991_1.R1039
5'-most EST	LIB3272-040-P1-K1-C5
Method	BLASTX
NCBI GI	g2494144
BLAST score	543
E value	2.0e-55
Match length	195
% identity	22
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	199729
Contig ID	62007_1.R1039
5'-most EST	LIB3272-040-P1-K1-F5
Method	BLASTX
NCBI GI	g4102723
BLAST score	563
E value	4.0e-58
Match length	120
% identity	68
NCBI Description	(AF015784) TATA-box binding protein [Phaseolus vulgaris]

Seq. No.	199730
Contig ID	62066_1.R1039
5'-most EST	LIB3272-041-P1-K1-D4

Seq. No.	199731
Contig ID	62094_1.R1039
5'-most EST	g5048460

Seq. No.	199732
Contig ID	62103_1.R1039
5'-most EST	uC-gsflmaxxa107b02b1
Method	BLASTX
NCBI GI	g4309738
BLAST score	161
E value	1.0e-10
Match length	67
% identity	51
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	199733

Contig ID	62122_1.R1039
5'-most EST	uC-gsflmaxxa091f05b1
Method	BLASTX
NCBI GI	g4512688
BLAST score	385
E value	5.0e-37
Match length	147
% identity	54
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199734
Contig ID	62147_1.R1039
5'-most EST	uC-gsflnu33B084c07b1

Seq. No.	199735
Contig ID	62185_1.R1039
5'-most EST	LIB3272-043-P1-K1-A10

Seq. No.	199736
Contig ID	62273_1.R1039
5'-most EST	LIB3272-044-P1-K1-A2

Seq. No.	199737
Contig ID	62298_1.R1039
5'-most EST	LIB3272-044-P1-K1-G7

Seq. No.	199738
Contig ID	62344_1.R1039
5'-most EST	LIB3272-044-P1-K1-G8
Method	BLASTX
NCBI GI	g4432840
BLAST score	175
E value	3.0e-14
Match length	107
% identity	47
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	199739
Contig ID	62357_1.R1039
5'-most EST	LIB3272-045-P1-K1-A11
Method	BLASTX
NCBI GI	g2160182
BLAST score	160
E value	7.0e-11
Match length	116
% identity	40
NCBI Description	(AC000132) ESTs gb|ATTS1236,gb|T43334,gb|N97019,gb|AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	199740
Contig ID	62361_1.R1039
5'-most EST	uC-gsflmaxxa093a01b1
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	3.0e-30
Match length	72

% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi|481909|pir||S40089 ribosomal protein S25 - tomato >gi|435679|emb|CAA54132| (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi|1584836|prf||2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	199741
Contig ID	62373_1.R1039
5'-most EST	LIB3272-045-P1-K1-B9

Seq. No.	199742
Contig ID	62428_1.R1039
5'-most EST	uC-gsflmaxxa095e11b1

Seq. No.	199743
Contig ID	62441_1.R1039
5'-most EST	uC-gsflnu33B004g09b1
Method	BLASTX
NCBI GI	g1076603
BLAST score	402
E value	5.0e-39
Match length	183
% identity	48
NCBI Description	vsf-1 protein - tomato

Seq. No.	199744
Contig ID	62453_1.R1039
5'-most EST	LIB3272-046-P1-K1-B8

Seq. No.	199745
Contig ID	62471_1.R1039
5'-most EST	g3326312
Method	BLASTN
NCBI GI	g3128143
BLAST score	40
E value	7.0e-13
Match length	218
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	199746
Contig ID	62478_1.R1039
5'-most EST	uC-gsronu33B168c09b1
Method	BLASTX
NCBI GI	g131754
BLAST score	338
E value	1.0e-31
Match length	126
% identity	52
NCBI Description	PPLZ02 PROTEIN >gi|99973|pir||S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi|19507|emb|CAA36069| (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Seq. No.	199747

Contig ID	62483_1.R1039
5'-most EST	LIB3272-046-P1-K1-E5

Seq. No.	199748
Contig ID	62512_1.R1039
5'-most EST	LIB3272-047-P1-K1-A10
Method	BLASTX
NCBI GI	g3878264
BLAST score	215
E value	4.0e-17
Match length	161
% identity	32
NCBI Description	(Z75712) Similarity to some prokaryotic esterases; cDNA EST EMBL:D71448 comes from this gene; cDNA EST EMBL:D74156 comes from this gene [Caenorhabditis elegans]

Seq. No.	199749
Contig ID	62566_1.R1039
5'-most EST	LIB3272-047-P1-K1-F4

Seq. No.	199750
Contig ID	62635_1.R1039
5'-most EST	LIB3272-048-P1-K1-E5
Method	BLASTX
NCBI GI	g1491776
BLAST score	348
E value	6.0e-33
Match length	85
% identity	78
NCBI Description	(M37636) cationic peroxidase [Arachis hypogaea]

Seq. No.	199751
Contig ID	62645_1.R1039
5'-most EST	g3326016
Method	BLASTX
NCBI GI	g3914237
BLAST score	154
E value	7.0e-10
Match length	107
% identity	33
NCBI Description	COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A) (RNP24) >gi|1212965|emb|CAA63069| (X92098) transmembrane protein [Homo sapiens]

Seq. No.	199752
Contig ID	62662_1.R1039
5'-most EST	uC-gsflmaxxa038f03b1
Method	BLASTX
NCBI GI	g4432860
BLAST score	328
E value	2.0e-30
Match length	109
% identity	61
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	199753

Contig ID	62678_1.R1039
5'-most EST	LIB3272-049-P1-K1-B10
Method	BLASTX
NCBI GI	g3811009
BLAST score	205
E value	4.0e-16
Match length	43
% identity	88
NCBI Description	(AB019328) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	199754
Contig ID	62713_1.R1039
5'-most EST	uC-gsflmaxxa041f05b1
Method	BLASTX
NCBI GI	g3281861
BLAST score	223
E value	3.0e-18
Match length	109
% identity	42
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	199755
Contig ID	62718_1.R1039
5'-most EST	uC-gsflnu33B101d04b1
Method	BLASTX
NCBI GI	g2288887
BLAST score	657
E value	1.0e-68
Match length	226
% identity	64
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi|3250736|emb|CAA76803| (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi|3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	199756
Contig ID	62829_1.R1039
5'-most EST	uC-gsflnu33B029f11b1
Method	BLASTX
NCBI GI	g3068705
BLAST score	330
E value	3.0e-30
Match length	199
% identity	38
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	199757
Contig ID	62845_1.R1039
5'-most EST	LIB3272-051-P1-K1-G2

Seq. No.	199758
Contig ID	62850_1.R1039
5'-most EST	LIB3272-051-P1-K1-C2
Method	BLASTX
NCBI GI	g2829894

BLAST score 160
E value 2.0e-10
Match length 87
% identity 46
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 199759
Contig ID 62872_1.R1039
5'-most EST uC-gsflnu33B100d07b1
Method BLASTX
NCBI GI g3372230
BLAST score 499
E value 1.0e-50
Match length 121
% identity 79
NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No. 199760
Contig ID 62885_1.R1039
5'-most EST uC-gsflnu33B099b11b1
Method BLASTX
NCBI GI g4262250
BLAST score 976
E value 1.0e-106
Match length 209
% identity 89
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 199761
Contig ID 62948_1.R1039
5'-most EST LIB3272-052-P1-K1-D9

Seq. No. 199762
Contig ID 62962_1.R1039
5'-most EST g5050549
Method BLASTX
NCBI GI g3786017
BLAST score 430
E value 5.0e-42
Match length 163
% identity 55
NCBI Description (AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No. 199763
Contig ID 62963_1.R1039
5'-most EST uC-gsflnu33B072d11b1
Method BLASTX
NCBI GI g3269293
BLAST score 280
E value 6.0e-25
Match length 90
% identity 64
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 199764

Contig ID	63028_1.R1039
5'-most EST	LIB3272-053-P1-K1-E1

Seq. No.	199765
Contig ID	63043_1.R1039
5'-most EST	g3325594
Method	BLASTX
NCBI GI	g3114658
BLAST score	188
E value	8.0e-14
Match length	109
% identity	35
NCBI Description	(AF060871) hypothetical alcohol dehydrogenase [Rhodococcus rhodochrous]

Seq. No.	199766
Contig ID	63124_1.R1039
5'-most EST	LIB3272-054-P1-K1-F8
Method	BLASTX
NCBI GI	g3236240
BLAST score	224
E value	5.0e-18
Match length	99
% identity	52
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	199767
Contig ID	63126_1.R1039
5'-most EST	uC-gsflnu33B051b08b1
Method	BLASTX
NCBI GI	g2370459
BLAST score	330
E value	1.0e-30
Match length	111
% identity	63
NCBI Description	(Y11987) FPF1 protein [Sinapis alba]

Seq. No.	199768
Contig ID	63157_1.R1039
5'-most EST	LIB3272-055-P1-K1-F3

Seq. No.	199769
Contig ID	63317_1.R1039
5'-most EST	uC-gsronu33B148f05b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	504
E value	5.0e-51
Match length	168
% identity	62
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	199770
Contig ID	63318_1.R1039
5'-most EST	uC-gsronu33B001b01b1

Seq. No.	199771
Contig ID	63323_1.R1039
5'-most EST	uC-gsflnu33B070b10b1

Seq. No.	199772
Contig ID	63366_1.R1039
5'-most EST	uC-gsflnu33B084f08b1
Method	BLASTX
NCBI GI	g3482933
BLAST score	288
E value	8.0e-26
Match length	89
% identity	65
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	199773
Contig ID	63372_1.R1039
5'-most EST	uC-gsronu33B001h08b1
Method	BLASTX
NCBI GI	g1362015
BLAST score	201
E value	2.0e-15
Match length	74
% identity	58
NCBI Description	zinc finger protein 1 - Arabidopsis thaliana >gi|2129779|pir||S71240 zinc finger protein 1 - Arabidopsis thaliana >gi|790673 (L39644) zinc finger protein [Arabidopsis thaliana] >gi|1297186 (U53501) zinc finger protein 1 [Arabidopsis thaliana]

Seq. No.	199774
Contig ID	63428_1.R1039
5'-most EST	uC-gsronu33B002h11b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	255
E value	1.0e-21
Match length	78
% identity	55
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	199775
Contig ID	63439_1.R1039
5'-most EST	uC-gsflnu33B005f05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	2.0e-09
Match length	34
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	199776
Contig ID	63444_1.R1039
5'-most EST	uC-gsronu33B166c02b2
Method	BLASTX

NCBI GI	g2982455
BLAST score	788
E value	1.0e-84
Match length	197
% identity	76
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Seq. No.	199777
Contig ID	63445_1.R1039
5'-most EST	uC-gsronu33B004b07b1

Seq. No.	199778
Contig ID	63468_1.R1039
5'-most EST	uC-gsflnu33B109d07b1

Seq. No.	199779
Contig ID	63496_1.R1039
5'-most EST	uC-gsronu33B005f04b1
Method	BLASTX
NCBI GI	g1403134
BLAST score	413
E value	2.0e-40
Match length	130
% identity	63
NCBI Description	(X98453) peroxidase [Arabidopsis thaliana]

Seq. No.	199780
Contig ID	63497_1.R1039
5'-most EST	uC-gsflnu33B128b10b1

Seq. No.	199781
Contig ID	63510_1.R1039
5'-most EST	uC-gsronu33B007a11b1

Seq. No.	199782
Contig ID	63536_1.R1039
5'-most EST	uC-gsflnu33B016h07b1
Method	BLASTX
NCBI GI	g3297815
BLAST score	257
E value	2.0e-23
Match length	96
% identity	60
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	199783
Contig ID	63539_1.R1039
5'-most EST	uC-gsronu33B007e11b1
Method	BLASTX
NCBI GI	g1755152
BLAST score	370
E value	2.0e-35
Match length	122
% identity	58
NCBI Description	(U75187) germin-like protein [Arabidopsis thaliana]

Seq. No. 199784
Contig ID 63573_1.R1039
5'-most EST g3326638

Seq. No. 199785
Contig ID 63577_1.R1039
5'-most EST uC-gsflmaxxa003d05b1
Method BLASTX
NCBI GI g2351374
BLAST score 992
E value 1.0e-112
Match length 235
% identity 89
NCBI Description (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No. 199786
Contig ID 63577_2.R1039
5'-most EST uC-gsflnu33B146d04b1

Seq. No. 199787
Contig ID 63578_1.R1039
5'-most EST uC-gsronu33B149g07b1

Seq. No. 199788
Contig ID 63596_1.R1039
5'-most EST uC-gsflnu33B084b04b1
Method BLASTX
NCBI GI g3912917
BLAST score 343
E value 6.0e-32
Match length 198
% identity 42
NCBI Description (AF001308) putative NAK-like ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 199789
Contig ID 63604_1.R1039
5'-most EST g5047177
Method BLASTX
NCBI GI g4455190
BLAST score 505
E value 2.0e-61
Match length 194
% identity 68
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 199790
Contig ID 63608_1.R1039
5'-most EST uC-gsronu33B164g08b2
Method BLASTX
NCBI GI g4455159
BLAST score 684
E value 3.0e-99
Match length 237
% identity 73
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	199791
Contig ID	63629_1.R1039
5'-most EST	uC-gsflmaxxa088b11b1
Method	BLASTX
NCBI GI	g3043612
BLAST score	296
E value	2.0e-26
Match length	229
% identity	37
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]

Seq. No.	199792
Contig ID	63641_1.R1039
5'-most EST	uC-gsronu33B011a08b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	383
E value	1.0e-36
Match length	177
% identity	46
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	199793
Contig ID	63648_1.R1039
5'-most EST	uC-gsronu33B109e12b1

Seq. No.	199794
Contig ID	63653_1.R1039
5'-most EST	uC-gsronu33B011c02b1
Method	BLASTX
NCBI GI	g3510264
BLAST score	449
E value	1.0e-44
Match length	97
% identity	73
NCBI Description	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]

Seq. No.	199795
Contig ID	63656_1.R1039
5'-most EST	uC-gsflnu33B140h11b1

Seq. No.	199796
Contig ID	63663_1.R1039
5'-most EST	uC-gsronu33B011d04b1
Method	BLASTX
NCBI GI	g3005576
BLAST score	781
E value	1.0e-115
Match length	238
% identity	63
NCBI Description	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No.	199797

Contig ID	63671_1.R1039
5'-most EST	uC-gsronu33B166b10b2
Method	BLASTX
NCBI GI	g1041702
BLAST score	316
E value	3.0e-29
Match length	80
% identity	68
NCBI Description	(U30476) expansin At-EXP1 [Arabidopsis thaliana]

Seq. No.	199798
Contig ID	63683_1.R1039
5'-most EST	uC-gsronu33B124a11b1
Method	BLASTX
NCBI GI	g4539660
BLAST score	405
E value	4.0e-50
Match length	155
% identity	59
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	199799
Contig ID	63707_1.R1039
5'-most EST	uC-gsflnu33B056g04b1
Method	BLASTX
NCBI GI	g3914467
BLAST score	840
E value	4.0e-90
Match length	204
% identity	84
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi|1864003|dbj|BAA19252| (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	199800
Contig ID	63744_1.R1039
5'-most EST	g5045582
Method	BLASTX
NCBI GI	g2245138
BLAST score	410
E value	8.0e-40
Match length	151
% identity	53
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199801
Contig ID	63758_1.R1039
5'-most EST	uC-gsronu33B012e10b1

Seq. No.	199802
Contig ID	63763_1.R1039
5'-most EST	uC-gsronu33B012f03b1

Seq. No.	199803
Contig ID	63782_1.R1039
5'-most EST	uC-gsronu33B012h03b1
Method	BLASTN

NCBI GI	g16131
BLAST score	115
E value	4.0e-58
Match length	119
% identity	99
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment

Seq. No.	199804
Contig ID	63790_1.R1039
5'-most EST	uC-gsronu33B012h11b1
Method	BLASTN
NCBI GI	g3510343
BLAST score	107
E value	7.0e-53
Match length	619
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	199805
Contig ID	63819_1.R1039
5'-most EST	uC-gsflmaxxa003e01b1
Method	BLASTX
NCBI GI	g4455232
BLAST score	707
E value	7.0e-75
Match length	156
% identity	80
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	199806
Contig ID	63846_1.R1039
5'-most EST	uC-gsflnu33B070f07b1
Method	BLASTX
NCBI GI	g4544369
BLAST score	196
E value	4.0e-15
Match length	131
% identity	38
NCBI Description	(AC006920) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199807
Contig ID	63857_1.R1039
5'-most EST	uC-gsronu33B015e02b1
Method	BLASTX
NCBI GI	g1370176
BLAST score	821
E value	6.0e-88
Match length	178
% identity	90
NCBI Description	(Z73937) RAB2A [Lotus japonicus]

Seq. No.	199808
Contig ID	63871_1.R1039
5'-most EST	uC-gsronu33B015f06b1

Seq. No.	199809
Contig ID	63925_1.R1039
5'-most EST	uC-gsronu33B156h01b1

Seq. No.	199810
Contig ID	63951_2.R1039
5'-most EST	uC-gsflnu33B108a01b1

Seq. No.	199811
Contig ID	63963_1.R1039
5'-most EST	uC-gsflnu33B074b11b1
Method	BLASTX
NCBI GI	g1657948
BLAST score	725
E value	7.0e-77
Match length	185
% identity	77
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	199812
Contig ID	63985_1.R1039
5'-most EST	uC-gsronu33B017c04b1
Method	BLASTX
NCBI GI	g2736075
BLAST score	675
E value	5.0e-71
Match length	209
% identity	64
NCBI Description	(AF016644) PAP-specific phosphatase; HAL2-like protein [Arabidopsis thaliana]

Seq. No.	199813
Contig ID	64024_1.R1039
5'-most EST	uC-gsronu33B017h07b1

Seq. No.	199814
Contig ID	64037_1.R1039
5'-most EST	uC-gsronu33B160h12b1

Seq. No.	199815
Contig ID	64051_1.R1039
5'-most EST	g5046411
Method	BLASTX
NCBI GI	g3201615
BLAST score	608
E value	5.0e-63
Match length	251
% identity	51
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	199816
Contig ID	64108_1.R1039
5'-most EST	uC-gsronu33B116d03b1

Seq. No.	199817
Contig ID	64111_1.R1039
5'-most EST	uC-gsflnu33B138d10b1

Method	BLASTX
NCBI GI	g2598575
BLAST score	233
E value	3.0e-19
Match length	134
% identity	39
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	199818
Contig ID	64157_1.R1039
5'-most EST	uC-gsronu33B019h02b1
Method	BLASTX
NCBI GI	g2673915
BLAST score	383
E value	2.0e-66
Match length	172
% identity	69
NCBI Description	(AC002561) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	199819
Contig ID	64164_1.R1039
5'-most EST	uC-gsronu33B166g03b2
Method	BLASTX
NCBI GI	g4063744
BLAST score	210
E value	1.0e-16
Match length	69
% identity	64
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199820
Contig ID	64175_1.R1039
5'-most EST	uC-gsronu33B077f11b1
Method	BLASTX
NCBI GI	g4090200
BLAST score	156
E value	3.0e-10
Match length	50
% identity	62
NCBI Description	(AJ012310) WUSCHEL protein [Arabidopsis thaliana]

Seq. No.	199821
Contig ID	64180_1.R1039
5'-most EST	uC-gsflnu33B018c01b1

Seq. No.	199822
Contig ID	64182_1.R1039
5'-most EST	uC-gsronu33B021b12b1

Seq. No.	199823
Contig ID	64193_1.R1039
5'-most EST	uC-gsronu33B021d01b1
Method	BLASTX
NCBI GI	g1931655
BLAST score	261
E value	3.0e-22
Match length	176

% identity	36
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	199824
Contig ID	64219_1.R1039
5'-most EST	uC-gsronu33B090a08b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	9.0e-09
Match length	34
% identity	59
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	199825
Contig ID	64221_1.R1039
5'-most EST	uC-gsronu33B021g02b1
Method	BLASTX
NCBI GI	g3184288
BLAST score	234
E value	2.0e-19
Match length	58
% identity	69
NCBI Description	(AC004136) unknown protein [Arabidopsis thaliana]

Seq. No.	199826
Contig ID	64231_1.R1039
5'-most EST	uC-gsflnu33B085h03b1
Method	BLASTX
NCBI GI	g2281633
BLAST score	162
E value	3.0e-19
Match length	119
% identity	52
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	199827
Contig ID	64322_1.R1039
5'-most EST	uC-gsronu33B029e11b1

Seq. No.	199828
Contig ID	64326_1.R1039
5'-most EST	uC-gsronu33B137d03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	46
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	199829
Contig ID	64333_1.R1039
5'-most EST	uC-gsflnu33B071g09b1

Seq. No. 199830

Contig ID	64335_1.R1039
5'-most EST	uC-gsronu33B048d03b1
Method	BLASTX
NCBI GI	g2493318
BLAST score	324
E value	1.0e-30
Match length	97
% identity	71
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi|562779|emb|CAA80963| (Z25471) blue copper protein [Pisum sativum] >gi|1098264|prf||2115352A blue Cu protein [Pisum sativum]

Seq. No.	199831
Contig ID	64340_1.R1039
5'-most EST	g5045472
Method	BLASTX
NCBI GI	g3702332
BLAST score	246
E value	1.0e-20
Match length	181
% identity	32
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	199832
Contig ID	64343_1.R1039
5'-most EST	uC-gsronu33B031b04b1
Method	BLASTX
NCBI GI	g1246403
BLAST score	389
E value	2.0e-37
Match length	178
% identity	48
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi|3406035 (AC005405) TINY [Arabidopsis thaliana]

Seq. No.	199833
Contig ID	64432_1.R1039
5'-most EST	g5046816
Method	BLASTX
NCBI GI	g2224911
BLAST score	814
E value	3.0e-87
Match length	182
% identity	85
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	199834
Contig ID	64457_1.R1039
5'-most EST	uC-gsronu33B109b01b1

Seq. No.	199835
Contig ID	64461_1.R1039
5'-most EST	uC-gsronu33B164c01b2

Seq. No.	199836
Contig ID	64472_1.R1039

5'-most EST	uC-gsflnu33B129h10b1
Seq. No.	199837
Contig ID	64498_1.R1039
5'-most EST	g5050382
Method	BLASTX
NCBI GI	g3335372
BLAST score	401
E value	1.0e-38
Match length	269
% identity	38
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.	199838
Contig ID	64520_1.R1039
5'-most EST	uC-gsronu33B037c05b1
Method	BLASTX
NCBI GI	g4220527
BLAST score	259
E value	2.0e-22
Match length	85
% identity	64
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	199839
Contig ID	64544_1.R1039
5'-most EST	uC-gsflnu33B049h01b1
Seq. No.	199840
Contig ID	64550_1.R1039
5'-most EST	g5045356
Method	BLASTX
NCBI GI	g4544432
BLAST score	808
E value	2.0e-86
Match length	180
% identity	82
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]
Seq. No.	199841
Contig ID	64567_1.R1039
5'-most EST	uC-gsflmaxxa095a11b1
Method	BLASTX
NCBI GI	g2213600
BLAST score	1034
E value	1.0e-113
Match length	290
% identity	69
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]
Seq. No.	199842
Contig ID	64597_1.R1039
5'-most EST	uC-gsflnu33B100a05b1
Seq. No.	199843
Contig ID	64610_1.R1039

5'-most EST	uC-gsronu33B038e12b1
Seq. No.	199844
Contig ID	64654_1.R1039
5'-most EST	uC-gsflnu33B146f03b1
Method	BLASTX
NCBI GI	g1644402
BLAST score	455
E value	3.0e-45
Match length	184
% identity	48
NCBI Description	(U73524) putative ATP/GTP-binding protein [Homo sapiens]
Seq. No.	199845
Contig ID	64668_1.R1039
5'-most EST	g5049407
Seq. No.	199846
Contig ID	64713_1.R1039
5'-most EST	g5044613
Method	BLASTX
NCBI GI	g1351856
BLAST score	804
E value	3.0e-86
Match length	174
% identity	84
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi|868003|dbj|BAA06108| (D29629) aconitase [Cucurbita sp.]
Seq. No.	199847
Contig ID	64716_1.R1039
5'-most EST	uC-gsronu33B040e12b1
Method	BLASTX
NCBI GI	g2316016
BLAST score	552
E value	1.0e-78
Match length	290
% identity	60
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
Seq. No.	199848
Contig ID	64720_1.R1039
5'-most EST	uC-gsronu33B040f08b1
Method	BLASTX
NCBI GI	g1657619
BLAST score	203
E value	2.0e-15
Match length	156
% identity	31
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi|3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.	199849
Contig ID	64726_1.R1039
5'-most EST	uC-gsflnu33B056h11b1
Method	BLASTX

NCBI GI	g4309730
BLAST score	232
E value	5.0e-19
Match length	111
% identity	44
NCBI Description	(AC006439) putative lipid transfer protein [Arabidopsis thaliana]

Seq. No.	199850
Contig ID	64727_1.R1039
5'-most EST	uC-gsronu33B040g12b1
Method	BLASTX
NCBI GI	g1212921
BLAST score	352
E value	2.0e-33
Match length	109
% identity	65
NCBI Description	(X95953) aquaporin [Helianthus annuus]

Seq. No.	199851
Contig ID	64771_1.R1039
5'-most EST	uC-gsronu33B041g05b1

Seq. No.	199852
Contig ID	64800_1.R1039
5'-most EST	uC-gsronu33B042e08b1
Method	BLASTX
NCBI GI	g2462760
BLAST score	424
E value	2.0e-41
Match length	174
% identity	52
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	199853
Contig ID	64853_1.R1039
5'-most EST	uC-gsflnu33B100a10b1

Seq. No.	199854
Contig ID	64854_1.R1039
5'-most EST	uC-gsronu33B147b03b1
Method	BLASTX
NCBI GI	g1706918
BLAST score	375
E value	5.0e-36
Match length	139
% identity	53
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi|498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	199855
Contig ID	64890_1.R1039
5'-most EST	g5046291
Method	BLASTX
NCBI GI	g1346754
BLAST score	1134
E value	1.0e-128

Match length	258
% identity	84
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 >gi|421851|pir||S31086 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP2) - Arabidopsis thaliana >gi|166797 (M93409) catalytic subunit [Arabidopsis thaliana]

Seq. No.	199856
Contig ID	64914_1.R1039
5'-most EST	g5050338

Seq. No.	199857
Contig ID	64937_1.R1039
5'-most EST	uC-gsronu33B047h01b1

Seq. No.	199858
Contig ID	64973_1.R1039
5'-most EST	g5050093
Method	BLASTX
NCBI GI	g1805654
BLAST score	358
E value	8.0e-34
Match length	159
% identity	48
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No.	199859
Contig ID	64974_1.R1039
5'-most EST	uC-gsronu33B154f10b2

Seq. No.	199860
Contig ID	64985_1.R1039
5'-most EST	uC-gsronu33B049d02b1
Method	BLASTX
NCBI GI	g4107103
BLAST score	207
E value	2.0e-16
Match length	61
% identity	62
NCBI Description	(AB015143) AHP3 [Arabidopsis thaliana]

Seq. No.	199861
Contig ID	65007_1.R1039
5'-most EST	uC-gsronu33B049g12b1

Seq. No.	199862
Contig ID	65020_1.R1039
5'-most EST	uC-gsronu33B150c12b1
Method	BLASTX
NCBI GI	g3269287
BLAST score	939
E value	1.0e-102
Match length	201
% identity	89
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	199863
Contig ID	65043_1.R1039
5'-most EST	uC-gsronu33B050c09b1
Method	BLASTX
NCBI GI	g2911040
BLAST score	514
E value	5.0e-52
Match length	186
% identity	55
NCBI Description	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	199864
Contig ID	65057_1.R1039
5'-most EST	uC-gsronu33B050e10b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	285
E value	3.0e-25
Match length	124
% identity	49
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	199865
Contig ID	65066_1.R1039
5'-most EST	uC-gsflnu33B146e08b1
Method	BLASTX
NCBI GI	g1755166
BLAST score	849
E value	4.0e-91
Match length	213
% identity	76
NCBI Description	(U75194) germin-like protein [Arabidopsis thaliana]

Seq. No.	199866
Contig ID	65087_1.R1039
5'-most EST	g5047189
Method	BLASTX
NCBI GI	g1723660
BLAST score	139
E value	4.0e-10
Match length	137
% identity	34
NCBI Description	HYPOTHETICAL 27.6 KD PROTEIN IN RPL26B-ACB1 INTERGENIC REGION >gi|2132589|pir||S64327 probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) >gi|1323019|emb|CAA97024| (Z72821) ORF YGR036c [Saccharomyces cerevisiae]

Seq. No.	199867
Contig ID	65100_1.R1039
5'-most EST	uC-gsronu33B051g11b1

Seq. No.	199868
Contig ID	65104_1.R1039
5'-most EST	uC-gsronu33B051h02b1

Seq. No.	199869
Contig ID	65181_1.R1039
5'-most EST	uC-gsronu33B108f08b1
Method	BLASTX
NCBI GI	g4105697
BLAST score	715
E value	1.0e-75
Match length	195
% identity	64
NCBI Description	(AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	199870
Contig ID	65185_1.R1039
5'-most EST	uC-gsronu33B057d08b1
Method	BLASTX
NCBI GI	g452519
BLAST score	146
E value	5.0e-09
Match length	78
% identity	24
NCBI Description	(D26362) similar to Human homolog of Drosophila female sterile homeotic mRNA (HUMFSHG) [Homo sapiens]

Seq. No.	199871
Contig ID	65195_1.R1039
5'-most EST	g5047412
Method	BLASTX
NCBI GI	g3335345
BLAST score	748
E value	3.0e-79
Match length	204
% identity	77
NCBI Description	(AC004512) Contains similarity to ABC transporter gb|1651790 from Synechocystis sp. gb|D90900. [Arabidopsis thaliana]

Seq. No.	199872
Contig ID	65223_1.R1039
5'-most EST	uC-gsflnu33B061g01b1

Seq. No.	199873
Contig ID	65285_1.R1039
5'-most EST	g5046882
Method	BLASTX
NCBI GI	g3953458
BLAST score	812
E value	7.0e-87
Match length	251
% identity	68
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	199874
Contig ID	65285_2.R1039
5'-most EST	uC-gsflnu33B109f06b1
Method	BLASTX
NCBI GI	g3953458

BLAST score 372
E value 1.0e-35
Match length 140
% identity 56
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 199875
Contig ID 65286_1.R1039
5'-most EST uC-gsflnu33B141f10b1
Method BLASTX
NCBI GI g3775999
BLAST score 575
E value 2.0e-59
Match length 169
% identity 69
NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 199876
Contig ID 65288_1.R1039
5'-most EST uC-gsronu33B110h02b1
Method BLASTN
NCBI GI g3775998
BLAST score 49
E value 2.0e-18
Match length 225
% identity 80
NCBI Description Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH11

Seq. No. 199877
Contig ID 65296_1.R1039
5'-most EST uC-gsflnu33B011f06b1
Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 2.0e-09
Match length 34
% identity 59
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 199878
Contig ID 65299_1.R1039
5'-most EST uC-gsronu33B061d05b1

Seq. No. 199879
Contig ID 65300_1.R1039
5'-most EST uC-gsronu33B061d07b1

Seq. No. 199880
Contig ID 65304_1.R1039
5'-most EST uC-gsronu33B060e05b1
Method BLASTX
NCBI GI g2244855
BLAST score 239
E value 4.0e-20
Match length 104
% identity 47
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199881
Contig ID	65307_1.R1039
5'-most EST	uC-gsronu33B061f06b1

Seq. No.	199882
Contig ID	65309_1.R1039
5'-most EST	g3326195
Method	BLASTX
NCBI GI	g1084349
BLAST score	454
E value	6.0e-45
Match length	106
% identity	85
NCBI Description	aldehyde dehydrogenase homolog btg-26 - rape >gi|913941|bbs|164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No.	199883
Contig ID	65377_1.R1039
5'-most EST	uC-gsronu33B062a12b1
Method	BLASTX
NCBI GI	g4559333
BLAST score	327
E value	2.0e-30
Match length	112
% identity	39
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	199884
Contig ID	65400_1.R1039
5'-most EST	uC-gsronu33B062e07b1
Method	BLASTX
NCBI GI	g3913633
BLAST score	111
E value	5.0e-11
Match length	56
% identity	70
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi|2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	199885
Contig ID	65422_1.R1039
5'-most EST	uC-gsflnu33B136h09b1
Method	BLASTX
NCBI GI	g1518113
BLAST score	151
E value	6.0e-10
Match length	35
% identity	74
NCBI Description	(U66193) SLL2 [Brassica napus]

Seq. No.	199886
Contig ID	65489_1.R1039
5'-most EST	uC-gsflnu33B140g05b1

Seq. No.	199887
Contig ID	65492_1.R1039
5'-most EST	uC-gsronu33B076f05b1
Method	BLASTX
NCBI GI	g4510379
BLAST score	310
E value	2.0e-28
Match length	125
% identity	50
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199888
Contig ID	65522_1.R1039
5'-most EST	uC-gsronu33B077a12b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	341
E value	6.0e-32
Match length	148
% identity	48
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	199889
Contig ID	65527_1.R1039
5'-most EST	g3326129
Method	BLASTX
NCBI GI	g4234941
BLAST score	261
E value	2.0e-22
Match length	208
% identity	25
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	199890
Contig ID	65528_1.R1039
5'-most EST	uC-gsflnu33B012d04b1

Seq. No.	199891
Contig ID	65549_1.R1039
5'-most EST	uC-gsronu33B077e01b1
Method	BLASTX
NCBI GI	g2739000
BLAST score	372
E value	2.0e-46
Match length	216
% identity	49
NCBI Description	(AF022459) CYP71D10p [Glycine max]

Seq. No.	199892
Contig ID	65549_2.R1039
5'-most EST	uC-gsronu33B169g01b1
Method	BLASTX
NCBI GI	g3334661
BLAST score	330
E value	2.0e-51
Match length	187

% identity	56
NCBI Description	(Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	199893
Contig ID	65617_1.R1039
5'-most EST	g5049306
Method	BLASTX
NCBI GI	g135535
BLAST score	870
E value	8.0e-94
Match length	220
% identity	81
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi|322602|pir||JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi|217871|dbj|BAA01955| (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi|2326265|dbj|BAA21772| (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	199894
Contig ID	65622_1.R1039
5'-most EST	uC-gsronu33B078d12b1

Seq. No.	199895
Contig ID	65630_1.R1039
5'-most EST	uC-gsronu33B078e11b1

Seq. No.	199896
Contig ID	65637_1.R1039
5'-most EST	uC-gsflnu33B142h02b1
Method	BLASTX
NCBI GI	g3236261
BLAST score	243
E value	9.0e-42
Match length	181
% identity	49
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	199897
Contig ID	65659_1.R1039
5'-most EST	uC-gsflmaxxa026f05b1
Method	BLASTX
NCBI GI	g3228668
BLAST score	144
E value	5.0e-09
Match length	71
% identity	41
NCBI Description	(AF069988) nitrilase 1 [Mus musculus]

Seq. No.	199898
Contig ID	65665_1.R1039
5'-most EST	uC-gsronu33B079a11b1
Method	BLASTX
NCBI GI	g1143511
BLAST score	773
E value	2.0e-82

Match length	157
% identity	92
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi|1586034|prf||2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No.	199899
Contig ID	65738_1.R1039
5'-most EST	uC-gsronu33b112d03b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	552
E value	1.0e-56
Match length	191
% identity	58
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	199900
Contig ID	65748_1.R1039
5'-most EST	uC-gsflnu33B058f03b1

Seq. No.	199901
Contig ID	65749_1.R1039
5'-most EST	g5044311
Method	BLASTX
NCBI GI	g1707412
BLAST score	428
E value	5.0e-42
Match length	195
% identity	45
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	199902
Contig ID	65804_1.R1039
5'-most EST	uC-gsronu33B143f01b1
Method	BLASTX
NCBI GI	g4522008
BLAST score	224
E value	2.0e-18
Match length	88
% identity	55
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199903
Contig ID	65806_1.R1039
5'-most EST	g3326581
Method	BLASTX
NCBI GI	g2829893
BLAST score	951
E value	1.0e-103
Match length	225
% identity	85
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	199904
Contig ID	65996_1.R1039

5'-most EST	uC-gsronu33B089d04b1
Method	BLASTX
NCBI GI	g2213597
BLAST score	334
E value	4.0e-31
Match length	119
% identity	54
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	199905
Contig ID	66023_1.R1039
5'-most EST	uC-gsflnu33B062f10b1
Method	BLASTX
NCBI GI	g3929333
BLAST score	194
E value	5.0e-24
Match length	145
% identity	41
NCBI Description	CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD) (PHENYLUREA DEALKYLASE) >gi|2370230|emb|CAA71054| (Y09920) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq. No.	199906
Contig ID	66026_1.R1039
5'-most EST	uC-gsflnu33B129f10b1

Seq. No.	199907
Contig ID	66027_1.R1039
5'-most EST	uC-gsflnu33B028b12b1
Method	BLASTX
NCBI GI	g3164222
BLAST score	169
E value	6.0e-12
Match length	131
% identity	35
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi|4206205 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	199908
Contig ID	66029_1.R1039
5'-most EST	uC-gsronu33B089h06b1

Seq. No.	199909
Contig ID	66057_1.R1039
5'-most EST	uC-gsronu33B090e02b1
Method	BLASTX
NCBI GI	g3702317
BLAST score	176
E value	9.0e-13
Match length	61
% identity	61
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana] >gi|4559376|gb|AAD23036.1|AC006526_1 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	199910

Contig ID	66062_1.R1039
5'-most EST	uC-gsronu33B090e09b1
Method	BLASTX
NCBI GI	g2570523
BLAST score	310
E value	2.0e-28
Match length	111
% identity	58
NCBI Description	(AF022873) inorganic phosphate transporter [Lycopersicon esculentum]

Seq. No.	199911
Contig ID	66072_1.R1039
5'-most EST	uC-gsronu33B132d09b1

Seq. No.	199912
Contig ID	66088_1.R1039
5'-most EST	uC-gsronu33B096b01b1

Seq. No.	199913
Contig ID	66099_1.R1039
5'-most EST	uC-gsflmaxxa058a10b1

Seq. No.	199914
Contig ID	66102_1.R1039
5'-most EST	g5046926

Seq. No.	199915
Contig ID	66107_1.R1039
5'-most EST	uC-gsronu33B098a10b1

Seq. No.	199916
Contig ID	66117_2.R1039
5'-most EST	uC-gsronu33B098c01b1
Method	BLASTX
NCBI GI	g3434975
BLAST score	351
E value	4.0e-33
Match length	148
% identity	54
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	199917
Contig ID	66146_1.R1039
5'-most EST	uC-gsflnu33B012g11b1

Seq. No.	199918
Contig ID	66156_1.R1039
5'-most EST	uC-gsronu33B106h05b2
Method	BLASTX
NCBI GI	g3850823
BLAST score	534
E value	1.0e-54
Match length	120
% identity	88
NCBI Description	(Y18351) U2 snRNP auxiliary factor, large subunit

[Nicotiana plumbaginifolia]

Seq. No.	199919
Contig ID	66182_1.R1039
5'-most EST	g5045858
Method	BLASTX
NCBI GI	g1706319
BLAST score	652
E value	5.0e-70
Match length	200
% identity	63
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi|481829|pir||S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi|416534|emb|CAA50719| (X71900) histidine decarboxylase [Lycopersicon esculentum]

Seq. No.	199920
Contig ID	66197_1.R1039
5'-most EST	uC-gsflmaxxa076c10b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	387
E value	2.0e-37
Match length	125
% identity	59
NCBI Description	(AL022604) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	199921
Contig ID	66224_1.R1039
5'-most EST	uC-gsronu33B099g08b1

Seq. No.	199922
Contig ID	66240_1.R1039
5'-most EST	uC-gsronu33B100a12b1
Method	BLASTX
NCBI GI	g4263522
BLAST score	140
E value	4.0e-09
Match length	55
% identity	42
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199923
Contig ID	66259_1.R1039
5'-most EST	g3325586
Method	BLASTX
NCBI GI	g1890317
BLAST score	1096
E value	1.0e-120
Match length	274
% identity	74
NCBI Description	(Y11791) peroxidase ATP26a [Arabidopsis thaliana]

Seq. No.	199924
Contig ID	66282_1.R1039
5'-most EST	uC-gsronu33B179a06b1

Method	BLASTX
NCBI GI	g2244952
BLAST score	212
E value	2.0e-17
Match length	75
% identity	63
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	199925
Contig ID	66307_1.R1039
5'-most EST	uC-gsronu33B101d02b1
Method	BLASTX
NCBI GI	g1208497
BLAST score	384
E value	5.0e-37
Match length	119
% identity	65
NCBI Description	(D38125) EREBP-4 [Nicotiana tabacum]

Seq. No.	199926
Contig ID	66333_1.R1039
5'-most EST	g3220218

Seq. No.	199927
Contig ID	66334_1.R1039
5'-most EST	uC-gsronu33B103a05b1

Seq. No.	199928
Contig ID	66338_1.R1039
5'-most EST	uC-gsronu33B162g04b2
Method	BLASTX
NCBI GI	g1055162
BLAST score	241
E value	3.0e-20
Match length	157
% identity	41
NCBI Description	(U40029) coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA yk7e12.5; co

Seq. No.	199929
Contig ID	66352_1.R1039
5'-most EST	uC-gsronu33B103c01b1
Method	BLASTX
NCBI GI	g3182950
BLAST score	175
E value	4.0e-12
Match length	98
% identity	39
NCBI Description	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) >gi|2645431 (AF006514) CHD2 [Homo sapiens] >gi|4557449|ref|NP_001262.1|pCHD2| chromodomain helicase DNA binding protein

Seq. No.	199930
Contig ID	66353_1.R1039
5'-most EST	uC-gsronu33B103c05b1
Method	BLASTX
NCBI GI	g2880042
BLAST score	310
E value	2.0e-28
Match length	87
% identity	64
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	199931
Contig ID	66370_1.R1039
5'-most EST	g5049689
Method	BLASTX
NCBI GI	g4220527
BLAST score	658
E value	8.0e-69
Match length	213
% identity	56
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	199932
Contig ID	66374_1.R1039
5'-most EST	uC-gsronu33B103e07b1
Method	BLASTX
NCBI GI	g2582971
BLAST score	331
E value	1.0e-30
Match length	98
% identity	66
NCBI Description	(D83711) TKRP125 [Nicotiana tabacum]

Seq. No.	199933
Contig ID	66390_1.R1039
5'-most EST	uC-gsronu33B103g04b1

Seq. No.	199934
Contig ID	66412_1.R1039
5'-most EST	uC-gsronu33B138d08b1
Method	BLASTX
NCBI GI	g4490309
BLAST score	870
E value	9.0e-94
Match length	222
% identity	73
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	199935
Contig ID	66419_1.R1039
5'-most EST	uC-gsflnu33B008c11b1

Seq. No.	199936
Contig ID	66507_1.R1039
5'-most EST	uC-gsronu33B143h07b1

Method	BLASTX
NCBI GI	g2677828
BLAST score	813
E value	3.0e-87
Match length	185
% identity	82
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	199937
Contig ID	66520_1.R1039
5'-most EST	uC-gsronu33B106e04b2
Method	BLASTX
NCBI GI	g3892058
BLAST score	528
E value	1.0e-53
Match length	229
% identity	48
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	199938
Contig ID	66542_1.R1039
5'-most EST	g5047549

Seq. No.	199939
Contig ID	66559_1.R1039
5'-most EST	uC-gsflmaxxa012b07b1
Method	BLASTX
NCBI GI	g4490735
BLAST score	463
E value	2.0e-46
Match length	138
% identity	67
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	199940
Contig ID	66599_1.R1039
5'-most EST	uC-gsronu33B145e12b1
Method	BLASTX
NCBI GI	g2739279
BLAST score	345
E value	2.0e-32
Match length	145
% identity	48
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi|2791348|emb|CAA11154| (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	199941
Contig ID	66614_1.R1039
5'-most EST	uC-gsflmaxxa046f04b1
Method	BLASTX
NCBI GI	g466044
BLAST score	197
E value	7.0e-15
Match length	55
% identity	58

NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi|630780|pir||S44909 ZK686.4 protein - Caenorhabditis elegans >gi|304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
Seq. No.	199942
Contig ID	66656_1.R1039
5'-most EST	uC-gsflnu33B130c09b1
Method	BLASTX
NCBI GI	g3482910
BLAST score	932
E value	1.0e-101
Match length	211
% identity	77
NCBI Description	(AC003970) Similar to rice water stress induced protein gi|537404 [Arabidopsis thaliana]
Seq. No.	199943
Contig ID	66657_1.R1039
5'-most EST	uC-gsflnu33B135h09b1
Method	BLASTX
NCBI GI	g4455129
BLAST score	202
E value	1.0e-15
Match length	118
% identity	47
NCBI Description	(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
Seq. No.	199944
Contig ID	66741_1.R1039
5'-most EST	uC-gsflnu33B046c06b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	33
E value	8.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.	199945
Contig ID	66795_1.R1039
5'-most EST	uC-gsflnu33B107g12b1
Seq. No.	199946
Contig ID	66815_1.R1039
5'-most EST	uC-gsronu33B145h06b1
Method	BLASTX
NCBI GI	g2558664
BLAST score	208
E value	2.0e-16
Match length	61
% identity	64
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]
Seq. No.	199947

Contig ID	66837_1.R1039
5'-most EST	uC-gsronu33B110h12b1
Method	BLASTX
NCBI GI	g3236238
BLAST score	374
E value	6.0e-36
Match length	76
% identity	89
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi|4519792|dbj|BAA75744.1| (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	199948
Contig ID	66849_1.R1039
5'-most EST	uC-gsflnu33B036d07b1
Method	BLASTX
NCBI GI	g4455342
BLAST score	597
E value	1.0e-61
Match length	192
% identity	60
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	199949
Contig ID	66852_1.R1039
5'-most EST	uC-gsronu33B111c02b1
Method	BLASTX
NCBI GI	g4539324
BLAST score	572
E value	5.0e-59
Match length	166
% identity	75
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	199950
Contig ID	66876_1.R1039
5'-most EST	uC-gsronu33B111e10b1
Method	BLASTX
NCBI GI	g2281103
BLAST score	288
E value	8.0e-26
Match length	97
% identity	55
NCBI Description	(AC002333) Glucan endo-1,3-beta glucosidase isolog [Arabidopsis thaliana]

Seq. No.	199951
Contig ID	66881_1.R1039
5'-most EST	uC-gsflnu33B036h07b1

Seq. No.	199952
Contig ID	66910_1.R1039
5'-most EST	g5044649
Method	BLASTX
NCBI GI	g3834302
BLAST score	956

E value	1.0e-104
Match length	250
% identity	77
NCBI Description	(AC005679) Similar to gb|D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb|F14272 and gb|F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	199953
Contig ID	66927_1.R1039
5'-most EST	uC-gsronu33B113c10b1

Seq. No.	199954
Contig ID	66933_1.R1039
5'-most EST	uC-gsronu33B113d07b1
Method	BLASTX
NCBI GI	g2281102
BLAST score	185
E value	9.0e-14
Match length	85
% identity	55
NCBI Description	(AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No.	199955
Contig ID	66976_1.R1039
5'-most EST	g3326265
Method	BLASTX
NCBI GI	g1706082
BLAST score	320
E value	9.0e-53
Match length	176
% identity	63
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi|629787|pir||S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi|619350|bbs|153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi|474392|emb|CAA55478| (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	199956
Contig ID	66976_2.R1039
5'-most EST	g5050714
Method	BLASTX
NCBI GI	g1706082
BLAST score	739
E value	2.0e-78
Match length	226
% identity	59
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi|629787|pir||S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi|619350|bbs|153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi|474392|emb|CAA55478| (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	199957

Contig ID	66977_1.R1039
5'-most EST	uC-gsronu33B114a06b1
Seq. No.	199958
Contig ID	66980_1.R1039
5'-most EST	g5044393
Method	BLASTX
NCBI GI	g2462825
BLAST score	202
E value	2.0e-15
Match length	60
% identity	62
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]
Seq. No.	199959
Contig ID	66983_1.R1039
5'-most EST	uC-gsronu33B114b07b1
Seq. No.	199960
Contig ID	66985_1.R1039
5'-most EST	uC-gsflmaxxa004h01b1
Seq. No.	199961
Contig ID	67020_1.R1039
5'-most EST	g5046019
Method	BLASTX
NCBI GI	g3901268
BLAST score	260
E value	2.0e-22
Match length	206
% identity	35
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]
Seq. No.	199962
Contig ID	67042_1.R1039
5'-most EST	uC-gsronu33B154d12b2
Seq. No.	199963
Contig ID	67053_1.R1039
5'-most EST	g5046217
Seq. No.	199964
Contig ID	67079_1.R1039
5'-most EST	uC-gsronu33B116e06b1
Method	BLASTX
NCBI GI	g3540201
BLAST score	759
E value	8.0e-81
Match length	218
% identity	72
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]
Seq. No.	199965
Contig ID	67136_1.R1039
5'-most EST	uC-gsronu33B117c08b1
Method	BLASTX

NCBI GI	g4490303
BLAST score	410
E value	6.0e-40
Match length	99
% identity	77
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	199966
Contig ID	67146_1.R1039
5'-most EST	uC-gsflnu33B136c12b1

Seq. No.	199967
Contig ID	67166_1.R1039
5'-most EST	uC-gsronu33B117f12b1

Seq. No.	199968
Contig ID	67173_1.R1039
5'-most EST	uC-gsronu33B168h03b1
Method	BLASTX
NCBI GI	g3702323
BLAST score	578
E value	2.0e-59
Match length	162
% identity	73
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	199969
Contig ID	67190_1.R1039
5'-most EST	uC-gsronu33B145a10b1
Method	BLASTX
NCBI GI	g2739309
BLAST score	187
E value	4.0e-19
Match length	123
% identity	31
NCBI Description	(Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No.	199970
Contig ID	67215_1.R1039
5'-most EST	uC-gsflnu33B079c05b1

Seq. No.	199971
Contig ID	67223_1.R1039
5'-most EST	uC-gsronu33B124b10b1

Seq. No.	199972
Contig ID	67250_1.R1039
5'-most EST	uC-gsronu33B124h06b1
Method	BLASTX
NCBI GI	g3183321
BLAST score	514
E value	5.0e-52
Match length	223
% identity	48
NCBI Description	HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I >gi|2330820|emb|CAB11050| (Z98530) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	199973
Contig ID	67275_1.R1039
5'-most EST	uC-gsronu33B124g09b1
Method	BLASTX
NCBI GI	g499068
BLAST score	736
E value	6.0e-78
Match length	187
% identity	79
NCBI Description	(X77301) GTPase [Glycine max]

Seq. No.	199974
Contig ID	67302_1.R1039
5'-most EST	uC-gsronu33B125b08b1

Seq. No.	199975
Contig ID	67328_1.R1039
5'-most EST	uC-gsronu33B146b04b1
Method	BLASTX
NCBI GI	g3935187
BLAST score	601
E value	2.0e-62
Match length	159
% identity	72
NCBI Description	(AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No.	199976
Contig ID	67380_1.R1039
5'-most EST	uC-gsflmaxxa027h05b1
Method	BLASTX
NCBI GI	g4218122
BLAST score	287
E value	1.0e-25
Match length	165
% identity	45
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	199977
Contig ID	67408_1.R1039
5'-most EST	g5048564
Method	BLASTX
NCBI GI	g2290532
BLAST score	553
E value	1.0e-56
Match length	168
% identity	64
NCBI Description	(U94748) AN11 [Petunia x hybrida]

Seq. No.	199978
Contig ID	67445_1.R1039
5'-most EST	uC-gsronu33B127b10b1
Method	BLASTX
NCBI GI	g2462749
BLAST score	289
E value	6.0e-26
Match length	95

% identity	64
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	199979
Contig ID	67470_1.R1039
5'-most EST	uC-gsronu33B127e10b1

Seq. No.	199980
Contig ID	67475_1.R1039
5'-most EST	uC-gsronu33B127f10b1
Method	BLASTX
NCBI GI	g3420239
BLAST score	917
E value	2.0e-99
Match length	173
% identity	100
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	199981
Contig ID	67482_1.R1039
5'-most EST	uC-gsronu33B127g02b1
Method	BLASTX
NCBI GI	g1279588
BLAST score	325
E value	3.0e-30
Match length	121
% identity	50
NCBI Description	(Z71749) glutathione S-transferase [Nicotiana plumbaginifolia]

Seq. No.	199982
Contig ID	67527_1.R1039
5'-most EST	uC-gsronu33B129c10b1
Method	BLASTX
NCBI GI	g3927825
BLAST score	345
E value	2.0e-32
Match length	75
% identity	88
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	199983
Contig ID	67595_1.R1039
5'-most EST	uC-gsronu33B130c07b1

Seq. No.	199984
Contig ID	67651_1.R1039
5'-most EST	g3326543
Method	BLASTX
NCBI GI	g2739004
BLAST score	490
E value	3.0e-49
Match length	215
% identity	50
NCBI Description	(AF022461) CYP82C1p [Glycine max]

Seq. No.	199985
Contig ID	67703_1.R1039
5'-most EST	g5048462
Method	BLASTX
NCBI GI	g4539386
BLAST score	590
E value	6.0e-61
Match length	246
% identity	33
NCBI Description	(AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No.	199986
Contig ID	67706_1.R1039
5'-most EST	uC-gsflnu33B012a04b1

Seq. No.	199987
Contig ID	67749_1.R1039
5'-most EST	uC-gsronu33B134d08b1

Seq. No.	199988
Contig ID	67752_1.R1039
5'-most EST	uC-gsronu33B144b09b1
Method	BLASTX
NCBI GI	g2213627
BLAST score	182
E value	1.0e-13
Match length	49
% identity	65
NCBI Description	(AC000103) F21J9.19 [Arabidopsis thaliana]

Seq. No.	199989
Contig ID	67762_1.R1039
5'-most EST	uC-gsflnu33B114f09b1
Method	BLASTX
NCBI GI	g3860333
BLAST score	340
E value	5.0e-32
Match length	115
% identity	57
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	199990
Contig ID	67806_1.R1039
5'-most EST	uC-gsronu33B136b03b1
Method	BLASTX
NCBI GI	g4567225
BLAST score	256
E value	6.0e-22
Match length	86
% identity	57
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	199991
Contig ID	67828_1.R1039
5'-most EST	uC-gsronu33B136d07b1
Method	BLASTX

NCBI GI	g4467157
BLAST score	237
E value	5.0e-20
Match length	105
% identity	48
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	199992
Contig ID	67849_1.R1039
5'-most EST	uC-gsronu33B138b08b1
Method	BLASTX
NCBI GI	g3046815
BLAST score	271
E value	1.0e-23
Match length	151
% identity	36
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	199993
Contig ID	67864_1.R1039
5'-most EST	uC-gsronu33B136h07b1

Seq. No.	199994
Contig ID	67878_1.R1039
5'-most EST	uC-gsronu33B137b01b1
Method	BLASTX
NCBI GI	g3859659
BLAST score	695
E value	3.0e-73
Match length	209
% identity	67
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	199995
Contig ID	67888_1.R1039
5'-most EST	uC-gsflnu33B131b09b1

Seq. No.	199996
Contig ID	67936_1.R1039
5'-most EST	uC-gsronu33B137h07b1
Method	BLASTX
NCBI GI	g285286
BLAST score	206
E value	3.0e-16
Match length	75
% identity	52
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	199997
Contig ID	67946_1.R1039
5'-most EST	uC-gsronu33B138a11b1
Method	BLASTN
NCBI GI	g4512656
BLAST score	54
E value	4.0e-21

Match length	496
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	199998
Contig ID	67958_1.R1039
5'-most EST	uC-gsronu33B138b09b1
Method	BLASTX
NCBI GI	g2979553
BLAST score	491
E value	2.0e-49
Match length	154
% identity	60
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	199999
Contig ID	67972_1.R1039
5'-most EST	uC-gsflnu33B137e11b1
Method	BLASTX
NCBI GI	g3080411
BLAST score	145
E value	4.0e-09
Match length	36
% identity	75
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	200000
Contig ID	67983_1.R1039
5'-most EST	uC-gsronu33B138e04b1

Seq. No.	200001
Contig ID	67990_1.R1039
5'-most EST	uC-gsflmaxxa106d11b1
Method	BLASTN
NCBI GI	g3510343
BLAST score	36
E value	9.0e-11
Match length	52
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	200002
Contig ID	68029_1.R1039
5'-most EST	g5044652

Seq. No.	200003
Contig ID	68121_1.R1039
5'-most EST	uC-gsronu33B141d07b1
Method	BLASTX
NCBI GI	g126120
BLAST score	265
E value	8.0e-23
Match length	116
% identity	47
NCBI Description	AGGLUTININ ALPHA CHAIN (MPA) >gi|81437|pir||S15825

agglutinin alpha chain - Osage orange
>gi|4139497|pdb|1JOT|A Chain A, Structure Of The Lectin Mpa Complexed With T-Antigen Disaccharide

Seq. No.	200004
Contig ID	68148_1.R1039
5'-most EST	uC-gsflmaxxa076d04b1

Seq. No.	200005
Contig ID	68153_1.R1039
5'-most EST	g5049889
Method	BLASTX
NCBI GI	g4510373
BLAST score	532
E value	3.0e-54
Match length	192
% identity	54
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	200006
Contig ID	68161_1.R1039
5'-most EST	g5045522
Method	BLASTX
NCBI GI	g2808531
BLAST score	123
E value	4.0e-09
Match length	180
% identity	20
NCBI Description	(Y12860) peroxisomal integral membrane protein [Homo sapiens]

Seq. No.	200007
Contig ID	68169_1.R1039
5'-most EST	g5047704
Method	BLASTX
NCBI GI	g4539395
BLAST score	754
E value	4.0e-80
Match length	256
% identity	56
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	200008
Contig ID	68226_1.R1039
5'-most EST	g5049203
Method	BLASTX
NCBI GI	g732207
BLAST score	163
E value	5.0e-11
Match length	79
% identity	44
NCBI Description	HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION >gi|626466|pir||S45131 probable membrane protein YNR008w - yeast (Saccharomyces cerevisiae) >gi|496725|emb|CAA54576| (X77395) N2042 [Saccharomyces cerevisiae] >gi|1302482|emb|CAA96285| (Z71623) ORF YNR008w

[Saccharomyces cerevisiae]

Seq. No.	200009
Contig ID	68246_1.R1039
5'-most EST	g5045745
Method	BLASTX
NCBI GI	g4455302
BLAST score	368
E value	6.0e-35
Match length	137
% identity	62
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	200010
Contig ID	68310_1.R1039
5'-most EST	uC-gsronu33B145b02b1

Seq. No.	200011
Contig ID	68318_1.R1039
5'-most EST	uC-gsronu33B145c03b1

Seq. No.	200012
Contig ID	68340_1.R1039
5'-most EST	uC-gsronu33B149b07b1

Seq. No.	200013
Contig ID	68373_1.R1039
5'-most EST	uC-gsflnu33B078g02b1
Method	BLASTX
NCBI GI	g2828241
BLAST score	262
E value	8.0e-23
Match length	68
% identity	68
NCBI Description	(AJ000885) Expansin [Brassica napus]

Seq. No.	200014
Contig ID	68402_1.R1039
5'-most EST	uC-gsronu33B146e01b1
Method	BLASTX
NCBI GI	g1730621
BLAST score	238
E value	6.0e-20
Match length	101
% identity	49
NCBI Description	HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION >gi|630106|pir||S48817 hypothetical protein YML079w - yeast (Saccharomyces cerevisiae) >gi|587531|emb|CAA86498| (Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum [Saccharomyces cerevisiae]

Seq. No.	200015
Contig ID	68417_1.R1039
5'-most EST	uC-gsflmaxxa042g07b1
Method	BLASTX
NCBI GI	g3153889

BLAST score	374
E value	9.0e-36
Match length	118
% identity	63
NCBI Description	(AF065444) root iron transporter protein [Pisum sativum]

Seq. No.	200016
Contig ID	68525_1.R1039
5'-most EST	uC-gsronu33B148d01b1
Method	BLASTX
NCBI GI	g4262233
BLAST score	253
E value	1.0e-21
Match length	139
% identity	46
NCBI Description	(AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200017
Contig ID	68555_1.R1039
5'-most EST	uC-gsronu33B148g11b1
Method	BLASTX
NCBI GI	g4006865
BLAST score	689
E value	9.0e-73
Match length	153
% identity	82
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	200018
Contig ID	68569_1.R1039
5'-most EST	uC-gsronu33B149a02b1
Method	BLASTX
NCBI GI	g3075393
BLAST score	483
E value	1.0e-48
Match length	122
% identity	75
NCBI Description	(AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200019
Contig ID	68656_1.R1039
5'-most EST	uC-gsflmaxxa047a02b1
Method	BLASTX
NCBI GI	g2392769
BLAST score	291
E value	7.0e-26
Match length	92
% identity	62
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	200020
Contig ID	68679_1.R1039
5'-most EST	uC-gsronu33B150d03b1

Seq. No.	200021
Contig ID	68743_1.R1039

5'-most EST	uC-gsronu33B153b09b2
Method	BLASTX
NCBI GI	g3005576
BLAST score	795
E value	4.0e-85
Match length	185
% identity	81
NCBI Description	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No.	200022
Contig ID	68744_1.R1039
5'-most EST	uC-gsflnu33B085c06b1

Seq. No.	200023
Contig ID	68772_1.R1039
5'-most EST	g5049526
Method	BLASTX
NCBI GI	g2495155
BLAST score	744
E value	5.0e-79
Match length	181
% identity	79
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi|1694926|dbj|BAA08910| (D50407) glutamyl-tRNA reductase [Cucumis sativus]

Seq. No.	200024
Contig ID	68779_1.R1039
5'-most EST	g5050586
Method	BLASTX
NCBI GI	g4006834
BLAST score	800
E value	1.0e-85
Match length	190
% identity	82
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	200025
Contig ID	68806_1.R1039
5'-most EST	uC-gsronu33B154a12b2
Method	BLASTX
NCBI GI	g2281090
BLAST score	277
E value	2.0e-24
Match length	131
% identity	46
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200026
Contig ID	68845_1.R1039
5'-most EST	uC-gsronu33b112e12b1
Method	BLASTX
NCBI GI	g4006882
BLAST score	638
E value	9.0e-67

Match length	160
% identity	78
NCBI Description	(Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	200027
Contig ID	68910_1.R1039
5'-most EST	uC-gsflnu33B082c08b1
Method	BLASTX
NCBI GI	g1755166
BLAST score	388
E value	1.0e-37
Match length	102
% identity	75
NCBI Description	(U75194) germin-like protein [Arabidopsis thaliana]

Seq. No.	200028
Contig ID	68922_1.R1039
5'-most EST	uC-gsronu33B155e01b2
Method	BLASTX
NCBI GI	g2384956
BLAST score	319
E value	4.0e-29
Match length	187
% identity	36
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	200029
Contig ID	68950_1.R1039
5'-most EST	uC-gsronu33B155g11b2

Seq. No.	200030
Contig ID	68983_1.R1039
5'-most EST	g5049793
Method	BLASTX
NCBI GI	g3915023
BLAST score	214
E value	4.0e-17
Match length	56
% identity	68
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi|2588888|dbj|BAA23213| (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	200031
Contig ID	68990_1.R1039
5'-most EST	uC-gsronu33B156f12b1
Method	BLASTX
NCBI GI	g3927830
BLAST score	342
E value	3.0e-32
Match length	134
% identity	37
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200032
Contig ID	69003_1.R1039
5'-most EST	uC-gsronu33B157a08b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	251
E value	9.0e-22
Match length	54
% identity	81
NCBI Description	(AL022604) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	200033
Contig ID	69007_1.R1039
5'-most EST	uC-gsflnu33B111g05b1
Method	BLASTX
NCBI GI	g2145356
BLAST score	747
E value	3.0e-79
Match length	207
% identity	72
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi|3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	200034
Contig ID	69023_1.R1039
5'-most EST	uC-gsronu33B157e02b1
Method	BLASTX
NCBI GI	g2231062
BLAST score	238
E value	1.0e-19
Match length	113
% identity	47
NCBI Description	(Z92911) beta-(1,3-1,4)-glucanase [Streptococcus bovis]

Seq. No.	200035
Contig ID	69033_1.R1039
5'-most EST	uC-gsflmaxxa045d04b1
Method	BLASTX
NCBI GI	g3860255
BLAST score	225
E value	3.0e-18
Match length	139
% identity	40
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200036
Contig ID	69041_1.R1039
5'-most EST	uC-gsronu33B157g07b1

Seq. No.	200037
Contig ID	69042_1.R1039
5'-most EST	uC-gsronu33B157g11b1
Method	BLASTX
NCBI GI	g4490705
BLAST score	172
E value	1.0e-12

Match length	41
% identity	83
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	200038
Contig ID	69090_1.R1039
5'-most EST	uC-gsflnu33B074a03b1

Seq. No.	200039
Contig ID	69100_1.R1039
5'-most EST	uC-gsflnu33B084e12b1
Method	BLASTX
NCBI GI	g2760837
BLAST score	369
E value	5.0e-35
Match length	228
% identity	36
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	200040
Contig ID	69110_1.R1039
5'-most EST	uC-gsflnu33B130c06b1
Method	BLASTX
NCBI GI	g2746086
BLAST score	333
E value	8.0e-31
Match length	226
% identity	36
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	200041
Contig ID	69133_1.R1039
5'-most EST	g5048037
Method	BLASTX
NCBI GI	g3256756
BLAST score	157
E value	3.0e-10
Match length	198
% identity	24
NCBI Description	(AP000002) 327aa long hypothetical galactose-1-phosphate uridyltransferase [Pyrococcus horikoshii]

Seq. No.	200042
Contig ID	69139_1.R1039
5'-most EST	uC-gsronu33B159b04b1
Method	BLASTX
NCBI GI	g2827536
BLAST score	255
E value	1.0e-21
Match length	101
% identity	48
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200043
Contig ID	69222_1.R1039

5'-most EST	uC-gsronu33B160c12b1
Method	BLASTX
NCBI GI	g2160166
BLAST score	446
E value	3.0e-44
Match length	162
% identity	55
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	200044
Contig ID	69285_1.R1039
5'-most EST	g5044327
Method	BLASTX
NCBI GI	g3257978
BLAST score	535
E value	2.0e-54
Match length	230
% identity	48
NCBI Description	(AP000006) 249aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	200045
Contig ID	69325_1.R1039
5'-most EST	uC-gsronu33B162g07b2
Method	BLASTX
NCBI GI	g4249419
BLAST score	244
E value	3.0e-32
Match length	99
% identity	77
NCBI Description	(AC006072) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	200046
Contig ID	69330_1.R1039
5'-most EST	g5044968
Method	BLASTX
NCBI GI	g2632106
BLAST score	150
E value	1.0e-09
Match length	30
% identity	93
NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	200047
Contig ID	69434_1.R1039
5'-most EST	uC-gsflnu33B115c08b1

Seq. No.	200048
Contig ID	69481_1.R1039
5'-most EST	uC-gsronu33B164h02b2
Method	BLASTX
NCBI GI	g1495251
BLAST score	384
E value	7.0e-37
Match length	181
% identity	48

NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.	200049
Contig ID	69504_1.R1039
5'-most EST	uC-gsflnu33B130a06b1
Seq. No.	200050
Contig ID	69540_1.R1039
5'-most EST	uC-gsflnu33B046g01b1
Method	BLASTX
NCBI GI	g3342802
BLAST score	699
E value	8.0e-74
Match length	163
% identity	79
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
Seq. No.	200051
Contig ID	69554_1.R1039
5'-most EST	uC-gsronu33B166h12b2
Seq. No.	200052
Contig ID	69561_1.R1039
5'-most EST	g3326622
Method	BLASTX
NCBI GI	g1709129
BLAST score	762
E value	1.0e-95
Match length	194
% identity	89
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 >gi|481018|pir||S37642 protein kinase MSK-3 (EC 2.7.1.-) - alfalfa >gi|313148|emb|CAA48472| (X68409) protein kinase [Medicago sativa]
Seq. No.	200053
Contig ID	69617_1.R1039
5'-most EST	g3326159
Method	BLASTX
NCBI GI	g1352439
BLAST score	186
E value	1.0e-22
Match length	104
% identity	58
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi|1008881 (L47221) eukaryotic initiation factor 5 [Phaseolus vulgaris]
Seq. No.	200054
Contig ID	69737_1.R1039
5'-most EST	uC-gsflnu33B115f05b1
Method	BLASTX
NCBI GI	g2144098
BLAST score	349
E value	1.0e-32
Match length	208

% identity	39
NCBI Description	SC2 - rat >gi|256994|bbs|115268 (S45663) SC2=synaptic glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]
Seq. No.	200055
Contig ID	69750_1.R1039
5'-most EST	g5049756
Method	BLASTX
NCBI GI	g3915039
BLAST score	891
E value	3.0e-96
Match length	211
% identity	82
NCBI Description	SUGAR CARRIER PROTEIN C >gi|169718 (L08196) sugar carrier protein [Ricinus communis]
Seq. No.	200056
Contig ID	69752_1.R1039
5'-most EST	uC-gsronu33B169f06b1
Method	BLASTX
NCBI GI	g2129855
BLAST score	1284
E value	1.0e-142
Match length	275
% identity	86
NCBI Description	mitogen-activated protein kinase MMK2 (EC 2.7.1.-) - alfalfa
Seq. No.	200057
Contig ID	69785_1.R1039
5'-most EST	g5050160
Method	BLASTX
NCBI GI	g3334276
BLAST score	267
E value	3.0e-23
Match length	131
% identity	43
NCBI Description	AUTOANTIGEN NGP-1 >gi|179285 (L05425) autoantigen [Homo sapiens]
Seq. No.	200058
Contig ID	69790_1.R1039
5'-most EST	g5046367
Method	BLASTX
NCBI GI	g4106395
BLAST score	1356
E value	1.0e-150
Match length	280
% identity	85
NCBI Description	(AF073744) raffinose synthase [Cucumis sativus]
Seq. No.	200059
Contig ID	69798_1.R1039
5'-most EST	uC-gsflnu33B114f03b1
Method	BLASTX
NCBI GI	g2622654
BLAST score	280

E value	3.0e-33
Match length	187
% identity	43
NCBI Description	(AE000913) heavy-metal transporting CPx-type ATPase [Methanobacterium thermoautotrophicum]

Seq. No.	200060
Contig ID	69814_1.R1039
5'-most EST	uC-gsronu33B170e07b1
Method	BLASTX
NCBI GI	g1168729
BLAST score	516
E value	2.0e-52
Match length	181
% identity	59
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-1 (CAD) >gi|282867|pir||S28044 ELI3-2 protein - Arabidopsis thaliana >gi|16267|emb|CAA48027| (X67816) Eli3-1 [Arabidopsis thaliana]

Seq. No.	200061
Contig ID	69869_1.R1039
5'-most EST	g5047393
Method	BLASTX
NCBI GI	g4544449
BLAST score	761
E value	5.0e-81
Match length	211
% identity	75
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	200062
Contig ID	69923_1.R1039
5'-most EST	g5048776
Method	BLASTX
NCBI GI	g4263712
BLAST score	490
E value	3.0e-49
Match length	138
% identity	68
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	200063
Contig ID	69959_1.R1039
5'-most EST	uC-gsronu33B178f05b1

Seq. No.	200064
Contig ID	70066_1.R1039
5'-most EST	uC-gsflnu33B128c12b1

Seq. No.	200065
Contig ID	70079_1.R1039
5'-most EST	uC-gsflmaxxa054d09b1
Method	BLASTX
NCBI GI	g3157951
BLAST score	987

E value	1.0e-107
Match length	218
% identity	93
NCBI Description	(AC002131) Contains similarity to vesicle trafficking protein gb|U91538 from Mus musculus. ESTs gb|F15494 and gb|F14097 come from this gene. [Arabidopsis thaliana]

Seq. No.	200066
Contig ID	70111_1.R1039
5'-most EST	uC-gsronu33b023h01b1
Method	BLASTX
NCBI GI	g3426039
BLAST score	320
E value	2.0e-29
Match length	146
% identity	46
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	200067
Contig ID	70138_1.R1039
5'-most EST	uC-gsronu33b025c04b1

Seq. No.	200068
Contig ID	70141_1.R1039
5'-most EST	uC-gsronu33b025c08b1
Method	BLASTX
NCBI GI	g1223579
BLAST score	253
E value	1.0e-22
Match length	72
% identity	72
NCBI Description	(X96481) cDNA101 [Arabidopsis thaliana]

Seq. No.	200069
Contig ID	70154_1.R1039
5'-most EST	uC-gsronu33b025d11b1
Method	BLASTX
NCBI GI	g2244996
BLAST score	396
E value	3.0e-38
Match length	179
% identity	12
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	200070
Contig ID	70172_1.R1039
5'-most EST	uC-gsronu33b025g03b1
Method	BLASTX
NCBI GI	g2230757
BLAST score	630
E value	1.0e-65
Match length	152
% identity	79
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 200071

Contig ID	70205_1.R1039
5'-most EST	uC-gsflnu33B005a07b1
Method	BLASTX
NCBI GI	g4510371
BLAST score	218
E value	3.0e-17
Match length	142
% identity	42
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	200072
Contig ID	70243_1.R1039
5'-most EST	uC-gsronu33b112f11b1
Method	BLASTX
NCBI GI	g2317729
BLAST score	394
E value	2.0e-38
Match length	125
% identity	71
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	200073
Contig ID	70263_1.R1039
5'-most EST	uC-gsronu33b112h12b1

Seq. No.	200074
Contig ID	70265_1.R1039
5'-most EST	uC-gsflmaxxa098d12b1
Method	BLASTX
NCBI GI	g3924604
BLAST score	299
E value	8.0e-27
Match length	227
% identity	16
NCBI Description	(AF069442) putative leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	200075
Contig ID	70282_1.R1039
5'-most EST	uC-gsflmaxxa040a04b1
Method	BLASTX
NCBI GI	g1706822
BLAST score	623
E value	6.0e-65
Match length	173
% identity	66
NCBI Description	FLAVONOL SYNTHASE (FLS) >gi|421946|pir||S33510 flavonol synthase - garden petunia >gi|311658|emb|CAA80264| (Z22543) flavonol synthase [Petunia x hybrida]

Seq. No.	200076
Contig ID	70305_1.R1039
5'-most EST	uC-gsflmaxxa060f01b1

Seq. No.	200077

Contig ID	70349_1.R1039
5'-most EST	uC-gsflmaxxa002d04b1
Method	BLASTX
NCBI GI	g3138972
BLAST score	254
E value	8.0e-22
Match length	64
% identity	75
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	200078
Contig ID	70383_1.R1039
5'-most EST	uC-gsflmaxxa057e03b1
Method	BLASTX
NCBI GI	g2252844
BLAST score	260
E value	2.0e-22
Match length	130
% identity	42
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	200079
Contig ID	70454_1.R1039
5'-most EST	uC-gsflmaxxa003h09b1

Seq. No.	200080
Contig ID	70468_1.R1039
5'-most EST	uC-gsflmaxxa060b05b1

Seq. No.	200081
Contig ID	70514_1.R1039
5'-most EST	uC-gsflmaxxa076d08b1

Seq. No.	200082
Contig ID	70532_1.R1039
5'-most EST	uC-gsflmaxxa047g06b1
Method	BLASTX
NCBI GI	g2979544
BLAST score	276
E value	2.0e-24
Match length	105
% identity	50
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	200083
Contig ID	70616_1.R1039
5'-most EST	uC-gsflmaxxa009c09b1

Seq. No.	200084
Contig ID	70617_1.R1039
5'-most EST	g5049277
Method	BLASTX
NCBI GI	g1711381
BLAST score	901

E value	2.0e-97
Match length	206
% identity	83
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi|1256204|dbj|BAA12206| (D84061) phosphoserine aminotransferase [Spinacia oleracea]

Seq. No.	200085
Contig ID	70637_1.R1039
5'-most EST	uC-gsflmaxxa009c11b1
Method	BLASTX
NCBI GI	g543565
BLAST score	203
E value	8.0e-16
Match length	78
% identity	49
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi|493721|dbj|BAA06462| (D30802) TED4 [Zinnia elegans] >gi|641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	200086
Contig ID	70639_1.R1039
5'-most EST	uC-gsflmaxxa009e09b1

Seq. No.	200087
Contig ID	70653_1.R1039
5'-most EST	uC-gsflmaxxa009e11b1

Seq. No.	200088
Contig ID	70686_1.R1039
5'-most EST	uC-gsflmaxxa070e12b1
Method	BLASTX
NCBI GI	g125889
BLAST score	376
E value	5.0e-36
Match length	131
% identity	55
NCBI Description	PROBABLE PECTATE LYASE P59 PRECURSOR >gi|280400|pir||S27098 pectate lyase (EC 4.2.2.2) LAT59 - tomato >gi|19271|emb|CAA33523| (X15499) P59 protein [Lycopersicon esculentum]

Seq. No.	200089
Contig ID	70686_2.R1039
5'-most EST	uC-gsflmaxxa043d09b1
Method	BLASTX
NCBI GI	g125889
BLAST score	224
E value	3.0e-18
Match length	86
% identity	50
NCBI Description	PROBABLE PECTATE LYASE P59 PRECURSOR >gi|280400|pir||S27098 pectate lyase (EC 4.2.2.2) LAT59 - tomato >gi|19271|emb|CAA33523| (X15499) P59 protein [Lycopersicon esculentum]

Seq. No.	200090
Contig ID	70690_1.R1039
5'-most EST	uC-gsflmaxxa010a05b1
Method	BLASTX
NCBI GI	g3810855
BLAST score	164
E value	5.0e-11
Match length	110
% identity	38
NCBI Description	(AL032684) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	200091
Contig ID	70715_1.R1039
5'-most EST	uC-gsflmaxxa010d05b1
Method	BLASTX
NCBI GI	g4056460
BLAST score	150
E value	2.0e-09
Match length	175
% identity	32
NCBI Description	(AC005990) Contains similarity to gb|L26505 Met30p from Saccharomyces cerevisiae. ESTs gb|F14133, gb|T46217, gb|AA404758 and gb|Z37647 come from this gene. [Arabidopsis thaliana]

Seq. No.	200092
Contig ID	70718_1.R1039
5'-most EST	uC-gsflnu33B060a03b1

Seq. No.	200093
Contig ID	70721_1.R1039
5'-most EST	g3325954

Seq. No.	200094
Contig ID	70748_1.R1039
5'-most EST	uC-gsflmaxxa011d02b1
Method	BLASTX
NCBI GI	g4063751
BLAST score	240
E value	5.0e-20
Match length	178
% identity	33
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi|4510409|gb|AAD21495.1| (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	200095
Contig ID	70759_1.R1039
5'-most EST	uC-gsflmaxxa045e06b1

Seq. No.	200096
Contig ID	70763_1.R1039
5'-most EST	uC-gsflmaxxa012b05b1

Seq. No.	200097
Contig ID	70769_1.R1039
5'-most EST	uC-gsflmaxxa012b12b1

Method	BLASTX
NCBI GI	g4206210
BLAST score	328
E value	1.0e-30
Match length	109
% identity	60
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi|4263043|gb|AAD15312| (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	200098
Contig ID	70818_1.R1039
5'-most EST	uC-gsflmaxxa015a03b1
Method	BLASTX
NCBI GI	g2129834
BLAST score	240
E value	3.0e-20
Match length	97
% identity	57
NCBI Description	low molecular weight heat shock protein precursor (clone Hsp22.3) - soybean >gi|710434 (U21723) Hsp22.3 [Glycine max]

Seq. No.	200099
Contig ID	70868_1.R1039
5'-most EST	g5050795
Method	BLASTX
NCBI GI	g2130139
BLAST score	154
E value	8.0e-10
Match length	106
% identity	33
NCBI Description	hypothetical protein - maize >gi|949980|emb|CAA61258| (X88779) orf [Zea mays]

Seq. No.	200100
Contig ID	70896_1.R1039
5'-most EST	uC-gsflmaxxa026f11b1
Method	BLASTN
NCBI GI	g2828188
BLAST score	34
E value	2.0e-09
Match length	90
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	200101
Contig ID	70919_1.R1039
5'-most EST	uC-gsflmaxxa090d10b1

Seq. No.	200102
Contig ID	70921_1.R1039
5'-most EST	g5049531
Method	BLASTX
NCBI GI	g2642429
BLAST score	222

E value	8.0e-18
Match length	55
% identity	20
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	200103
Contig ID	70947_1.R1039
5'-most EST	uC-gsflnu33B114e05b1
Method	BLASTN
NCBI GI	g510879
BLAST score	63
E value	9.0e-27
Match length	175
% identity	84
NCBI Description	B.oleracea mRNA for aspartic protease

Seq. No.	200104
Contig ID	70995_1.R1039
5'-most EST	g5047167
Method	BLASTX
NCBI GI	g3063709
BLAST score	193
E value	1.0e-30
Match length	286
% identity	34
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	200105
Contig ID	71011_1.R1039
5'-most EST	uC-gsflmaxxa028c12b1

Seq. No.	200106
Contig ID	71017_1.R1039
5'-most EST	uC-gsflmaxxa045a09b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	237
E value	5.0e-20
Match length	56
% identity	36
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	200107
Contig ID	71018_1.R1039
5'-most EST	uC-gsflmaxxa028d09b1
Method	BLASTX
NCBI GI	g4539459
BLAST score	302
E value	2.0e-27
Match length	80
% identity	70
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	200108
Contig ID	71056_1.R1039

5'-most EST	uC-gsflmaxxa028h05b1
Method	BLASTX
NCBI GI	g1871526
BLAST score	166
E value	3.0e-11
Match length	124
% identity	31
NCBI Description	(X81997) leucine-rich-repeat protein [Helianthus annuus]

Seq. No.	200109
Contig ID	71178_1.R1039
5'-most EST	uC-gsflmaxxa038g06b1
Method	BLASTX
NCBI GI	g2583128
BLAST score	711
E value	4.0e-75
Match length	168
% identity	83
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200110
Contig ID	71197_1.R1039
5'-most EST	uC-gsflmaxxa039a01b1

Seq. No.	200111
Contig ID	71209_1.R1039
5'-most EST	uC-gsflmaxxa054g10b1
Method	BLASTX
NCBI GI	g1169451
BLAST score	494
E value	8.0e-50
Match length	153
% identity	59
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi|322510|pir||S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi|22677|emb|CAA49853| (X70409) A6 [Arabidopsis thaliana] >gi|2244764|emb|CAB10187| (Z97335) AMP-binding protein [Arabidopsis thaliana]

Seq. No.	200112
Contig ID	71253_1.R1039
5'-most EST	uC-gsflmaxxa039g01b1
Method	BLASTX
NCBI GI	g2642443
BLAST score	320
E value	1.0e-29
Match length	111
% identity	54
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	200113
Contig ID	71258_1.R1039
5'-most EST	uC-gsflmaxxa039g10b1

Seq. No.	200114

Contig ID	71263_1.R1039
5'-most EST	g3325654

Seq. No.	200115
Contig ID	71303_1.R1039
5'-most EST	uC-gsflmaxxa040d04b1
Method	BLASTX
NCBI GI	g2435406
BLAST score	273
E value	4.0e-24
Match length	91
% identity	57
NCBI Description	(U83490) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	200116
Contig ID	71312_1.R1039
5'-most EST	uC-gsflmaxxa040d12b1
Method	BLASTX
NCBI GI	g1076625
BLAST score	365
E value	7.0e-35
Match length	108
% identity	57
NCBI Description	glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor - common tobacco >gi|473102|emb|CAA82271| (Z28697) beta-1,3-glucanase [Nicotiana tabacum]

Seq. No.	200117
Contig ID	71322_1.R1039
5'-most EST	uC-gsflmaxxa040e10b1
Method	BLASTX
NCBI GI	g2808420
BLAST score	274
E value	6.0e-24
Match length	184
% identity	35
NCBI Description	(Z97632) HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1 [Homo sapiens]

Seq. No.	200118
Contig ID	71327_1.R1039
5'-most EST	uC-gsflmaxxa040f03b1

Seq. No.	200119
Contig ID	71339_1.R1039
5'-most EST	uC-gsflmaxxa040g03b1
Method	BLASTX
NCBI GI	g3108161
BLAST score	261
E value	1.0e-22
Match length	82
% identity	62
NCBI Description	(AF061106) putative monosaccharide transporter 1 [Petunia x hybrida]

Seq. No.	200120
Contig ID	71343_1.R1039

5'-most EST	uC-gsflnu33B139a06b1
Seq. No.	200121
Contig ID	71352_1.R1039
5'-most EST	uC-gsflmaxxa054g05b1
Seq. No.	200122
Contig ID	71357_1.R1039
5'-most EST	uC-gsflmaxxa040h12b1
Seq. No.	200123
Contig ID	71360_1.R1039
5'-most EST	uC-gsflmaxxa041g07b1
Seq. No.	200124
Contig ID	71377_1.R1039
5'-most EST	uC-gsflmaxxa041b11b1
Seq. No.	200125
Contig ID	71419_1.R1039
5'-most EST	uC-gsflmaxxa041f10b1
Seq. No.	200126
Contig ID	71425_1.R1039
5'-most EST	uC-gsflmaxxa041g03b1
Method	BLASTX
NCBI GI	g3581838
BLAST score	313
E value	2.0e-28
Match length	187
% identity	38
NCBI Description	(AL031541) putative secreted arabinosidase [Streptomyces coelicolor]
Seq. No.	200127
Contig ID	71460_1.R1039
5'-most EST	uC-gsflmaxxa042b07b1
Seq. No.	200128
Contig ID	71473_1.R1039
5'-most EST	g5047100
Method	BLASTX
NCBI GI	g2627181
BLAST score	725
E value	1.0e-86
Match length	184
% identity	75
NCBI Description	(D89619) cycloartenol synthase [Pisum sativum]
Seq. No.	200129
Contig ID	71494_1.R1039
5'-most EST	uC-gsflmaxxa042e11b1
Method	BLASTX
NCBI GI	g1169451
BLAST score	393
E value	4.0e-38
Match length	135

% identity	53
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi|322510|pir||S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi|22677|emb|CAA49853| (X70409) A6 [Arabidopsis thaliana] >gi|2244764|emb|CAB10187| (Z97335) AMP-binding protein [Arabidopsis thaliana]

Seq. No.	200130
Contig ID	71500_1.R1039
5'-most EST	uC-gsflmaxxa042f07b1
Method	BLASTX
NCBI GI	g2459445
BLAST score	284
E value	4.0e-25
Match length	89
% identity	29
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	200131
Contig ID	71523_1.R1039
5'-most EST	g5048964
Method	BLASTX
NCBI GI	g4220474
BLAST score	499
E value	4.0e-50
Match length	246
% identity	53
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	200132
Contig ID	71533_1.R1039
5'-most EST	uC-gsflmaxxa043b03b1
Method	BLASTX
NCBI GI	g3763918
BLAST score	319
E value	3.0e-29
Match length	68
% identity	84
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	200133
Contig ID	71540_1.R1039
5'-most EST	uC-gsflmaxxa043c02b1
Method	BLASTX
NCBI GI	g3258635
BLAST score	260
E value	2.0e-22
Match length	132
% identity	39
NCBI Description	(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No.	200134

Contig ID	71543_1.R1039
5'-most EST	uC-gsflmaxxa043c08b1
Method	BLASTN
NCBI GI	g2062691
BLAST score	33
E value	5.0e-09
Match length	33
% identity	61
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	200135
Contig ID	71559_1.R1039
5'-most EST	uC-gsflmaxxa043d12b1
Method	BLASTX
NCBI GI	g2317904
BLAST score	295
E value	6.0e-42
Match length	118
% identity	73
NCBI Description	(U89959) Similar to rice chalcone synthase homolog, gp|U90341|2507617 and anther specific protein, gp|Y14507|2326772 [Arabidopsis thaliana]

Seq. No.	200136
Contig ID	71567_1.R1039
5'-most EST	uC-gsflmaxxa043e09b1
Method	BLASTX
NCBI GI	g2244970
BLAST score	578
E value	1.0e-59
Match length	180
% identity	59
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi|2326365|emb|CAA74765| (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	200137
Contig ID	71627_1.R1039
5'-most EST	uC-gsflmaxxa045d12b1

Seq. No.	200138
Contig ID	71628_1.R1039
5'-most EST	uC-gsflmaxxa060g03b1
Method	BLASTX
NCBI GI	g3790441
BLAST score	237
E value	3.0e-44
Match length	164
% identity	71
NCBI Description	(AF030515) chaperonin 60 alpha subunit [Canavalia lineata]

Seq. No.	200139
Contig ID	71629_1.R1039
5'-most EST	uC-gsflmaxxa045e03b1
Method	BLASTN
NCBI GI	g21090

BLAST score	71
E value	2.0e-31
Match length	292
% identity	81
NCBI Description	Castor-bean mRNA for Rubisco subunit binding-protein alpha subunit

Seq. No.	200140
Contig ID	71642_1.R1039
5'-most EST	g5050118
Method	BLASTX
NCBI GI	g1084429
BLAST score	367
E value	7.0e-35
Match length	186
% identity	42
NCBI Description	pectin esterase - Petunia inflata

Seq. No.	200141
Contig ID	71753_1.R1039
5'-most EST	uC-gsflmaxxa047b01b1

Seq. No.	200142
Contig ID	71786_1.R1039
5'-most EST	uC-gsflmaxxa047e05b1
Method	BLASTX
NCBI GI	g2827713
BLAST score	969
E value	1.0e-105
Match length	221
% identity	82
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]

Seq. No.	200143
Contig ID	71791_1.R1039
5'-most EST	uC-gsflnu33B113b06b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	731
E value	1.0e-77
Match length	155
% identity	94
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	200144
Contig ID	71826_1.R1039
5'-most EST	uC-gsflmaxxa048a03b1

Seq. No.	200145
Contig ID	71839_1.R1039
5'-most EST	uC-gsflmaxxa048b07b1

Seq. No.	200146
Contig ID	71847_1.R1039
5'-most EST	uC-gsflmaxxa089g03b1

Seq. No.	200147
Contig ID	71909_1.R1039
5'-most EST	uC-gsflmaxxa049a09b1

Seq. No.	200148
Contig ID	71921_1.R1039
5'-most EST	uC-gsflmaxxa049c05b1
Method	BLASTX
NCBI GI	g3881505
BLAST score	150
E value	2.0e-09
Match length	62
% identity	45
NCBI Description	(Z47357) similar to the mouse hypothetical protein D15Kz1 (PIR accession number A30222); cDNA EST EMBL:C08599 comes from this gene; cDNA EST EMBL:C07385 comes from this gene; cDNA EST EMBL:C08733 comes from this gene; cDNA EST

Seq. No.	200149
Contig ID	71941_1.R1039
5'-most EST	uC-gsflmaxxa049e10b1
Method	BLASTX
NCBI GI	g2052510
BLAST score	663
E value	5.0e-75
Match length	195
% identity	79
NCBI Description	(U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No.	200150
Contig ID	71952_1.R1039
5'-most EST	uC-gsflmaxxa088c11b1
Method	BLASTX
NCBI GI	g2529683
BLAST score	260
E value	2.0e-22
Match length	77
% identity	68
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	200151
Contig ID	71963_1.R1039
5'-most EST	uC-gsflmaxxa049h11b1

Seq. No.	200152
Contig ID	72087_1.R1039
5'-most EST	uC-gsflmaxxa096a09b1
Method	BLASTX
NCBI GI	g1871185
BLAST score	397
E value	1.0e-38
Match length	120
% identity	63
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	200153
Contig ID	72099_1.R1039
5'-most EST	uC-gsflmaxxa057d09b1
Method	BLASTX
NCBI GI	g4337202
BLAST score	179
E value	7.0e-22
Match length	104
% identity	53
NCBI Description	(AC006403) putative endosperm-specific protein [Arabidopsis thaliana]

Seq. No.	200154
Contig ID	72170_1.R1039
5'-most EST	g5049060
Method	BLASTX
NCBI GI	g3176680
BLAST score	861
E value	1.0e-92
Match length	246
% identity	31
NCBI Description	(AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb|U63373. EST gb|AA404878 comes from this gene. [Arabidopsis thaliana]

Seq. No.	200155
Contig ID	72203_1.R1039
5'-most EST	uC-gsflmaxxa058a07b1
Method	BLASTX
NCBI GI	g2447107
BLAST score	364
E value	8.0e-35
Match length	124
% identity	55
NCBI Description	(U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No.	200156
Contig ID	72217_1.R1039
5'-most EST	uC-gsflmaxxa058b09b1
Method	BLASTX
NCBI GI	g2443886
BLAST score	527
E value	1.0e-53
Match length	127
% identity	84
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	200157
Contig ID	72267_1.R1039
5'-most EST	g5048596

Seq. No.	200158
Contig ID	72268_1.R1039
5'-most EST	g5047328
Method	BLASTX
NCBI GI	g3608515
BLAST score	816

E value	2.0e-87
Match length	199
% identity	76
NCBI Description	(AF090734) putative glycerol-3-phosphate acyltransferase [Vicia faba]

Seq. No.	200159
Contig ID	72277_1.R1039
5'-most EST	uC-gsflmaxxa096d03b1

Seq. No.	200160
Contig ID	72322_1.R1039
5'-most EST	uC-gsflnu33B074e05b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	326
E value	6.0e-30
Match length	198
% identity	39
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	200161
Contig ID	72397_1.R1039
5'-most EST	uC-gsflmaxxa090b08b1
Method	BLASTX
NCBI GI	g2367392
BLAST score	296
E value	1.0e-26
Match length	108
% identity	53
NCBI Description	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]

Seq. No.	200162
Contig ID	72427_1.R1039
5'-most EST	g5046085
Method	BLASTX
NCBI GI	g1072187
BLAST score	146
E value	2.0e-10
Match length	83
% identity	46
NCBI Description	(U40941) coded for by C. elegans cDNA CEESB82F; coded for by C. elegans cDNA CEESE93F [Caenorhabditis elegans]

Seq. No.	200163
Contig ID	72434_1.R1039
5'-most EST	uC-gsflmaxxa064c11b1

Seq. No.	200164
Contig ID	72456_1.R1039
5'-most EST	uC-gsflnu33B001e08b1

Seq. No.	200165
Contig ID	72476_1.R1039
5'-most EST	g5049749

Method	BLASTX
NCBI GI	g3860321
BLAST score	707
E value	9.0e-75
Match length	156
% identity	82
NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No.	200166
Contig ID	72551_1.R1039
5'-most EST	g5050690
Method	BLASTX
NCBI GI	g2529663
BLAST score	540
E value	4.0e-55
Match length	127
% identity	76
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi|3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	200167
Contig ID	72611_1.R1039
5'-most EST	g5045430
Method	BLASTX
NCBI GI	g401621
BLAST score	271
E value	1.0e-23
Match length	143
% identity	43
NCBI Description	HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION >gi|290561 (L10328) o188 [Escherichia coli] >gi|1790149 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No.	200168
Contig ID	72616_1.R1039
5'-most EST	g3326315
Method	BLASTX
NCBI GI	g4325345
BLAST score	271
E value	2.0e-23
Match length	117
% identity	16
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	200169
Contig ID	72697_1.R1039
5'-most EST	uC-gsflmaxxa076f10b1

Seq. No.	200170
Contig ID	72800_1.R1039
5'-most EST	uC-gsflmaxxa107a05b1
Method	BLASTX
NCBI GI	g1546700

BLAST score	462
E value	3.0e-46
Match length	147
% identity	65
NCBI Description	(X98804) peroxidase ATP18a [Arabidopsis thaliana]

Seq. No.	200171
Contig ID	72808_1.R1039
5'-most EST	g5045759
Method	BLASTX
NCBI GI	g1213629
BLAST score	446
E value	5.0e-44
Match length	204
% identity	49
NCBI Description	(X95991) pectinesterase [Prunus persica]

Seq. No.	200172
Contig ID	72809_1.R1039
5'-most EST	uC-gsflmaxxa089b07b1

Seq. No.	200173
Contig ID	72872_1.R1039
5'-most EST	uC-gsflmaxxa090a01b1
Method	BLASTX
NCBI GI	g1305531
BLAST score	297
E value	1.0e-26
Match length	122
% identity	43
NCBI Description	(U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi|1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No.	200174
Contig ID	72938_1.R1039
5'-most EST	uC-gsflnu33B141d08b1
Method	BLASTX
NCBI GI	g2894599
BLAST score	519
E value	6.0e-53
Match length	128
% identity	76
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	200175
Contig ID	72940_1.R1039
5'-most EST	g5044704
Method	BLASTX
NCBI GI	g4006876
BLAST score	315
E value	2.0e-28
Match length	258
% identity	48
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200176
Contig ID	72978_1.R1039
5'-most EST	uC-gsflnu33B093a08b1

Seq. No.	200177
Contig ID	73009_1.R1039
5'-most EST	g3326458
Method	BLASTX
NCBI GI	g1652678
BLAST score	757
E value	2.0e-80
Match length	332
% identity	45
NCBI Description	(D90907) amidase [Synechocystis sp.]

Seq. No.	200178
Contig ID	73034_1.R1039
5'-most EST	g5045151
Method	BLASTX
NCBI GI	g2507426
BLAST score	876
E value	2.0e-94
Match length	188
% identity	82
NCBI Description	ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (ALANINE--TRNA LIGASE) (ALARS) >gi|1673365|emb|CAA80380| (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No.	200179
Contig ID	73143_1.R1039
5'-most EST	uC-gsflmaxxa096b07b1
Method	BLASTX
NCBI GI	g3834306
BLAST score	377
E value	6.0e-36
Match length	99
% identity	69
NCBI Description	(AC005679) EST gb|R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	200180
Contig ID	73181_1.R1039
5'-most EST	uC-gsflnu33B063f03b1
Method	BLASTX
NCBI GI	g1076802
BLAST score	152
E value	9.0e-10
Match length	94
% identity	41
NCBI Description	extensin-like protein - maize >gi|600118|emb|CAA84230| (Z34465) extensin-like protein [Zea mays] >gi|1096557|prf||2111476A extensin-like domain [Zea mays]

Seq. No.	200181
Contig ID	73189_1.R1039
5'-most EST	uC-gsflmaxxa096g04b1

Method	BLASTX
NCBI GI	g4512675
BLAST score	574
E value	4.0e-59
Match length	155
% identity	73
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	200182
Contig ID	73202_1.R1039
5'-most EST	uC-gsflmaxxa098c06b1
Method	BLASTX
NCBI GI	g3096945
BLAST score	432
E value	2.0e-42
Match length	102
% identity	81
NCBI Description	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	200183
Contig ID	73266_1.R1039
5'-most EST	uC-gsflmaxxa097g12b1

Seq. No.	200184
Contig ID	73281_1.R1039
5'-most EST	g5048685
Method	BLASTX
NCBI GI	g3831444
BLAST score	419
E value	6.0e-41
Match length	115
% identity	70
NCBI Description	(AC005819) putative protein kinase [Arabidopsis thaliana]

Seq. No.	200185
Contig ID	73293_1.R1039
5'-most EST	g5049391
Method	BLASTX
NCBI GI	g3128218
BLAST score	749
E value	1.0e-79
Match length	231
% identity	68
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	200186
Contig ID	73315_1.R1039
5'-most EST	g5048662
Method	BLASTX
NCBI GI	g3650037
BLAST score	1258
E value	1.0e-139
Match length	291
% identity	84
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	200187
Contig ID	73335_1.R1039
5'-most EST	uC-gsflmaxxa098f06b1
Method	BLASTX
NCBI GI	g2673906
BLAST score	681
E value	8.0e-72
Match length	167
% identity	79
NCBI Description	(AC002561) putative DNA polymerase delta small subunit [Arabidopsis thaliana]

Seq. No.	200188
Contig ID	73384_1.R1039
5'-most EST	uC-gsflmaxxa106f07b1
Method	BLASTX
NCBI GI	g4193320
BLAST score	648
E value	9.0e-68
Match length	203
% identity	63
NCBI Description	(AF045473) histone deacetylase [Zea mays]

Seq. No.	200189
Contig ID	73556_1.R1039
5'-most EST	uC-gsflnu33B002g03b1

Seq. No.	200190
Contig ID	73571_1.R1039
5'-most EST	uC-gsflnu33B003a07b1
Method	BLASTX
NCBI GI	g3668069
BLAST score	978
E value	1.0e-106
Match length	208
% identity	89
NCBI Description	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No.	200191
Contig ID	73688_1.R1039
5'-most EST	g5046145
Method	BLASTX
NCBI GI	g3033394
BLAST score	207
E value	6.0e-16
Match length	137
% identity	31
NCBI Description	(AC004238) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	200192
Contig ID	73689_1.R1039
5'-most EST	uC-gsflnu33B005c03b1
Method	BLASTX
NCBI GI	g4455351
BLAST score	249

E value 4.0e-27
Match length 93
% identity 68
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 200193
Contig ID 73741_1.R1039
5'-most EST uC-gsflnu33B006a01b1

Seq. No. 200194
Contig ID 73808_1.R1039
5'-most EST g5050145
Method BLASTX
NCBI GI g1352458
BLAST score 989
E value 1.0e-108
Match length 221
% identity 89
NCBI Description INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD) >gi|2117507|pir||JC4999 IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana >gi|1100063 (L34684) IMP dehydrogenase [Arabidopsis thaliana]

Seq. No. 200195
Contig ID 73810_1.R1039
5'-most EST g5047922
Method BLASTX
NCBI GI g99992
BLAST score 193
E value 2.0e-14
Match length 79
% identity 30
NCBI Description protein disulfide-isomerase (EC 5.3.4.1) precursor - alfalfa (clone B2) >gi|166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No. 200196
Contig ID 73832_1.R1039
5'-most EST uC-gsflnu33B008d02b1
Method BLASTX
NCBI GI g1663722
BLAST score 545
E value 2.0e-98
Match length 241
% identity 72
NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 200197
Contig ID 73936_1.R1039
5'-most EST uC-gsflnu33B011a07b1
Method BLASTX
NCBI GI g2245030
BLAST score 426
E value 9.0e-48
Match length 162
% identity 59
NCBI Description (Z97341) apetala2 domain TINY homolog [Arabidopsis

thaliana]

Seq. No.	200198
Contig ID	74022_1.R1039
5'-most EST	g5047506
Method	BLASTX
NCBI GI	g4335763
BLAST score	679
E value	2.0e-71
Match length	161
% identity	80
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	200199
Contig ID	74120_1.R1039
5'-most EST	uC-gsflnu33B013g01b1
Method	BLASTX
NCBI GI	g3386613
BLAST score	358
E value	2.0e-34
Match length	80
% identity	84
NCBI Description	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	200200
Contig ID	74125_1.R1039
5'-most EST	uC-gsflnu33B115e08b1
Method	BLASTX
NCBI GI	g4176420
BLAST score	161
E value	7.0e-11
Match length	138
% identity	36
NCBI Description	(AB008097) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	200201
Contig ID	74184_1.R1039
5'-most EST	uC-gsflnu33B015e06b1
Method	BLASTX
NCBI GI	g1361983
BLAST score	345
E value	3.0e-32
Match length	173
% identity	44
NCBI Description	ARP protein - Arabidopsis thaliana >gi|886434|emb|CAA89858| (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	200202
Contig ID	74276_1.R1039
5'-most EST	uC-gsflnu33B016h11b1
Method	BLASTX
NCBI GI	g2827529
BLAST score	454
E value	3.0e-45
Match length	161
% identity	50

NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]
Seq. No.	200203
Contig ID	74279_1.R1039
5'-most EST	uC-gsflnu33B018a02b1
Seq. No.	200204
Contig ID	74306_1.R1039
5'-most EST	uC-gsflnu33B018c10b1
Method	BLASTX
NCBI GI	g4580469
BLAST score	163
E value	6.0e-11
Match length	166
% identity	30
NCBI Description	(AC006081) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	200205
Contig ID	74323_1.R1039
5'-most EST	uC-gsflnu33B018e05b1
Method	BLASTX
NCBI GI	g3033389
BLAST score	386
E value	4.0e-37
Match length	187
% identity	9
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
Seq. No.	200206
Contig ID	74343_1.R1039
5'-most EST	uC-gsflnu33B018g11b1
Method	BLASTX
NCBI GI	g2494041
BLAST score	609
E value	5.0e-63
Match length	196
% identity	62
NCBI Description	DIAMINOPIMELATE EPIMERASE >gi|1653875|dbj|BAA18785| (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.	200207
Contig ID	74475_1.R1039
5'-most EST	g5046655
Method	BLASTX
NCBI GI	g2739385
BLAST score	238
E value	1.0e-19
Match length	66
% identity	71
NCBI Description	(AC002505) putative beta-1,3-glucanase [Arabidopsis thaliana]
Seq. No.	200208
Contig ID	74500_1.R1039
5'-most EST	g5049787

Seq. No.	200209
Contig ID	74513_1.R1039
5'-most EST	g5049288
Method	BLASTX
NCBI GI	g507275
BLAST score	165
E value	3.0e-11
Match length	131
% identity	31
NCBI Description	(L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama guanicoe]

Seq. No.	200210
Contig ID	74515_1.R1039
5'-most EST	uC-gsflnu33B023c07b1

Seq. No.	200211
Contig ID	74594_1.R1039
5'-most EST	g5050649
Method	BLASTX
NCBI GI	g2244994
BLAST score	953
E value	1.0e-103
Match length	224
% identity	78
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	200212
Contig ID	74676_1.R1039
5'-most EST	g5047438

Seq. No.	200213
Contig ID	74681_1.R1039
5'-most EST	uC-gsflnu33B026g12b1

Seq. No.	200214
Contig ID	74715_1.R1039
5'-most EST	g5050434

Seq. No.	200215
Contig ID	74719_1.R1039
5'-most EST	g5049906
Method	BLASTX
NCBI GI	g2983986
BLAST score	160
E value	2.0e-10
Match length	86
% identity	47
NCBI Description	(AE000749) ribosomal protein L15 [Aquifex aeolicus]

Seq. No.	200216
Contig ID	74749_1.R1039
5'-most EST	uC-gsflnu33B031f11b1
Method	BLASTX
NCBI GI	g4006917
BLAST score	459

E value	2.0e-45
Match length	202
% identity	46
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	200217
Contig ID	74755_1.R1039
5'-most EST	g5050301

Seq. No.	200218
Contig ID	74790_1.R1039
5'-most EST	g5048125
Method	BLASTN
NCBI GI	g2924734
BLAST score	38
E value	1.0e-11
Match length	155
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	200219
Contig ID	74799_1.R1039
5'-most EST	uC-gsflnu33B028h02b1
Method	BLASTX
NCBI GI	g3805960
BLAST score	384
E value	9.0e-40
Match length	115
% identity	69
NCBI Description	(Y13771) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	200220
Contig ID	74922_1.R1039
5'-most EST	g3326006
Method	BLASTX
NCBI GI	g3059129
BLAST score	386
E value	4.0e-37
Match length	180
% identity	49
NCBI Description	(AJ000477) cytochrome P450 [Helianthus tuberosus]

Seq. No.	200221
Contig ID	74951_1.R1039
5'-most EST	uC-gsflnu33B031h05b1
Method	BLASTX
NCBI GI	g3928097
BLAST score	373
E value	8.0e-36
Match length	132
% identity	62
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	200222
Contig ID	75028_1.R1039

5'-most EST	uC-gsflnu33B036f11b1
Seq. No.	200223
Contig ID	75072_1.R1039
5'-most EST	uC-gsflnu33B100f03b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	281
E value	4.0e-25
Match length	117
% identity	48
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]
Seq. No.	200224
Contig ID	75078_1.R1039
5'-most EST	uC-gsflnu33B037e12b1
Seq. No.	200225
Contig ID	75090_1.R1039
5'-most EST	uC-gsflnu33B059f11b1
Seq. No.	200226
Contig ID	75095_1.R1039
5'-most EST	g5047876
Seq. No.	200227
Contig ID	75114_1.R1039
5'-most EST	uC-gsflnu33B046b02b1
Method	BLASTX
NCBI GI	g1619321
BLAST score	282
E value	4.0e-25
Match length	97
% identity	55
NCBI Description	(Y07563) hin1 [Nicotiana tabacum]
Seq. No.	200228
Contig ID	75241_1.R1039
5'-most EST	g3326374
Method	BLASTX
NCBI GI	g1170660
BLAST score	528
E value	9.0e-54
Match length	180
% identity	56
NCBI Description	MEVALONATE KINASE (MK) >gi|541880|pir||S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi|456614|emb|CAA54820| (X77793) mevalonate kinase [Arabidopsis thaliana]
Seq. No.	200229
Contig ID	75292_1.R1039
5'-most EST	uC-gsflnu33B050h08b1
Method	BLASTX
NCBI GI	g1362019
BLAST score	257

E value	4.0e-22
Match length	104
% identity	56
NCBI Description	zinc finger protein 6 - Arabidopsis thaliana >gi|790683 (L39649) zinc finger protein [Arabidopsis thaliana]

Seq. No.	200230
Contig ID	75521_1.R1039
5'-most EST	uC-gsflnu33B057d05b1

Seq. No.	200231
Contig ID	75653_1.R1039
5'-most EST	uC-gsflnu33B059d08b1

Seq. No.	200232
Contig ID	75788_1.R1039
5'-most EST	uC-gsflnu33B061c03b1
Method	BLASTX
NCBI GI	g4056457
BLAST score	530
E value	5.0e-54
Match length	129
% identity	75
NCBI Description	(AC005990) ESTs gb|234051 and gb|F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	200233
Contig ID	75836_1.R1039
5'-most EST	uC-gsflnu33B061h05b1

Seq. No.	200234
Contig ID	76086_1.R1039
5'-most EST	g5048006
Method	BLASTX
NCBI GI	g4206787
BLAST score	406
E value	1.0e-57
Match length	166
% identity	72
NCBI Description	(AF112863) syntaxin-related protein Nt-syr1 [Nicotiana tabacum]

Seq. No.	200235
Contig ID	76150_1.R1039
5'-most EST	uC-gsflnu33B068h07b1
Method	BLASTX
NCBI GI	g2832644
BLAST score	195
E value	5.0e-15
Match length	113
% identity	50
NCBI Description	(AL021710) teosinte branched1 - like protein [Arabidopsis thaliana]

Seq. No.	200236
Contig ID	76204_1.R1039
5'-most EST	g5047119

Method	BLASTX
NCBI GI	g498707
BLAST score	1311
E value	1.0e-147
Match length	426
% identity	62
NCBI Description	(X78422) HYP1 [Arabidopsis thaliana]

Seq. No.	200237
Contig ID	76213_1.R1039
5'-most EST	uC-gsflnu33B126h11b1

Seq. No.	200238
Contig ID	76277_1.R1039
5'-most EST	g5050456
Method	BLASTX
NCBI GI	g3415115
BLAST score	258
E value	4.0e-22
Match length	129
% identity	50
NCBI Description	(AF081202) villin 2 [Arabidopsis thaliana]

Seq. No.	200239
Contig ID	76305_1.R1039
5'-most EST	uC-gsflnu33B072b02b1

Seq. No.	200240
Contig ID	76334_1.R1039
5'-most EST	uC-gsflnu33B100f01b1
Method	BLASTX
NCBI GI	g2739385
BLAST score	567
E value	2.0e-58
Match length	156
% identity	69
NCBI Description	(AC002505) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	200241
Contig ID	76547_1.R1039
5'-most EST	uC-gsflnu33B082b12b1

Seq. No.	200242
Contig ID	76550_1.R1039
5'-most EST	uC-gsflnu33B082c01b1
Method	BLASTX
NCBI GI	g3033379
BLAST score	279
E value	1.0e-24
Match length	80
% identity	69
NCBI Description	(AC004238) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	200243
Contig ID	76553_1.R1039

5'-most EST	uC-gsflnu33B076c12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	200244
Contig ID	76559_1.R1039
5'-most EST	uC-gsflnu33B076e10b1

Seq. No.	200245
Contig ID	76561_1.R1039
5'-most EST	uC-gsflnu33B076e08b1

Seq. No.	200246
Contig ID	76566_1.R1039
5'-most EST	uC-gsflnu33B076f01b1
Method	BLASTX
NCBI GI	g2924509
BLAST score	272
E value	7.0e-24
Match length	111
% identity	48
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	200247
Contig ID	76568_1.R1039
5'-most EST	uC-gsflnu33B082f07b1

Seq. No.	200248
Contig ID	76570_1.R1039
5'-most EST	uC-gsflnu33B082g01b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	641
E value	6.0e-67
Match length	197
% identity	62
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	200249
Contig ID	76571_1.R1039
5'-most EST	uC-gsflnu33B082g03b1

Seq. No.	200250
Contig ID	76577_1.R1039
5'-most EST	uC-gsflnu33B082h03b1

Seq. No.	200251
Contig ID	76581_1.R1039
5'-most EST	uC-gsflnu33B083a05b1
Method	BLASTX
NCBI GI	g4262236

BLAST score 416
E value 7.0e-49
Match length 139
% identity 72
NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 200252
Contig ID 76585_1.R1039
5'-most EST uC-gsflnu33B083a01b1

Seq. No. 200253
Contig ID 76586_1.R1039
5'-most EST uC-gsflnu33B083c07b1

Seq. No. 200254
Contig ID 76595_1.R1039
5'-most EST uC-gsflnu33B083e10b1
Method BLASTX
NCBI GI g2144191
BLAST score 166
E value 1.0e-11
Match length 108
% identity 39
NCBI Description glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Microbispora bispora >gi|149826 (L06134) glucan-glucohydrolase [Microbispora bispora]

Seq. No. 200255
Contig ID 76602_1.R1039
5'-most EST uC-gsflnu33B083f04b1

Seq. No. 200256
Contig ID 76673_1.R1039
5'-most EST uC-gsflnu33B078h06b1
Method BLASTX
NCBI GI g3005576
BLAST score 716
E value 6.0e-76
Match length 163
% identity 85
NCBI Description (AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No. 200257
Contig ID 76682_1.R1039
5'-most EST uC-gsflnu33B085a06b1

Seq. No. 200258
Contig ID 76686_1.R1039
5'-most EST uC-gsflnu33B085b02b1

Seq. No. 200259
Contig ID 76707_1.R1039
5'-most EST uC-gsflnu33B085d06b1

Seq. No. 200260

Contig ID 76721_1.R1039
5'-most EST uC-gsflnu33B085f07b1
Method BLASTX
NCBI GI g1905910
BLAST score 587
E value 6.0e-61
Match length 139
% identity 78
NCBI Description (AD000092) putative human phenylalanine tRNA synthetase [Homo sapiens]

Seq. No. 200261
Contig ID 76730_1.R1039
5'-most EST uC-gsflnu33B085g06b1

Seq. No. 200262
Contig ID 76739_1.R1039
5'-most EST uC-gsflnu33B085h05b1
Method BLASTX
NCBI GI g4538898
BLAST score 226
E value 2.0e-18
Match length 153
% identity 48
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 200263
Contig ID 76741_1.R1039
5'-most EST g3326842
Method BLASTX
NCBI GI g3935168
BLAST score 178
E value 2.0e-24
Match length 138
% identity 53
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 200264
Contig ID 76789_1.R1039
5'-most EST g3325619

Seq. No. 200265
Contig ID 76794_1.R1039
5'-most EST g5046721

Seq. No. 200266
Contig ID 76800_1.R1039
5'-most EST g3326833
Method BLASTX
NCBI GI g4406773
BLAST score 187
E value 1.0e-13
Match length 67
% identity 34
NCBI Description (AC006836) putative cell division control protein 48 [Arabidopsis thaliana]

Seq. No. 200267
Contig ID 76836_1.R1039
5'-most EST g3326307

Seq. No. 200268
Contig ID 76853_1.R1039
5'-most EST g5047223
Method BLASTX
NCBI GI g3036793
BLAST score 229
E value 1.0e-18
Match length 101
% identity 49
NCBI Description (AL022373) putative protein [Arabidopsis thaliana] >gi|3805855|emb|CAA21475| (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 200269
Contig ID 76902_1.R1039
5'-most EST uC-gsflnu33B082f02b1
Method BLASTX
NCBI GI g2129854
BLAST score 667
E value 9.0e-70
Match length 212
% identity 58
NCBI Description early nodulin 8 precursor - alfalfa >gi|304037 (L18899) early nodulin [Medicago sativa]

Seq. No. 200270
Contig ID 76916_1.R1039
5'-most EST g5048391
Method BLASTX
NCBI GI g2827630
BLAST score 354
E value 4.0e-50
Match length 176
% identity 60
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 200271
Contig ID 77017_1.R1039
5'-most EST uC-gsflnu33B084b06b1
Method BLASTX
NCBI GI g3559814
BLAST score 877
E value 1.0e-94
Match length 199
% identity 86
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]

Seq. No. 200272
Contig ID 77032_1.R1039
5'-most EST uC-gsflnu33B084d07b1

Seq. No. 200273
Contig ID 77051_1.R1039

5'-most EST	uC-gsflnu33B084f01b1
Method	BLASTX
NCBI GI	g627424
BLAST score	198
E value	2.0e-15
Match length	113
% identity	35
NCBI Description	dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50kD subunit - human >gi|2135018|pir||S66254 dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50K chain - human

Seq. No.	200274
Contig ID	77156_1.R1039
5'-most EST	uC-gsflnu33B088c03b1

Seq. No.	200275
Contig ID	77195_1.R1039
5'-most EST	g5044219
Method	BLASTX
NCBI GI	g3123130
BLAST score	320
E value	2.0e-29
Match length	115
% identity	58
NCBI Description	HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN T32G6.2 IN CHROMOSOME II >gi|2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi|3241948 (AC004625) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No.	200276
Contig ID	77243_1.R1039
5'-most EST	uC-gsflnu33B089f08b1
Method	BLASTX
NCBI GI	g1723242
BLAST score	153
E value	8.0e-10
Match length	57
% identity	56
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I >gi|1177363|emb|CAA93239| (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]

Seq. No.	200277
Contig ID	77270_1.R1039
5'-most EST	uC-gsflnu33B090b07b1
Method	BLASTX
NCBI GI	g3334665
BLAST score	398
E value	8.0e-39
Match length	125
% identity	66
NCBI Description	(Y10492) putative cytochrome P450 [Glycine max]

Seq. No.	200278
Contig ID	77272_1.R1039

5'-most EST	uC-gsflnu33B090a11b1
Method	BLASTX
NCBI GI	g2059326
BLAST score	245
E value	1.0e-20
Match length	176
% identity	31
NCBI Description	(D67067) thymic epithelial cell surface antigen [Mus musculus]

Seq. No.	200279
Contig ID	77288_1.R1039
5'-most EST	g5050290
Method	BLASTX
NCBI GI	g4063007
BLAST score	473
E value	2.0e-47
Match length	149
% identity	36
NCBI Description	(AB021706) uncoupling protein [Arabidopsis thaliana]

Seq. No.	200280
Contig ID	77301_1.R1039
5'-most EST	uC-gsflnu33B129e10b1
Method	BLASTX
NCBI GI	g4105798
BLAST score	258
E value	3.0e-22
Match length	70
% identity	66
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	200281
Contig ID	77404_1.R1039
5'-most EST	g5047169

Seq. No.	200282
Contig ID	77588_1.R1039
5'-most EST	g3325856
Method	BLASTX
NCBI GI	g2342724
BLAST score	348
E value	2.0e-38
Match length	104
% identity	80
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	200283
Contig ID	77688_1.R1039
5'-most EST	uC-gsflnu33B099f08b1
Method	BLASTX
NCBI GI	g2388566
BLAST score	129
E value	2.0e-20
Match length	93
% identity	64
NCBI Description	(AC000098) Similar to Arabidopsis Fe(II) transport protein

(gb|U27590). [Arabidopsis thaliana]

Seq. No.	200284
Contig ID	77739_1.R1039
5'-most EST	uC-gsflnu33B100f04b1

Seq. No.	200285
Contig ID	77828_1.R1039
5'-most EST	uC-gsflnu33B107a02b1
Method	BLASTX
NCBI GI	g478790
BLAST score	111
E value	1.0e-10
Match length	180
% identity	36
NCBI Description	luciferase YG - luminescent click beetle (Pyrophorus plagiophthalmus)

Seq. No.	200286
Contig ID	77878_1.R1039
5'-most EST	g5049272
Method	BLASTX
NCBI GI	g2842490
BLAST score	427
E value	5.0e-55
Match length	213
% identity	55
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	200287
Contig ID	77914_1.R1039
5'-most EST	g3326504
Method	BLASTX
NCBI GI	g2290681
BLAST score	960
E value	1.0e-108
Match length	269
% identity	72
NCBI Description	(AF000135) acidic cellulase [Citrus sinensis]

Seq. No.	200288
Contig ID	78080_1.R1039
5'-most EST	uC-gsflnu33B111b02b1
Method	BLASTX
NCBI GI	g3080371
BLAST score	339
E value	9.0e-32
Match length	91
% identity	65
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	200289
Contig ID	78116_1.R1039
5'-most EST	uC-gsflnu33B146h04b1
Method	BLASTX
NCBI GI	g3023535

BLAST score	721
E value	1.0e-108
Match length	241
% identity	79
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi|662871|emb|CAA88107| (Z48047) Cnx2 [Arabidopsis thaliana]

Seq. No.	200290
Contig ID	78132_1.R1039
5'-most EST	g5048169
Method	BLASTX
NCBI GI	g1657615
BLAST score	758
E value	1.0e-80
Match length	183
% identity	77
NCBI Description	(U72502) G1p [Arabidopsis thaliana] >gi|3068706 (AF049236) putative transmembrane protein G1p [Arabidopsis thaliana]

Seq. No.	200291
Contig ID	78252_1.R1039
5'-most EST	uC-gsflnu33B113e09b1

Seq. No.	200292
Contig ID	78261_1.R1039
5'-most EST	uC-gsflnu33B113f10b1
Method	BLASTN
NCBI GI	g167346
BLAST score	39
E value	2.0e-12
Match length	397
% identity	83
NCBI Description	Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds

Seq. No.	200293
Contig ID	78315_1.R1039
5'-most EST	g5044328
Method	BLASTX
NCBI GI	g3746594
BLAST score	639
E value	1.0e-66
Match length	221
% identity	54
NCBI Description	(AF064611) RNA polymerase II subunit 2 [Periploca graeca]

Seq. No.	200294
Contig ID	78316_1.R1039
5'-most EST	uC-gsflnu33B114d04b1

Seq. No.	200295
Contig ID	78457_1.R1039
5'-most EST	uC-gsflnu33B126d01b1
Method	BLASTX
NCBI GI	g4455350
BLAST score	580

E value	1.0e-59
Match length	231
% identity	55
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	200296
Contig ID	78462_1.R1039
5'-most EST	uC-gsflnu33B136e08b1

Seq. No.	200297
Contig ID	78574_1.R1039
5'-most EST	uC-gsflnu33B128b05b1
Method	BLASTX
NCBI GI	g4191774
BLAST score	366
E value	5.0e-35
Match length	90
% identity	72
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	200298
Contig ID	78638_1.R1039
5'-most EST	g5048226
Method	BLASTX
NCBI GI	g4204281
BLAST score	210
E value	2.0e-16
Match length	123
% identity	36
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	200299
Contig ID	78641_1.R1039
5'-most EST	uC-gsflnu33B142g03b1

Seq. No.	200300
Contig ID	78672_1.R1039
5'-most EST	uC-gsflnu33B129f06b1
Method	BLASTX
NCBI GI	g3560261
BLAST score	145
E value	7.0e-09
Match length	91
% identity	33
NCBI Description	(AL031535) RNA binding protein [Schizosaccharomyces pombe]

Seq. No.	200301
Contig ID	78715_1.R1039
5'-most EST	g5049931
Method	BLASTX
NCBI GI	g2244852
BLAST score	358
E value	1.0e-33
Match length	102
% identity	66
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200302
Contig ID	78721_1.R1039
5'-most EST	g3325963

Seq. No.	200303
Contig ID	78757_1.R1039
5'-most EST	uC-gsflnu33B130h04b1
Method	BLASTX
NCBI GI	g2281090
BLAST score	559
E value	3.0e-57
Match length	219
% identity	59
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200304
Contig ID	78870_1.R1039
5'-most EST	uC-gsflnu33B133g12b1
Method	BLASTX
NCBI GI	g3549652
BLAST score	520
E value	4.0e-53
Match length	127
% identity	80
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	200305
Contig ID	78940_1.R1039
5'-most EST	uC-gsflnu33B135e06b1
Method	BLASTX
NCBI GI	g3193326
BLAST score	175
E value	9.0e-13
Match length	39
% identity	92
NCBI Description	(AF069299) contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R proteins [Arabidopsis thaliana]

Seq. No.	200306
Contig ID	79046_1.R1039
5'-most EST	uC-gsflnu33B137c08b1

Seq. No.	200307
Contig ID	79081_1.R1039
5'-most EST	uC-gsflnu33B137g03b1
Method	BLASTX
NCBI GI	g2773404
BLAST score	352
E value	2.0e-37
Match length	177
% identity	51
NCBI Description	(AF041255) pyridoxal kinase [Sus scrofa]

Seq. No. 200308

Contig ID	79119_1.R1039
5'-most EST	g5044705
Seq. No.	200309
Contig ID	79204_1.R1039
5'-most EST	g5048511
Seq. No.	200310
Contig ID	79254_1.R1039
5'-most EST	g2604014
Method	BLASTX
NCBI GI	g136636
BLAST score	560
E value	1.0e-57
Match length	106
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi|1076424|pir||S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi|442594|pdb|1AAK| Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi|2981894|pdb|2AAK| Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi|166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi|431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	200311
Contig ID	79316_1.R1039
5'-most EST	uC-gsflnu33B142a02b1
Method	BLASTX
NCBI GI	g3650033
BLAST score	348
E value	1.0e-32
Match length	94
% identity	76
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]
Seq. No.	200312
Contig ID	79399_1.R1039
5'-most EST	g5044387
Seq. No.	200313
Contig ID	79456_1.R1039
5'-most EST	uC-gsflnu33B144b04b1
Seq. No.	200314
Contig ID	79576_1.R1039
5'-most EST	uC-gsflnu33B145f06b1
Method	BLASTX
NCBI GI	g21309
BLAST score	341
E value	4.0e-32
Match length	81
% identity	42
NCBI Description	(X57955) 28kD RNA binding protein [Spinacia oleracea]
Seq. No.	200315

Contig ID	79607_1.R1039
5'-most EST	g5047331
Method	BLASTX
NCBI GI	g2804278
BLAST score	1094
E value	1.0e-137
Match length	323
% identity	76
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	200316
Contig ID	79804_1.R1039
5'-most EST	g5047156
Method	BLASTX
NCBI GI	g2129656
BLAST score	696
E value	2.0e-73
Match length	166
% identity	78
NCBI Description	OBP33pep protein - Arabidopsis thaliana (fragment) >gi|1022801 (U37699) OBP33pep [Arabidopsis thaliana]

Seq. No.	200317
Contig ID	79932_1.R1039
5'-most EST	g3325740

Seq. No.	200318
Contig ID	80006_1.R1039
5'-most EST	g5049217
Method	BLASTX
NCBI GI	g1944132
BLAST score	638
E value	2.0e-66
Match length	146
% identity	79
NCBI Description	(AB002560) CUC2 [Arabidopsis thaliana]

Seq. No.	200319
Contig ID	80028_1.R1039
5'-most EST	g5049834
Method	BLASTX
NCBI GI	g3367591
BLAST score	552
E value	3.0e-56
Match length	220
% identity	51
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	200320
Contig ID	80179_1.R1039
5'-most EST	g3326009

Seq. No.	200321
Contig ID	80223_1.R1039
5'-most EST	g5045831
Method	BLASTX
NCBI GI	g3128195

BLAST score	710
E value	2.0e-74
Match length	208
% identity	73
NCBI Description	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No.	200322
Contig ID	80292_1.R1039
5'-most EST	g3326102
Method	BLASTX
NCBI GI	g729092
BLAST score	350
E value	7.0e-33
Match length	91
% identity	84
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi|477484|pir||A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi|304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	200323
Contig ID	80313_1.R1039
5'-most EST	g5046296
Method	BLASTX
NCBI GI	g2642153
BLAST score	227
E value	3.0e-18
Match length	246
% identity	36
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi|2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	200324
Contig ID	80342_1.R1039
5'-most EST	g5044663
Method	BLASTX
NCBI GI	g3264778
BLAST score	476
E value	1.0e-47
Match length	189
% identity	57
NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	200325
Contig ID	80478_1.R1039
5'-most EST	g5047347
Method	BLASTX
NCBI GI	g1922246
BLAST score	438
E value	5.0e-43
Match length	201
% identity	48

NCBI Description	(Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No.	200326
Contig ID	80614_1.R1039
5'-most EST	g5047927
Method	BLASTX
NCBI GI	g4454452
BLAST score	436
E value	8.0e-64
Match length	233
% identity	42
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	200327
Contig ID	80727_1.R1039
5'-most EST	g3326535
Method	BLASTX
NCBI GI	g3033375
BLAST score	312
E value	2.0e-28
Match length	207
% identity	38
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	200328
Contig ID	80958_1.R1039
5'-most EST	g5050602
Method	BLASTX
NCBI GI	g3860255
BLAST score	239
E value	1.0e-19
Match length	190
% identity	36
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200329
Contig ID	81065_1.R1039
5'-most EST	g5044284
Method	BLASTX
NCBI GI	g3021513
BLAST score	986
E value	1.0e-107
Match length	215
% identity	85
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]

Seq. No.	200330
Contig ID	81095_1.R1039
5'-most EST	g5044254
Method	BLASTX
NCBI GI	g1703318
BLAST score	291
E value	3.0e-26
Match length	65
% identity	85

NCBI Description	ANNEXIN-LIKE PROTEIN RJ4 >gi|1362037|pir||S56674 annexin homolog RJ4 (clone RJ4) - garden strawberry (fragment) >gi|643076 (U19941) annexin [Fragaria x ananassa]

Seq. No.	200331
Contig ID	81098_1.R1039
5'-most EST	g5046802

Seq. No.	200332
Contig ID	81117_1.R1039
5'-most EST	g5050557
Method	BLASTX
NCBI GI	g4008006
BLAST score	373
E value	2.0e-35
Match length	128
% identity	40
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	200333
Contig ID	81130_1.R1039
5'-most EST	g5050547
Method	BLASTX
NCBI GI	g2738996
BLAST score	547
E value	6.0e-56
Match length	220
% identity	51
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	200334
Contig ID	81138_1.R1039
5'-most EST	g5047500
Method	BLASTX
NCBI GI	g417745
BLAST score	1029
E value	1.0e-112
Match length	212
% identity	92
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi|170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No.	200335
Contig ID	81150_1.R1039
5'-most EST	g5050678
Method	BLASTX
NCBI GI	g3540209
BLAST score	205
E value	8.0e-16
Match length	77
% identity	49
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	200336
Contig ID	81165_1.R1039

5'-most EST	g5044404
Method	BLASTX
NCBI GI	g3912926
BLAST score	292
E value	5.0e-26
Match length	175
% identity	38
NCBI Description	(AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]

Seq. No.	200337
Contig ID	81171_1.R1039
5'-most EST	g5044410
Method	BLASTX
NCBI GI	g3335368
BLAST score	264
E value	1.0e-22
Match length	134
% identity	42
NCBI Description	(AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200338
Contig ID	81211_1.R1039
5'-most EST	g5044304
Method	BLASTX
NCBI GI	g3482979
BLAST score	682
E value	9.0e-72
Match length	160
% identity	76
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi|4567258|gb|AAD23672.1|AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200339
Contig ID	81246_1.R1039
5'-most EST	g5050893
Method	BLASTX
NCBI GI	g2642450
BLAST score	821
E value	4.0e-88
Match length	201
% identity	81
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi|3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	200340
Contig ID	81253_1.R1039
5'-most EST	g5044347
Method	BLASTX
NCBI GI	g3600054
BLAST score	627
E value	3.0e-65
Match length	188
% identity	60
NCBI Description	(AF080120) No definition line found [Arabidopsis thaliana]

Seq. No.	200341
Contig ID	81255_1.R1039
5'-most EST	g5044349
Method	BLASTX
NCBI GI	g4558664
BLAST score	331
E value	1.0e-30
Match length	204
% identity	8
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200342
Contig ID	81280_1.R1039
5'-most EST	g5044444
Method	BLASTX
NCBI GI	g2982451
BLAST score	421
E value	4.0e-41
Match length	215
% identity	52
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	200343
Contig ID	81291_1.R1039
5'-most EST	g5044455
Method	BLASTX
NCBI GI	g4559371
BLAST score	877
E value	2.0e-94
Match length	265
% identity	62
NCBI Description	(AC006585) putative peroxidase [Arabidopsis thaliana]

Seq. No.	200344
Contig ID	81304_1.R1039
5'-most EST	g5044469
Method	BLASTX
NCBI GI	g3337367
BLAST score	520
E value	1.0e-52
Match length	250
% identity	43
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200345
Contig ID	81319_1.R1039
5'-most EST	g5045608
Method	BLASTX
NCBI GI	g629592
BLAST score	940
E value	1.0e-101
Match length	317
% identity	58
NCBI Description	hypothetical protein - rape

Seq. No.	200346
Contig ID	81330_1.R1039

5'-most EST	g5044495
Seq. No.	200347
Contig ID	81334_1.R1039
5'-most EST	g5048546
Method	BLASTX
NCBI GI	g4567279
BLAST score	570
E value	1.0e-58
Match length	162
% identity	67
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	200348
Contig ID	81381_1.R1039
5'-most EST	g5050666
Method	BLASTX
NCBI GI	g3451463
BLAST score	217
E value	3.0e-19
Match length	141
% identity	41
NCBI Description	(AL031349) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	200349
Contig ID	81407_1.R1039
5'-most EST	g5044872
Method	BLASTX
NCBI GI	g4510385
BLAST score	326
E value	5.0e-30
Match length	108
% identity	60
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	200350
Contig ID	81417_1.R1039
5'-most EST	g5044584
Seq. No.	200351
Contig ID	81467_1.R1039
5'-most EST	g5048132
Method	BLASTX
NCBI GI	g2499569
BLAST score	751
E value	8.0e-80
Match length	195
% identity	73
NCBI Description	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi|2129700|pir||S66344 protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) - Arabidopsis thaliana >gi|1322021 (U31288) L-isoaspartyl methyltransferase [Arabidopsis thaliana]

Seq. No.	200352
Contig ID	81486_1.R1039
5'-most EST	g5044656

Seq. No.	200353
Contig ID	81499_1.R1039
5'-most EST	g5044669
Method	BLASTX
NCBI GI	g4567282
BLAST score	594
E value	2.0e-61
Match length	198
% identity	60
NCBI Description	(AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	200354
Contig ID	81507_1.R1039
5'-most EST	g5046951
Method	BLASTX
NCBI GI	g461753
BLAST score	172
E value	7.0e-12
Match length	158
% identity	23
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi|419773|pir||S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi|169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	200355
Contig ID	81523_1.R1039
5'-most EST	g5044694

Seq. No.	200356
Contig ID	81550_1.R1039
5'-most EST	g5044724
Method	BLASTX
NCBI GI	g3935152
BLAST score	816
E value	2.0e-87
Match length	215
% identity	73
NCBI Description	(AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No.	200357
Contig ID	81564_1.R1039
5'-most EST	g5044738
Method	BLASTX
NCBI GI	g3695392
BLAST score	430
E value	3.0e-42
Match length	169
% identity	51
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 200358

Contig ID	81567_1.R1039
5'-most EST	g5044742
Method	BLASTX
NCBI GI	g2217970
BLAST score	170
E value	1.0e-11
Match length	127
% identity	12
NCBI Description	(Z97074) p40 [Homo sapiens]

Seq. No.	200359
Contig ID	81599_1.R1039
5'-most EST	g5044776
Method	BLASTX
NCBI GI	g2443886
BLAST score	147
E value	5.0e-09
Match length	139
% identity	30
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	200360
Contig ID	81600_1.R1039
5'-most EST	g5044777
Method	BLASTX
NCBI GI	g2673961
BLAST score	203
E value	1.0e-15
Match length	127
% identity	17
NCBI Description	(U70477) astrocytic NOVA-like RNA-binding protein [Homo sapiens]

Seq. No.	200361
Contig ID	81609_1.R1039
5'-most EST	g5048050
Method	BLASTX
NCBI GI	g4510381
BLAST score	224
E value	3.0e-18
Match length	157
% identity	39
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	200362
Contig ID	81634_1.R1039
5'-most EST	g5044811
Method	BLASTX
NCBI GI	g1652779
BLAST score	214
E value	7.0e-17
Match length	90
% identity	48
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	200363
Contig ID	81641_1.R1039

5'-most EST	g5044818
Method	BLASTX
NCBI GI	g3913437
BLAST score	1044
E value	1.0e-114
Match length	212
% identity	93
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi|1402875|emb|CAA66825| (X98130) RNA helicase [Arabidopsis thaliana] >gi|1495271|emb|CAA66613| (X97970) RNA helicase [Arabidopsis thaliana]

Seq. No.	200364
Contig ID	81650_1.R1039
5'-most EST	g5044827
Method	BLASTX
NCBI GI	g3522949
BLAST score	459
E value	1.0e-45
Match length	100
% identity	76
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200365
Contig ID	81673_1.R1039
5'-most EST	g5047894
Method	BLASTX
NCBI GI	g4191344
BLAST score	158
E value	2.0e-10
Match length	131
% identity	32
NCBI Description	(AF085199) golgin-84 [Homo sapiens]

Seq. No.	200366
Contig ID	81680_1.R1039
5'-most EST	g5044857
Method	BLASTX
NCBI GI	g2129698
BLAST score	645
E value	3.0e-67
Match length	230
% identity	60
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi|1054633|emb|CAA63387| (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	200367
Contig ID	81727_1.R1039
5'-most EST	g5047868
Method	BLASTX
NCBI GI	g121881
BLAST score	468
E value	1.0e-46
Match length	237
% identity	40
NCBI Description	DNA GYRASE SUBUNIT A >gi|80350|pir||F22930 DNA

topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Bacillus subtilis >gi|40019|emb|CAA26222| (X02369) ORF 821 (aa 1-821) [Bacillus subtilis] >gi|467397|dbj|BAA05243| (D26185) A subunit of DNA gyrase [Bacillus subtilis] >gi|2632274|emb|CAB11783| (Z99104) DNA gyrase (subunit A) [Bacillus subtilis]

Seq. No.	200368
Contig ID	81827_1.R1039
5'-most EST	g5045007
Method	BLASTX
NCBI GI	g2760839
BLAST score	1563
E value	1.0e-174
Match length	562
% identity	57
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	200369
Contig ID	81934_1.R1039
5'-most EST	g5047733
Method	BLASTN
NCBI GI	g13185
BLAST score	213
E value	1.0e-116
Match length	229
% identity	98
NCBI Description	Oenothera berteriana mitochondrial gene for 26S ribosomal RNA

Seq. No.	200370
Contig ID	82088_1.R1039
5'-most EST	g5045624
Method	BLASTX
NCBI GI	g2498732
BLAST score	616
E value	5.0e-64
Match length	158
% identity	73
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi|1362014|pir||S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi|886430|emb|CAA89262| (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	200371
Contig ID	82091_1.R1039
5'-most EST	g5049589
Method	BLASTX
NCBI GI	g2213867
BLAST score	647
E value	1.0e-67
Match length	172
% identity	75
NCBI Description	(AF003124) fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Seq. No. 200372

Contig ID	82274_1.R1039
5'-most EST	g5046374
Method	BLASTX
NCBI GI	g3935145
BLAST score	218
E value	2.0e-17
Match length	115
% identity	42
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	200373
Contig ID	82381_1.R1039
5'-most EST	g5047756
Method	BLASTX
NCBI GI	g2660673
BLAST score	221
E value	9.0e-18
Match length	185
% identity	10
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	200374
Contig ID	82424_1.R1039
5'-most EST	g5045613
Method	BLASTX
NCBI GI	g3047104
BLAST score	1382
E value	1.0e-153
Match length	330
% identity	82
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	200375
Contig ID	82598_1.R1039
5'-most EST	g5045787
Method	BLASTX
NCBI GI	g3176710
BLAST score	657
E value	8.0e-69
Match length	186
% identity	68
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	200376
Contig ID	82913_1.R1039
5'-most EST	g5050109

Seq. No.	200377
Contig ID	82927_1.R1039
5'-most EST	g5046117
Method	BLASTX
NCBI GI	g4262147
BLAST score	470
E value	6.0e-47
Match length	202
% identity	49
NCBI Description	(AC005275) putative homolog of transport inhibitor response

1 [Arabidopsis thaliana]

Seq. No.	200378
Contig ID	82985_1.R1039
5'-most EST	g5047726
Method	BLASTX
NCBI GI	g4455223
BLAST score	363
E value	3.0e-34
Match length	95
% identity	26
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	200379
Contig ID	83144_1.R1039
5'-most EST	g5046336
Method	BLASTX
NCBI GI	g2191152
BLAST score	258
E value	4.0e-22
Match length	158
% identity	39
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	200380
Contig ID	83146_1.R1039
5'-most EST	g5049833
Method	BLASTX
NCBI GI	g2252871
BLAST score	322
E value	5.0e-34
Match length	160
% identity	53
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	200381
Contig ID	83182_1.R1039
5'-most EST	g5046376
Method	BLASTX
NCBI GI	g282873
BLAST score	228
E value	1.0e-18
Match length	69
% identity	67
NCBI Description	transforming protein (myb) homolog - Arabidopsis thaliana >gi|217859|dbj|BAA01730| (D10936) ATMYB1 protein [Arabidopsis thaliana]

Seq. No.	200382
Contig ID	83202_1.R1039
5'-most EST	g5049814
Method	BLASTX
NCBI GI	g282964
BLAST score	592
E value	3.0e-61

Match length	190
% identity	72
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi|20563|emb|CAA78386| (Z13996) protein 1 [Petunia x hybrida]

Seq. No.	200383
Contig ID	83204_1.R1039
5'-most EST	g5049887
Method	BLASTX
NCBI GI	g3402686
BLAST score	780
E value	3.0e-83
Match length	214
% identity	71
NCBI Description	(AC004697) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	200384
Contig ID	83213_1.R1039
5'-most EST	g5049862
Method	BLASTX
NCBI GI	g2708532
BLAST score	372
E value	2.0e-35
Match length	155
% identity	26
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No.	200385
Contig ID	83268_1.R1039
5'-most EST	g5049821
Method	BLASTX
NCBI GI	g4262186
BLAST score	632
E value	6.0e-66
Match length	150
% identity	81
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	200386
Contig ID	83322_1.R1039
5'-most EST	g5049538

Seq. No.	200387
Contig ID	83336_1.R1039
5'-most EST	g5046535
Method	BLASTX
NCBI GI	g3702333
BLAST score	521
E value	7.0e-53
Match length	172
% identity	63
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 200388

Contig ID	83352_1.R1039
5'-most EST	g5046551
Method	BLASTX
NCBI GI	g1086900
BLAST score	367
E value	8.0e-35
Match length	197
% identity	38
NCBI Description	(U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]

Seq. No.	200389
Contig ID	83400_1.R1039
5'-most EST	g5047870
Method	BLASTX
NCBI GI	g1370172
BLAST score	156
E value	7.0e-10
Match length	118
% identity	36
NCBI Description	(Z73935) RAB1X [Lotus japonicus]

Seq. No.	200390
Contig ID	83415_1.R1039
5'-most EST	g5046999
Method	BLASTX
NCBI GI	g3033398
BLAST score	808
E value	4.0e-97
Match length	213
% identity	81
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	200391
Contig ID	83431_1.R1039
5'-most EST	g5046631

Seq. No.	200392
Contig ID	83435_1.R1039
5'-most EST	g5046635
Method	BLASTX
NCBI GI	g2842490
BLAST score	574
E value	6.0e-59
Match length	135
% identity	78
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	200393
Contig ID	83469_1.R1039
5'-most EST	g5046669
Method	BLASTX
NCBI GI	g3355486
BLAST score	626
E value	3.0e-65

Match length	191
% identity	62
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	200394
Contig ID	83489_1.R1039
5'-most EST	g5048292
Method	BLASTX
NCBI GI	g4490310
BLAST score	532
E value	4.0e-54
Match length	172
% identity	60
NCBI Description	(AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No.	200395
Contig ID	83492_1.R1039
5'-most EST	g5047135
Method	BLASTX
NCBI GI	g2499608
BLAST score	622
E value	8.0e-65
Match length	138
% identity	86
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi|2129645|pir||S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi|457400|dbj|BAA04867| (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No.	200396
Contig ID	83511_1.R1039
5'-most EST	g5048514
Method	BLASTX
NCBI GI	g4559334
BLAST score	267
E value	6.0e-23
Match length	210
% identity	31
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	200397
Contig ID	83527_1.R1039
5'-most EST	g5046727
Method	BLASTX
NCBI GI	g1723242
BLAST score	158
E value	3.0e-10
Match length	74
% identity	45
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I >gi|1177363|emb|CAA93239| (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]

Seq. No.	200398
Contig ID	83565_1.R1039

5'-most EST	g5047397
Method	BLASTX
NCBI GI	g2792304
BLAST score	664
E value	1.0e-69
Match length	210
% identity	60
NCBI Description	(AF039896) putative aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	200399
Contig ID	83576_1.R1039
5'-most EST	g5048463
Method	BLASTX
NCBI GI	g1297190
BLAST score	254
E value	2.0e-21
Match length	190
% identity	37
NCBI Description	(U53501) Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	200400
Contig ID	83612_1.R1039
5'-most EST	g5046889
Method	BLASTX
NCBI GI	g169959
BLAST score	892
E value	4.0e-96
Match length	339
% identity	59
NCBI Description	(L01448) G-box binding factor [Glycine max]

Seq. No.	200401
Contig ID	83614_1.R1039
5'-most EST	g5046891
Method	BLASTX
NCBI GI	g3935181
BLAST score	1109
E value	1.0e-121
Match length	222
% identity	88
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	200402
Contig ID	83647_1.R1039
5'-most EST	g5050490
Method	BLASTX
NCBI GI	g3885341
BLAST score	282
E value	6.0e-25
Match length	126
% identity	47
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	200403
Contig ID	83651_1.R1039

5'-most EST	g5046788
Method	BLASTX
NCBI GI	g3785990
BLAST score	386
E value	4.0e-37
Match length	135
% identity	61
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi|4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200404
Contig ID	83696_1.R1039
5'-most EST	g5049223
Method	BLASTX
NCBI GI	g2827658
BLAST score	581
E value	7.0e-60
Match length	212
% identity	56
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	200405
Contig ID	83708_1.R1039
5'-most EST	g5046847
Method	BLASTX
NCBI GI	g4510421
BLAST score	676
E value	6.0e-71
Match length	278
% identity	56
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	200406
Contig ID	83772_1.R1039
5'-most EST	g5050715
Method	BLASTN
NCBI GI	g3849811
BLAST score	53
E value	1.0e-20
Match length	129
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	200407
Contig ID	83777_1.R1039
5'-most EST	g5046983

Seq. No.	200408
Contig ID	83848_1.R1039
5'-most EST	g5050774
Method	BLASTX
NCBI GI	g3482933
BLAST score	207
E value	4.0e-16
Match length	170

% identity	36
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	200409
Contig ID	83875_1.R1039
5'-most EST	g5050146
Method	BLASTX
NCBI GI	g2497964
BLAST score	173
E value	4.0e-12
Match length	126
% identity	42
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX3 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX3) >gi|662873|emb|CAA88106| (Z48046) Cnx3 [Arabidopsis thaliana]

Seq. No.	200410
Contig ID	83932_1.R1039
5'-most EST	g5048066
Method	BLASTX
NCBI GI	g1086249
BLAST score	912
E value	2.0e-98
Match length	390
% identity	48
NCBI Description	subtilisin-like protease - Alnus glutinosa >gi|757522|emb|CAA59964| (X85975) subtilisin-like protease [Alnus glutinosa]

Seq. No.	200411
Contig ID	83957_1.R1039
5'-most EST	g5047168
Method	BLASTX
NCBI GI	g4467128
BLAST score	518
E value	1.0e-52
Match length	145
% identity	69
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	200412
Contig ID	84014_1.R1039
5'-most EST	g5050333
Method	BLASTX
NCBI GI	g3059131
BLAST score	589
E value	2.0e-73
Match length	240
% identity	56
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	200413
Contig ID	84045_1.R1039
5'-most EST	g5048106
Method	BLASTX
NCBI GI	g4314356

BLAST score	394
E value	6.0e-38
Match length	225
% identity	39
NCBI Description	(AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No.	200414
Contig ID	84089_1.R1039
5'-most EST	g5049927
Method	BLASTX
NCBI GI	g2832618
BLAST score	604
E value	2.0e-62
Match length	225
% identity	32
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	200415
Contig ID	84098_1.R1039
5'-most EST	g5048122
Method	BLASTX
NCBI GI	g4512624
BLAST score	963
E value	1.0e-104
Match length	239
% identity	76
NCBI Description	(AC004793) Strong similarity to gi|3033401 F19I3.29 putative potassium transporter from Arabidopsis thaliana BAC gb|AC004238

Seq. No.	200416
Contig ID	84101_1.R1039
5'-most EST	g5050582
Method	BLASTX
NCBI GI	g266410
BLAST score	155
E value	4.0e-13
Match length	90
% identity	54
NCBI Description	CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi|82507|pir||S13934 protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice >gi|20194|emb|CAA41172| (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa]

Seq. No.	200417
Contig ID	84102_1.R1039
5'-most EST	g5047318
Method	BLASTX
NCBI GI	g4455332
BLAST score	329
E value	4.0e-30
Match length	106
% identity	60
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	200418

Contig ID	84105_1.R1039
5'-most EST	g5047322
Method	BLASTX
NCBI GI	g3377851
BLAST score	844
E value	8.0e-91
Match length	204
% identity	80
NCBI Description	(AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05) [Arabidopsis thaliana]

Seq. No.	200419
Contig ID	84107_1.R1039
5'-most EST	g5050793
Method	BLASTX
NCBI GI	g2245005
BLAST score	270
E value	2.0e-23
Match length	114
% identity	51
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200420
Contig ID	84199_1.R1039
5'-most EST	g5048529

Seq. No.	200421
Contig ID	84218_1.R1039
5'-most EST	g5047442
Method	BLASTX
NCBI GI	g2281627
BLAST score	372
E value	2.0e-35
Match length	90
% identity	80
NCBI Description	(AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]

Seq. No.	200422
Contig ID	84244_1.R1039
5'-most EST	g5050710
Method	BLASTX
NCBI GI	g4538920
BLAST score	247
E value	8.0e-21
Match length	76
% identity	40
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	200423
Contig ID	84249_1.R1039
5'-most EST	g5050518
Method	BLASTX
NCBI GI	g3426037
BLAST score	1164

E value	1.0e-128
Match length	252
% identity	44
NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No.	200424
Contig ID	84304_1.R1039
5'-most EST	g5050482
Method	BLASTX
NCBI GI	g4249418
BLAST score	272
E value	1.0e-23
Match length	116
% identity	22
NCBI Description	(AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H type domains), 5' partial [Arabidopsis thaliana]

Seq. No.	200425
Contig ID	84307_1.R1039
5'-most EST	g5047535
Method	BLASTX
NCBI GI	g4160298
BLAST score	411
E value	4.0e-40
Match length	168
% identity	54
NCBI Description	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]

Seq. No.	200426
Contig ID	84315_1.R1039
5'-most EST	g5048980
Method	BLASTX
NCBI GI	g2245131
BLAST score	264
E value	7.0e-23
Match length	164
% identity	42
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200427
Contig ID	84341_1.R1039
5'-most EST	g5047571

Seq. No.	200428
Contig ID	84370_1.R1039
5'-most EST	g5047601
Method	BLASTX
NCBI GI	g3377822
BLAST score	560
E value	2.0e-57
Match length	193
% identity	66
NCBI Description	(AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No. 200429

Contig ID	84589_1.R1039
5'-most EST	g5047830
Method	BLASTX
NCBI GI	g4262225
BLAST score	551
E value	2.0e-56
Match length	192
% identity	56
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	200430
Contig ID	84652_1.R1039
5'-most EST	g5047895
Method	BLASTX
NCBI GI	g2765817
BLAST score	837
E value	5.0e-90
Match length	208
% identity	73
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi|3892049|gb|AAC78258.1|AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	200431
Contig ID	84657_1.R1039
5'-most EST	g5048459

Seq. No.	200432
Contig ID	84677_1.R1039
5'-most EST	g5047920
Method	BLASTX
NCBI GI	g3924604
BLAST score	384
E value	7.0e-37
Match length	205
% identity	24
NCBI Description	(AF069442) putative leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	200433
Contig ID	84745_1.R1039
5'-most EST	g5050497
Method	BLASTX
NCBI GI	g1110502
BLAST score	483
E value	2.0e-48
Match length	190
% identity	54
NCBI Description	(U40387) coil protein [Medicago sativa]

Seq. No.	200434
Contig ID	84879_1.R1039
5'-most EST	g5048127
Method	BLASTX
NCBI GI	g3169883
BLAST score	731

E value	2.0e-77
Match length	246
% identity	59
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi|3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	200435
Contig ID	85002_1.R1039
5'-most EST	g5049908
Method	BLASTX
NCBI GI	g3894194
BLAST score	463
E value	8.0e-46
Match length	259
% identity	39
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	200436
Contig ID	85114_1.R1039
5'-most EST	g5048373
Method	BLASTX
NCBI GI	g2244904
BLAST score	162
E value	1.0e-10
Match length	240
% identity	19
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	200437
Contig ID	85137_1.R1039
5'-most EST	g5050569
Method	BLASTX
NCBI GI	g3482927
BLAST score	314
E value	1.0e-28
Match length	146
% identity	49
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	200438
Contig ID	85304_1.R1039
5'-most EST	g5048569
Method	BLASTX
NCBI GI	g266410
BLAST score	645
E value	2.0e-67
Match length	140
% identity	89
NCBI Description	CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi|82507|pir||S13934 protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice >gi|20194|emb|CAA41172| (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa]

Seq. No.	200439
Contig ID	85315_1.R1039
5'-most EST	g5048580
Method	BLASTX
NCBI GI	g3738297
BLAST score	839
E value	1.0e-105
Match length	249
% identity	38
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	200440
Contig ID	85662_1.R1039
5'-most EST	g5049684
Method	BLASTX
NCBI GI	g2829902
BLAST score	491
E value	3.0e-58
Match length	183
% identity	66
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	200441
Contig ID	85977_1.R1039
5'-most EST	g5049253
Method	BLASTX
NCBI GI	g2129662
BLAST score	572
E value	7.0e-59
Match length	214
% identity	48
NCBI Description	ovule-specific homeotic protein homolog A20 - Arabidopsis thaliana >gi|1881536 (U37589) A20 [Arabidopsis thaliana]

Seq. No.	200442
Contig ID	86232_1.R1039
5'-most EST	g5049686

Seq. No.	200443
Contig ID	86479_1.R1039
5'-most EST	g5049758
Method	BLASTX
NCBI GI	g730326
BLAST score	177
E value	1.0e-12
Match length	110
% identity	35
NCBI Description	PHOSPHATIDYLINOSITOL-GLYCAN BIOSYNTHESIS, CLASS F PROTEIN (PIG-F) >gi|1082413|pir||A46097 GPI-anchor biosynthesis protein PIG-F - human >gi|303616|dbj|BAA02697| (D13435) PIG-F [Homo sapiens] >gi|4505797|ref|NP_002634.1|pPIGF| phosphatidylinositol glycan, class F

Seq. No.	200444
Contig ID	86554_1.R1039
5'-most EST	g5049836

Method	BLASTX
NCBI GI	g3323581
BLAST score	332
E value	9.0e-31
Match length	95
% identity	74
NCBI Description	(AF057281) two-component response regulator homolog [Arabidopsis thaliana]

Seq. No.	200445
Contig ID	86933_1.R1039
5'-most EST	g5050223

Seq. No.	200446
Contig ID	86935_1.R1039
5'-most EST	g5050225
Method	BLASTX
NCBI GI	g2842477
BLAST score	454
E value	6.0e-45
Match length	127
% identity	73
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	200447
Contig ID	86961_1.R1039
5'-most EST	g5050253
Method	BLASTX
NCBI GI	g3334138
BLAST score	324
E value	7.0e-30
Match length	128
% identity	52
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]

Seq. No.	200448
Contig ID	86979_1.R1039
5'-most EST	g5050619
Method	BLASTX
NCBI GI	g2498731
BLAST score	683
E value	7.0e-72
Match length	224
% identity	60
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi|1362013|pir||S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi|886428|emb|CAA89838| (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	200449
Contig ID	87518_1.R1039
5'-most EST	g5050840
Method	BLASTX
NCBI GI	g1438881
BLAST score	298

E value	6.0e-27
Match length	77
% identity	69
NCBI Description	(U43839) GmCK2p [Glycine max]

Seq. No.	200450
Contig ID	87526_1.R1039
5'-most EST	g5050842
Method	BLASTX
NCBI GI	g3402686
BLAST score	495
E value	6.0e-50
Match length	174
% identity	17
NCBI Description	(AC004697) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	200451
Seq. ID	LIB3048-001-Q1-L1-A11
Method	BLASTX
NCBI GI	g4106061
BLAST score	177
E value	9.0e-13
Match length	59
% identity	56
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	200452
Seq. ID	LIB3048-001-Q1-L1-A2
Method	BLASTX
NCBI GI	g1326165
BLAST score	360
E value	2.0e-34
Match length	108
% identity	61
NCBI Description	(U55032) aspartic protease [Brassica napus]

Seq. No.	200453
Seq. ID	LIB3048-001-Q1-L1-A3
Method	BLASTX
NCBI GI	g2129597
BLAST score	546
E value	4.0e-56
Match length	107
% identity	96
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	200454
Seq. ID	LIB3048-001-Q1-L1-A5
Method	BLASTX
NCBI GI	g2558512
BLAST score	142
E value	9.0e-09
Match length	92

% identity	43
NCBI Description	(AJ002020) proton pump interactor [Arabidopsis thaliana]

Seq. No.	200455
Seq. ID	LIB3048-001-Q1-L1-A8
Method	BLASTX
NCBI GI	g1747296
BLAST score	544
E value	6.0e-56
Match length	128
% identity	84
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	200456
Seq. ID	LIB3048-001-Q1-L1-B10
Method	BLASTX
NCBI GI	g4519507
BLAST score	405
E value	1.0e-39
Match length	129
% identity	67
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No.	200457
Seq. ID	LIB3048-001-Q1-L1-B11
Method	BLASTX
NCBI GI	g3292829
BLAST score	241
E value	2.0e-20
Match length	81
% identity	63
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	200458
Seq. ID	LIB3048-001-Q1-L1-B4
Method	BLASTX
NCBI GI	g1572819
BLAST score	192
E value	1.0e-14
Match length	81
% identity	48
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	200459
Seq. ID	LIB3048-001-Q1-L1-B5
Method	BLASTX
NCBI GI	g3775989
BLAST score	238
E value	4.0e-20
Match length	50
% identity	84
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No.	200460

Seq. ID	LIB3048-001-Q1-L1-B6
Method	BLASTX
NCBI GI	g729470
BLAST score	243
E value	1.0e-20
Match length	130
% identity	56
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	200461
Seq. ID	LIB3048-001-Q1-L1-B8
Method	BLASTX
NCBI GI	g3876865
BLAST score	164
E value	2.0e-11
Match length	76
% identity	38
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	200462
Seq. ID	LIB3048-001-Q1-L1-C1
Method	BLASTX
NCBI GI	g3980417
BLAST score	263
E value	4.0e-23
Match length	106
% identity	55
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	200463
Seq. ID	LIB3048-001-Q1-L1-C10
Method	BLASTX
NCBI GI	g3335351
BLAST score	323
E value	5.0e-30
Match length	123
% identity	11
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	200464
Seq. ID	LIB3048-001-Q1-L1-C11
Method	BLASTX
NCBI GI	g1708062
BLAST score	129
E value	2.0e-13
Match length	68
% identity	61

NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG PRECURSOR >gi_2129599_pir__S71250 glutathione peroxidase - Arabidopsis thaliana >gi_1061036_emb_CAA61965_ (X89866) glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	200465
Seq. ID	LIB3048-001-Q1-L1-C2
Method	BLASTX
NCBI GI	g4218535
BLAST score	445
E value	3.0e-44
Match length	121
% identity	66
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	200466
Seq. ID	LIB3048-001-Q1-L1-C6
Method	BLASTX
NCBI GI	g4102703
BLAST score	273
E value	4.0e-24
Match length	90
% identity	67
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	200467
Seq. ID	LIB3048-001-Q1-L1-C8
Method	BLASTX
NCBI GI	g4539335
BLAST score	190
E value	1.0e-14
Match length	103
% identity	36
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	200468
Seq. ID	LIB3048-001-Q1-L1-C9
Method	BLASTX
NCBI GI	g2443329
BLAST score	402
E value	3.0e-39
Match length	127
% identity	64
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	200469
Seq. ID	LIB3048-001-Q1-L1-D11
Method	BLASTX
NCBI GI	g547653
BLAST score	129
E value	6.0e-15
Match length	96
% identity	54
NCBI Description	HYDROXYMETHYLGLUTARYL-COA LYASE (HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE) >gi_482999_pir__B45470 hydroxymethylglutaryl-CoA lyase (EC

4.1.3.4) - chicken

Seq. No.	200470
Seq. ID	LIB3048-001-Q1-L1-D5
Method	BLASTX
NCBI GI	g3152576
BLAST score	183
E value	9.0e-14
Match length	101
% identity	45
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	200471
Seq. ID	LIB3048-001-Q1-L1-D7
Method	BLASTX
NCBI GI	g4454052
BLAST score	149
E value	1.0e-09
Match length	99
% identity	40
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200472
Seq. ID	LIB3048-001-Q1-L1-D8
Method	BLASTX
NCBI GI	g4335751
BLAST score	287
E value	6.0e-26
Match length	89
% identity	57
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	200473
Seq. ID	LIB3048-001-Q1-L1-E10
Method	BLASTX
NCBI GI	g4508073
BLAST score	205
E value	3.0e-16
Match length	66
% identity	64
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	200474
Seq. ID	LIB3048-001-Q1-L1-E2
Method	BLASTX
NCBI GI	g1370166
BLAST score	579
E value	5.0e-60
Match length	132
% identity	87
NCBI Description	(Z73932) RAB1C [Lotus japonicus]

Seq. No.	200475
Seq. ID	LIB3048-001-Q1-L1-E5
Method	BLASTX

NCBI GI	g3033375
BLAST score	150
E value	4.0e-10
Match length	81
% identity	37
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	200476
Seq. ID	LIB3048-001-Q1-L1-E7
Method	BLASTX
NCBI GI	g4539315
BLAST score	259
E value	2.0e-22
Match length	132
% identity	46
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	200477
Seq. ID	LIB3048-001-Q1-L1-E8
Method	BLASTX
NCBI GI	g1107526
BLAST score	141
E value	3.0e-09
Match length	53
% identity	49
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	200478
Seq. ID	LIB3048-001-Q1-L1-F3
Method	BLASTX
NCBI GI	g548774
BLAST score	299
E value	2.0e-27
Match length	83
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	200479
Seq. ID	LIB3048-001-Q1-L1-F5
Method	BLASTX
NCBI GI	g3549691
BLAST score	211
E value	2.0e-17
Match length	41
% identity	90
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	200480
Seq. ID	LIB3048-001-Q1-L1-F6
Method	BLASTX
NCBI GI	g2213629
BLAST score	312
E value	6.0e-29

Match length	74
% identity	73
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	200481
Seq. ID	LIB3048-001-Q1-L1-F7
Method	BLASTX
NCBI GI	g3242705
BLAST score	369
E value	2.0e-35
Match length	83
% identity	80
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	200482
Seq. ID	LIB3048-001-Q1-L1-F9
Method	BLASTX
NCBI GI	g1173257
BLAST score	230
E value	4.0e-31
Match length	103
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_1076674_pir__S47642 ribosomal protein S4 - potato >gi_457803_emb_CAA54095_ (X76651) ribosomal protein S4 [Solanum tuberosum]

Seq. No.	200483
Seq. ID	LIB3048-001-Q1-L1-G7
Method	BLASTX
NCBI GI	g4325324
BLAST score	644
E value	1.0e-67
Match length	129
% identity	92
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	200484
Seq. ID	LIB3048-001-Q1-L1-G8
Method	BLASTX
NCBI GI	g3236478
BLAST score	247
E value	3.0e-33
Match length	89
% identity	89
NCBI Description	(AF071196) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	200485
Seq. ID	LIB3048-001-Q1-L1-H2
Method	BLASTX
NCBI GI	g4115371
BLAST score	176
E value	9.0e-13
Match length	107
% identity	40

NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	200486
Seq. ID	LIB3048-001-Q1-L1-H5
Method	BLASTX
NCBI GI	g2129597
BLAST score	259
E value	2.0e-22
Match length	104
% identity	64
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	200487
Seq. ID	LIB3048-001-Q1-L1-H7
Method	BLASTX
NCBI GI	g2978452
BLAST score	408
E value	6.0e-40
Match length	113
% identity	70
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	200488
Seq. ID	LIB3048-001-Q1-L1-H9
Method	BLASTX
NCBI GI	g3236476
BLAST score	338
E value	5.0e-32
Match length	81
% identity	86
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	200489
Seq. ID	LIB3048-002-Q1-L1-A1
Method	BLASTX
NCBI GI	g2262170
BLAST score	217
E value	1.0e-17
Match length	95
% identity	46
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	200490
Seq. ID	LIB3048-002-Q1-L1-A11
Method	BLASTX
NCBI GI	g3955021
BLAST score	410
E value	3.0e-40
Match length	93
% identity	86
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	200491
Seq. ID	LIB3048-002-Q1-L1-A2
Method	BLASTX
NCBI GI	g1928981
BLAST score	518
E value	6.0e-53
Match length	107
% identity	94
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	200492
Seq. ID	LIB3048-002-Q1-L1-A3
Method	BLASTX
NCBI GI	g1402912
BLAST score	228
E value	7.0e-19
Match length	102
% identity	51
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	200493
Seq. ID	LIB3048-002-Q1-L1-A5
Method	BLASTX
NCBI GI	g2501850
BLAST score	518
E value	5.0e-53
Match length	106
% identity	93
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	200494
Seq. ID	LIB3048-002-Q1-L1-A6
Method	BLASTX
NCBI GI	g1001135
BLAST score	175
E value	7.0e-13
Match length	51
% identity	69
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	200495
Seq. ID	LIB3048-002-Q1-L1-A7
Method	BLASTX
NCBI GI	g480450
BLAST score	265
E value	3.0e-36
Match length	120
% identity	69
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	200496
Seq. ID	LIB3048-002-Q1-L1-A8
Method	BLASTX

NCBI GI	g1173253
BLAST score	469
E value	4.0e-47
Match length	107
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_543317_pir__S41170 ribosomal protein S3 - mouse >gi_57728_emb_CAA35916_ (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi_439522_emb_CAA54167_ (X76772) ribosomal protein S3 [Mus musculus]

Seq. No.	200497
Seq. ID	LIB3048-002-Q1-L1-A9
Method	BLASTX
NCBI GI	g2642158
BLAST score	508
E value	8.0e-52
Match length	112
% identity	80
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200498
Seq. ID	LIB3048-002-Q1-L1-B1
Method	BLASTX
NCBI GI	g3641837
BLAST score	406
E value	7.0e-40
Match length	121
% identity	71
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	200499
Seq. ID	LIB3048-002-Q1-L1-B2
Method	BLASTX
NCBI GI	g2196466
BLAST score	219
E value	7.0e-18
Match length	103
% identity	50
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	200500
Seq. ID	LIB3048-002-Q1-L1-B4
Method	BLASTX
NCBI GI	g1709358
BLAST score	310
E value	2.0e-28
Match length	117
% identity	52
NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859 nucleoside triphosphatase - garden pea >gi_2129890_pir__S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	200501
Seq. ID	LIB3048-002-Q1-L1-B5
Method	BLASTX
NCBI GI	g232024
BLAST score	305
E value	6.0e-28
Match length	105
% identity	61
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	200502
Seq. ID	LIB3048-002-Q1-L1-B6
Method	BLASTX
NCBI GI	g1703108
BLAST score	701
E value	2.0e-74
Match length	130
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	200503
Seq. ID	LIB3048-002-Q1-L1-B7
Method	BLASTX
NCBI GI	g4115379
BLAST score	164
E value	2.0e-11
Match length	51
% identity	61
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	200504
Seq. ID	LIB3048-002-Q1-L1-C1
Method	BLASTX
NCBI GI	g3218396
BLAST score	193
E value	8.0e-15
Match length	72
% identity	53
NCBI Description	(AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	200505
Seq. ID	LIB3048-002-Q1-L1-C10
Method	BLASTX
NCBI GI	g3024756
BLAST score	213

E value	4.0e-17
Match length	124
% identity	35
NCBI Description	TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi_1926403_emb_CAA71604_ (Y10582) type II DNA topoisomerase subunit B [Sulfolobus shibatae]

Seq. No.	200506
Seq. ID	LIB3048-002-Q1-L1-C3
Method	BLASTX
NCBI GI	g4249382
BLAST score	408
E value	5.0e-40
Match length	106
% identity	68
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	200507
Seq. ID	LIB3048-002-Q1-L1-C7
Method	BLASTX
NCBI GI	g1335862
BLAST score	454
E value	2.0e-45
Match length	100
% identity	87
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	200508
Seq. ID	LIB3048-002-Q1-L1-C8
Method	BLASTX
NCBI GI	g633110
BLAST score	607
E value	2.0e-63
Match length	123
% identity	95
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	200509
Seq. ID	LIB3048-002-Q1-L1-D1
Method	BLASTX
NCBI GI	g2129597
BLAST score	506
E value	2.0e-51
Match length	100
% identity	96
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	200510
Seq. ID	LIB3048-002-Q1-L1-D2
Method	BLASTX
NCBI GI	g3805845
BLAST score	214

E value	1.0e-17
Match length	76
% identity	55
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	200511
Seq. ID	LIB3048-002-Q1-L1-D3
Method	BLASTX
NCBI GI	g1350680
BLAST score	474
E value	9.0e-48
Match length	121
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	200512
Seq. ID	LIB3048-002-Q1-L1-D6
Method	BLASTX
NCBI GI	g2252846
BLAST score	317
E value	2.0e-29
Match length	92
% identity	67
NCBI Description	(AF013293) Similar to phospholipase D [Arabidopsis thaliana]

Seq. No.	200513
Seq. ID	LIB3048-002-Q1-L1-D7
Method	BLASTX
NCBI GI	g1350680
BLAST score	340
E value	5.0e-32
Match length	119
% identity	56
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	200514
Seq. ID	LIB3048-002-Q1-L1-D8
Method	BLASTX
NCBI GI	g167367
BLAST score	676
E value	2.0e-71
Match length	128
% identity	99
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	200515
Seq. ID	LIB3048-002-Q1-L1-D9
Method	BLASTX
NCBI GI	g4406809
BLAST score	146
E value	3.0e-09
Match length	82
% identity	49
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	200516

Seq. ID	LIB3048-002-Q1-L1-E1
Method	BLASTX
NCBI GI	g544250
BLAST score	439
E value	1.0e-43
Match length	106
% identity	78
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	200517
Seq. ID	LIB3048-002-Q1-L1-E10
Method	BLASTX
NCBI GI	g2062167
BLAST score	196
E value	2.0e-30
Match length	102
% identity	68
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	200518
Seq. ID	LIB3048-002-Q1-L1-E11
Method	BLASTX
NCBI GI	g633110
BLAST score	622
E value	4.0e-65
Match length	126
% identity	95
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	200519
Seq. ID	LIB3048-002-Q1-L1-E12
Method	BLASTN
NCBI GI	g4388705
BLAST score	39
E value	1.0e-12
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	200520
Seq. ID	LIB3048-002-Q1-L1-E4
Method	BLASTX
NCBI GI	g82065
BLAST score	414
E value	9.0e-41
Match length	114
% identity	74
NCBI Description	ribosomal protein S3a - Madagascar periwinkle >gi_217903_dbj_BAA00860_ (D01058) ORF [Catharanthus roseus]

Seq. No.	200521
Seq. ID	LIB3048-002-Q1-L1-E5
Method	BLASTX

NCBI GI g3152576
BLAST score 368
E value 3.0e-35
Match length 123
% identity 59
NCBI Description (AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No. 200522
Seq. ID LIB3048-002-Q1-L1-E9
Method BLASTX
NCBI GI g3435196
BLAST score 602
E value 1.0e-62
Match length 128
% identity 86
NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 200523
Seq. ID LIB3048-002-Q1-L1-F10
Method BLASTX
NCBI GI g2191183
BLAST score 299
E value 3.0e-27
Match length 113
% identity 48
NCBI Description (AF007271) similar to the ligand-gated ionic channels family [Arabidopsis thaliana]

Seq. No. 200524
Seq. ID LIB3048-002-Q1-L1-F12
Method BLASTX
NCBI GI g2388710
BLAST score 306
E value 4.0e-28
Match length 60
% identity 82
NCBI Description (AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No. 200525
Seq. ID LIB3048-002-Q1-L1-F2
Method BLASTX
NCBI GI g1658197
BLAST score 500
E value 9.0e-51
Match length 97
% identity 92
NCBI Description (U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No. 200526
Seq. ID LIB3048-002-Q1-L1-F3
Method BLASTX
NCBI GI g2342728
BLAST score 216
E value 2.0e-17

Match length	88
% identity	43
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	200527
Seq. ID	LIB3048-002-Q1-L1-F4
Method	BLASTX
NCBI GI	g1107526
BLAST score	385
E value	3.0e-37
Match length	117
% identity	68
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	200528
Seq. ID	LIB3048-002-Q1-L1-F5
Method	BLASTX
NCBI GI	g2062167
BLAST score	190
E value	4.0e-27
Match length	100
% identity	63
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	200529
Seq. ID	LIB3048-002-Q1-L1-F6
Method	BLASTX
NCBI GI	g2129597
BLAST score	506
E value	2.0e-51
Match length	100
% identity	96
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	200530
Seq. ID	LIB3048-002-Q1-L1-F8
Method	BLASTX
NCBI GI	g2642158
BLAST score	472
E value	2.0e-47
Match length	130
% identity	71
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200531
Seq. ID	LIB3048-002-Q1-L1-G11
Method	BLASTX
NCBI GI	g4433048
BLAST score	390
E value	6.0e-38
Match length	120
% identity	63

NCBI Description	(D26578) DNA-binding protein [Daucus carota]
Seq. No.	200532
Seq. ID	LIB3048-002-Q1-L1-G12
Method	BLASTX
NCBI GI	g1895084
BLAST score	301
E value	2.0e-27
Match length	59
% identity	95
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]
Seq. No.	200533
Seq. ID	LIB3048-002-Q1-L1-G2
Method	BLASTX
NCBI GI	g1762148
BLAST score	513
E value	3.0e-52
Match length	111
% identity	87
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]
Seq. No.	200534
Seq. ID	LIB3048-002-Q1-L1-G3
Method	BLASTX
NCBI GI	g3334147
BLAST score	494
E value	5.0e-50
Match length	136
% identity	72
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]
Seq. No.	200535
Seq. ID	LIB3048-002-Q1-L1-G4
Method	BLASTX
NCBI GI	g2129597
BLAST score	314
E value	5.0e-29
Match length	101
% identity	65
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]
Seq. No.	200536
Seq. ID	LIB3048-002-Q1-L1-G5
Method	BLASTX
NCBI GI	g2462826
BLAST score	224
E value	2.0e-18
Match length	118
% identity	41
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]
Seq. No.	200537

Seq. ID	LIB3048-002-Q1-L1-G6
Method	BLASTN
NCBI GI	g2656025
BLAST score	45
E value	4.0e-16
Match length	69
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	200538
Seq. ID	LIB3048-002-Q1-L1-G9
Method	BLASTX
NCBI GI	g1698548
BLAST score	551
E value	8.0e-57
Match length	126
% identity	82
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	200539
Seq. ID	LIB3048-002-Q1-L1-H10
Method	BLASTX
NCBI GI	g4314384
BLAST score	224
E value	2.0e-18
Match length	94
% identity	49
NCBI Description	(AC006232) putative cysteine proteinase [Arabidopsis thaliana]

Seq. No.	200540
Seq. ID	LIB3048-002-Q1-L1-H11
Method	BLASTX
NCBI GI	g3402693
BLAST score	155
E value	2.0e-10
Match length	88
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200541
Seq. ID	LIB3048-002-Q1-L1-H12
Method	BLASTX
NCBI GI	g3123515
BLAST score	497
E value	2.0e-50
Match length	105
% identity	90
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	200542
Seq. ID	LIB3048-002-Q1-L1-H3
Method	BLASTX
NCBI GI	g1143322
BLAST score	237
E value	2.0e-20

Match length	58
% identity	76
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	200543
Seq. ID	LIB3048-002-Q1-L1-H5
Method	BLASTX
NCBI GI	g1946368
BLAST score	178
E value	4.0e-13
Match length	101
% identity	37
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	200544
Seq. ID	LIB3048-002-Q1-L1-H7
Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200545
Seq. ID	LIB3048-002-Q1-L1-H9
Method	BLASTX
NCBI GI	g2500399
BLAST score	456
E value	1.0e-45
Match length	105
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098) ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls, embryos, Peptide, 253 aa] [Ambystoma mexicanum]

Seq. No.	200546
Seq. ID	LIB3048-003-Q1-L1-A1
Method	BLASTX
NCBI GI	g3738285
BLAST score	239
E value	4.0e-20
Match length	48
% identity	90
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	200547
Seq. ID	LIB3048-003-Q1-L1-A10
Method	BLASTX
NCBI GI	g3152576
BLAST score	372
E value	9.0e-36
Match length	124
% identity	59
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	200548
Seq. ID	LIB3048-003-Q1-L1-A11
Method	BLASTX
NCBI GI	g1002800
BLAST score	514
E value	2.0e-52
Match length	119
% identity	76
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	200549
Seq. ID	LIB3048-003-Q1-L1-A2
Method	BLASTX
NCBI GI	g3152609
BLAST score	340
E value	6.0e-32
Match length	119
% identity	55
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	200550
Seq. ID	LIB3048-003-Q1-L1-A3
Method	BLASTX
NCBI GI	g4160402
BLAST score	173
E value	2.0e-12
Match length	130
% identity	38
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No.	200551
Seq. ID	LIB3048-003-Q1-L1-A5
Method	BLASTX
NCBI GI	g4115379
BLAST score	256
E value	4.0e-22
Match length	87
% identity	61
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	200552
Seq. ID	LIB3048-003-Q1-L1-A8
Method	BLASTX
NCBI GI	g3876092
BLAST score	303
E value	1.0e-27
Match length	134
% identity	49
NCBI Description	(Z69635) Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	200553

Seq. ID	LIB3048-003-Q1-L1-A9
Method	BLASTX
NCBI GI	g3047082
BLAST score	566
E value	2.0e-58
Match length	123
% identity	82
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	200554
Seq. ID	LIB3048-003-Q1-L1-B1
Method	BLASTX
NCBI GI	g2597826
BLAST score	317
E value	3.0e-29
Match length	109
% identity	60
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	200555
Seq. ID	LIB3048-003-Q1-L1-B11
Method	BLASTX
NCBI GI	g2062167
BLAST score	196
E value	9.0e-28
Match length	89
% identity	72
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	200556
Seq. ID	LIB3048-003-Q1-L1-B3
Method	BLASTX
NCBI GI	g2407790
BLAST score	293
E value	2.0e-26
Match length	123
% identity	16
NCBI Description	(AF019910) grr1 [Glycine max]

Seq. No.	200557
Seq. ID	LIB3048-003-Q1-L1-B4
Method	BLASTX
NCBI GI	g4100433
BLAST score	337
E value	1.0e-31
Match length	98
% identity	67
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	200558
Seq. ID	LIB3048-003-Q1-L1-B5
Method	BLASTX
NCBI GI	g4309698
BLAST score	550
E value	1.0e-56

Match length	133
% identity	84
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	200559
Seq. ID	LIB3048-003-Q1-L1-B7
Method	BLASTX
NCBI GI	g1928981
BLAST score	578
E value	7.0e-60
Match length	121
% identity	63
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	200560
Seq. ID	LIB3048-003-Q1-L1-B8
Method	BLASTX
NCBI GI	g1407705
BLAST score	605
E value	5.0e-63
Match length	137
% identity	82
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	200561
Seq. ID	LIB3048-003-Q1-L1-B9
Method	BLASTX
NCBI GI	g3894387
BLAST score	145
E value	3.0e-09
Match length	113
% identity	4
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	200562
Seq. ID	LIB3048-003-Q1-L1-C10
Method	BLASTX
NCBI GI	g4490318
BLAST score	595
E value	6.0e-62
Match length	127
% identity	87
NCBI Description	(AL035678) 2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana]

Seq. No.	200563
Seq. ID	LIB3048-003-Q1-L1-C11
Method	BLASTX
NCBI GI	g4106061
BLAST score	105
E value	2.0e-10
Match length	57
% identity	53
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	200564
Seq. ID	LIB3048-003-Q1-L1-C2
Method	BLASTX
NCBI GI	g2281115
BLAST score	681
E value	6.0e-72
Match length	140
% identity	91
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	200565
Seq. ID	LIB3048-003-Q1-L1-C3
Method	BLASTX
NCBI GI	g3212866
BLAST score	185
E value	8.0e-14
Match length	127
% identity	35
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	200566
Seq. ID	LIB3048-003-Q1-L1-C6
Method	BLASTX
NCBI GI	g2444178
BLAST score	504
E value	3.0e-51
Match length	138
% identity	76
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	200567
Seq. ID	LIB3048-003-Q1-L1-C7
Method	BLASTX
NCBI GI	g4508068
BLAST score	231
E value	3.0e-19
Match length	135
% identity	45
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	200568
Seq. ID	LIB3048-003-Q1-L1-C8
Method	BLASTX
NCBI GI	g4432860
BLAST score	392
E value	4.0e-38
Match length	136
% identity	16
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	200569
Seq. ID	LIB3048-003-Q1-L1-D10
Method	BLASTX
NCBI GI	g119350
BLAST score	290

E value	3.0e-26
Match length	96
% identity	67
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	200570
Seq. ID	LIB3048-003-Q1-L1-D11
Method	BLASTX
NCBI GI	g3775989
BLAST score	154
E value	3.0e-10
Match length	40
% identity	68
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No.	200571
Seq. ID	LIB3048-003-Q1-L1-D12
Method	BLASTX
NCBI GI	g4432860
BLAST score	421
E value	1.0e-41
Match length	120
% identity	15
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	200572
Seq. ID	LIB3048-003-Q1-L1-D4
Method	BLASTX
NCBI GI	g2129769
BLAST score	282
E value	6.0e-32
Match length	88
% identity	80
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	200573
Seq. ID	LIB3048-003-Q1-L1-D6
Method	BLASTX
NCBI GI	g3132696
BLAST score	353
E value	1.0e-33
Match length	89
% identity	83
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	200574
Seq. ID	LIB3048-003-Q1-L1-D8
Method	BLASTX
NCBI GI	g232024
BLAST score	323

E value	5.0e-30
Match length	117
% identity	61
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	200575
Seq. ID	LIB3048-003-Q1-L1-E10
Method	BLASTX
NCBI GI	g1143188
BLAST score	529
E value	3.0e-54
Match length	109
% identity	36
NCBI Description	(U32627) ubiquitin precursor [Candida albicans]

Seq. No.	200576
Seq. ID	LIB3048-003-Q1-L1-E11
Method	BLASTX
NCBI GI	g3281848
BLAST score	141
E value	1.0e-08
Match length	61
% identity	54
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	200577
Seq. ID	LIB3048-003-Q1-L1-E12
Method	BLASTX
NCBI GI	g4508068
BLAST score	190
E value	2.0e-14
Match length	66
% identity	62
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	200578
Seq. ID	LIB3048-003-Q1-L1-E2
Method	BLASTX
NCBI GI	g3249105
BLAST score	441
E value	8.0e-44
Match length	136
% identity	61
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	200579
Seq. ID	LIB3048-003-Q1-L1-E3
Method	BLASTX
NCBI GI	g3334659
BLAST score	265
E value	4.0e-23
Match length	139

% identity	42
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	200580
Seq. ID	LIB3048-003-Q1-L1-E8
Method	BLASTX
NCBI GI	g3461815
BLAST score	182
E value	1.0e-22
Match length	76
% identity	75
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200581
Seq. ID	LIB3048-003-Q1-L1-F10
Method	BLASTX
NCBI GI	g2243118
BLAST score	221
E value	4.0e-18
Match length	54
% identity	74
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	200582
Seq. ID	LIB3048-003-Q1-L1-F12
Method	BLASTX
NCBI GI	g1107526
BLAST score	366
E value	4.0e-35
Match length	117
% identity	64
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	200583
Seq. ID	LIB3048-003-Q1-L1-F2
Method	BLASTX
NCBI GI	g1129145
BLAST score	650
E value	3.0e-68
Match length	140
% identity	89
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	200584
Seq. ID	LIB3048-003-Q1-L1-F3
Method	BLASTX
NCBI GI	g1483218
BLAST score	463
E value	2.0e-46
Match length	138
% identity	59
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	200585
Seq. ID	LIB3048-003-Q1-L1-F4
Method	BLASTX

NCBI GI	g3249105
BLAST score	329
E value	8.0e-36
Match length	131
% identity	55
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	200586
Seq. ID	LIB3048-003-Q1-L1-F6
Method	BLASTX
NCBI GI	g3775989
BLAST score	285
E value	2.0e-25
Match length	71
% identity	76
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No.	200587
Seq. ID	LIB3048-003-Q1-L1-F7
Method	BLASTX
NCBI GI	g1483218
BLAST score	428
E value	3.0e-42
Match length	130
% identity	58
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	200588
Seq. ID	LIB3048-003-Q1-L1-F8
Method	BLASTX
NCBI GI	g1762148
BLAST score	559
E value	1.0e-57
Match length	112
% identity	94
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]

Seq. No.	200589
Seq. ID	LIB3048-003-Q1-L1-F9
Method	BLASTX
NCBI GI	g3549691
BLAST score	196
E value	2.0e-37
Match length	118
% identity	67
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	200590
Seq. ID	LIB3048-003-Q1-L1-G12
Method	BLASTX
NCBI GI	g2980770
BLAST score	232
E value	1.0e-19
Match length	69
% identity	62

NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	200591
Seq. ID	LIB3048-003-Q1-L1-G3
Method	BLASTX
NCBI GI	g3047114
BLAST score	361
E value	2.0e-34
Match length	79
% identity	81
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	200592
Seq. ID	LIB3048-003-Q1-L1-G5
Method	BLASTX
NCBI GI	g483057
BLAST score	224
E value	2.0e-18
Match length	113
% identity	44
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	200593
Seq. ID	LIB3048-003-Q1-L1-G6
Method	BLASTX
NCBI GI	g1009232
BLAST score	199
E value	2.0e-15
Match length	72
% identity	60
NCBI Description	(L38828) EF-1-alpha-related GTP-binding protein [Nicotiana tabacum]

Seq. No.	200594
Seq. ID	LIB3048-003-Q1-L1-G9
Method	BLASTX
NCBI GI	g2230757
BLAST score	290
E value	3.0e-26
Match length	116
% identity	56
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	200595
Seq. ID	LIB3048-003-Q1-L1-H1
Method	BLASTX
NCBI GI	g1708236
BLAST score	457
E value	1.0e-45
Match length	98
% identity	91
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana

>gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	200596
Seq. ID	LIB3048-003-Q1-L1-H10
Method	BLASTX
NCBI GI	g119354
BLAST score	464
E value	1.0e-46
Match length	103
% identity	87
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	200597
Seq. ID	LIB3048-003-Q1-L1-H11
Method	BLASTX
NCBI GI	g1129145
BLAST score	586
E value	7.0e-61
Match length	126
% identity	89
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	200598
Seq. ID	LIB3048-003-Q1-L1-H2
Method	BLASTX
NCBI GI	g1399275
BLAST score	564
E value	3.0e-58
Match length	130
% identity	83
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	200599
Seq. ID	LIB3048-003-Q1-L1-H3
Method	BLASTX
NCBI GI	g1107526
BLAST score	461
E value	4.0e-46
Match length	114
% identity	75
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	200600
Seq. ID	LIB3048-003-Q1-L1-H6
Method	BLASTX
NCBI GI	g2738949
BLAST score	586

E value	8.0e-61
Match length	118
% identity	92
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	200601
Seq. ID	LIB3048-003-Q1-L1-H9
Method	BLASTX
NCBI GI	g3158376
BLAST score	274
E value	2.0e-24
Match length	109
% identity	52
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	200602
Seq. ID	LIB3048-004-Q1-L1-A10
Method	BLASTX
NCBI GI	g1657374
BLAST score	457
E value	1.0e-45
Match length	102
% identity	83
NCBI Description	(X96853) endo-beta-1,4-glucanase [Prunus persica] >gi_1657380_emb_CAA65600_ (X96856) endo-beta-1,4-glucanase [Prunus persica]

Seq. No.	200603
Seq. ID	LIB3048-004-Q1-L1-A11
Method	BLASTX
NCBI GI	g1657374
BLAST score	147
E value	2.0e-09
Match length	93
% identity	38
NCBI Description	(X96853) endo-beta-1,4-glucanase [Prunus persica] >gi_1657380_emb_CAA65600_ (X96856) endo-beta-1,4-glucanase [Prunus persica]

Seq. No.	200604
Seq. ID	LIB3048-004-Q1-L1-A12
Method	BLASTN
NCBI GI	g2829205
BLAST score	124
E value	3.0e-63
Match length	387
% identity	21
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	200605
Seq. ID	LIB3048-004-Q1-L1-A9
Method	BLASTX
NCBI GI	g3924597
BLAST score	192
E value	1.0e-14

Match length	102
% identity	38
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	200606
Seq. ID	LIB3048-004-Q1-L1-B10
Method	BLASTX
NCBI GI	g4335752
BLAST score	226
E value	1.0e-18
Match length	115
% identity	43
NCBI Description	(AC006284) putative myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	200607
Seq. ID	LIB3048-004-Q1-L1-B11
Method	BLASTX
NCBI GI	g224321
BLAST score	329
E value	4.0e-31
Match length	81
% identity	33
NCBI Description	ubiquitin precursor [Saccharomyces cerevisiae]

Seq. No.	200608
Seq. ID	LIB3048-004-Q1-L1-B9
Method	BLASTX
NCBI GI	g2895866
BLAST score	190
E value	2.0e-14
Match length	73
% identity	55
NCBI Description	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]

Seq. No.	200609
Seq. ID	LIB3048-004-Q1-L1-C11
Method	BLASTX
NCBI GI	g2979555
BLAST score	255
E value	4.0e-22
Match length	108
% identity	52
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	200610
Seq. ID	LIB3048-004-Q1-L1-C12
Method	BLASTX
NCBI GI	g3892712
BLAST score	559
E value	1.0e-57
Match length	130
% identity	83
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	200611
Seq. ID	LIB3048-004-Q1-L1-D10
Method	BLASTX
NCBI GI	g132939
BLAST score	502
E value	5.0e-51
Match length	115
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	200612
Seq. ID	LIB3048-004-Q1-L1-D9
Method	BLASTN
NCBI GI	g556421
BLAST score	43
E value	6.0e-15
Match length	55
% identity	95
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No.	200613
Seq. ID	LIB3048-004-Q1-L1-E10
Method	BLASTX
NCBI GI	g3024756
BLAST score	206
E value	3.0e-16
Match length	124
% identity	35
NCBI Description	TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi_1926403_emb_CAA71604_ (Y10582) type II DNA topoisomerase subunit B [Sulfolobus shibatae]

Seq. No.	200614
Seq. ID	LIB3048-004-Q1-L1-E12
Method	BLASTX
NCBI GI	g2462746
BLAST score	502
E value	6.0e-51
Match length	116
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	200615
Seq. ID	LIB3048-004-Q1-L1-F10
Method	BLASTX
NCBI GI	g3892712
BLAST score	545
E value	4.0e-56
Match length	126
% identity	83
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	200616
Seq. ID	LIB3048-004-Q1-L1-F12
Method	BLASTX
NCBI GI	g1168536
BLAST score	517
E value	9.0e-53
Match length	129
% identity	74
NCBI Description	PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE) >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-) precursor - barley >gi_18904_emb_CAA39602_ (X56136) aspartic proteinase [Hordeum vulgare]

Seq. No.	200617
Seq. ID	LIB3048-004-Q1-L1-G10
Method	BLASTX
NCBI GI	g3329294
BLAST score	142
E value	8.0e-09
Match length	115
% identity	30
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	200618
Seq. ID	LIB3048-004-Q1-L1-G11
Method	BLASTX
NCBI GI	g2791278
BLAST score	259
E value	2.0e-22
Match length	118
% identity	39
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	200619
Seq. ID	LIB3048-004-Q1-L1-H11
Method	BLASTX
NCBI GI	g629602
BLAST score	602
E value	1.0e-62
Match length	126
% identity	88
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	200620
Seq. ID	LIB3048-004-Q1-L1-H9
Method	BLASTX
NCBI GI	g3687235
BLAST score	306
E value	4.0e-28
Match length	118
% identity	62
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	200621
Seq. ID	LIB3048-005-Q1-L1-A1
Method	BLASTX
NCBI GI	g3047114
BLAST score	237
E value	2.0e-20
Match length	80
% identity	59
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	200622
Seq. ID	LIB3048-005-Q1-L1-A12
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	98
% identity	83
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	200623
Seq. ID	LIB3048-005-Q1-L1-A5
Method	BLASTX
NCBI GI	g1170028
BLAST score	488
E value	2.0e-49
Match length	102
% identity	92
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	200624
Seq. ID	LIB3048-005-Q1-L1-A6
Method	BLASTX
NCBI GI	g2281115
BLAST score	353
E value	3.0e-36
Match length	97
% identity	84
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	200625
Seq. ID	LIB3048-005-Q1-L1-B11
Method	BLASTX
NCBI GI	g1617270
BLAST score	493
E value	2.0e-55
Match length	132
% identity	78
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	200626
Seq. ID	LIB3048-005-Q1-L1-B12
Method	BLASTX
NCBI GI	g1617270
BLAST score	158
E value	1.0e-10
Match length	120
% identity	38
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	200627
Seq. ID	LIB3048-005-Q1-L1-B3
Method	BLASTX
NCBI GI	g529353
BLAST score	223
E value	3.0e-18
Match length	109
% identity	49
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	200628
Seq. ID	LIB3048-005-Q1-L1-B4
Method	BLASTX
NCBI GI	g2129851
BLAST score	190
E value	2.0e-14
Match length	52
% identity	69
NCBI Description	tRNA adenylyltransferase (EC 2.7.7.25) - white lupine >gi_1139585 (U15930) tRNA nucleotidyltransferase [Lupinus albus]

Seq. No.	200629
Seq. ID	LIB3048-005-Q1-L1-B6
Method	BLASTX
NCBI GI	g4204295
BLAST score	187
E value	5.0e-14
Match length	107
% identity	42
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	200630
Seq. ID	LIB3048-005-Q1-L1-B7
Method	BLASTX
NCBI GI	g3834314
BLAST score	243
E value	3.0e-36
Match length	117
% identity	72
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	200631
Seq. ID	LIB3048-005-Q1-L1-C11
Method	BLASTX
NCBI GI	g1709498
BLAST score	528
E value	5.0e-54
Match length	116
% identity	82
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	200632
Seq. ID	LIB3048-005-Q1-L1-C12
Method	BLASTX
NCBI GI	g3152576
BLAST score	409
E value	4.0e-40
Match length	132
% identity	61
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	200633
Seq. ID	LIB3048-005-Q1-L1-C2
Method	BLASTX
NCBI GI	g2642158
BLAST score	259
E value	2.0e-22
Match length	128
% identity	51
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200634
Seq. ID	LIB3048-005-Q1-L1-C7
Method	BLASTX
NCBI GI	g2760837
BLAST score	225
E value	2.0e-18
Match length	109
% identity	37
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	200635
Seq. ID	LIB3048-005-Q1-L1-C8
Method	BLASTX
NCBI GI	g2911052
BLAST score	562
E value	5.0e-58
Match length	132
% identity	80
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	200636
Seq. ID	LIB3048-005-Q1-L1-D11
Method	BLASTX

NCBI GI	g4510406
BLAST score	381
E value	8.0e-37
Match length	114
% identity	65
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	200637
Seq. ID	LIB3048-005-Q1-L1-D12
Method	BLASTX
NCBI GI	g1076668
BLAST score	555
E value	3.0e-57
Match length	130
% identity	79
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	200638
Seq. ID	LIB3048-005-Q1-L1-D3
Method	BLASTX
NCBI GI	g120667
BLAST score	361
E value	2.0e-34
Match length	103
% identity	69
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	200639
Seq. ID	LIB3048-005-Q1-L1-D4
Method	BLASTX
NCBI GI	g3047082
BLAST score	438
E value	2.0e-43
Match length	124
% identity	67
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	200640
Seq. ID	LIB3048-005-Q1-L1-D5
Method	BLASTX
NCBI GI	g3249105
BLAST score	375
E value	3.0e-36
Match length	109
% identity	65
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	200641
Seq. ID	LIB3048-005-Q1-L1-D6
Method	BLASTX
NCBI GI	g483057
BLAST score	189
E value	2.0e-14
Match length	106
% identity	40
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	200642
Seq. ID	LIB3048-005-Q1-L1-D8
Method	BLASTX
NCBI GI	g1361983
BLAST score	481
E value	2.0e-48
Match length	131
% identity	74
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	200643
Seq. ID	LIB3048-005-Q1-L1-E11
Method	BLASTX
NCBI GI	g2130149
BLAST score	615
E value	3.0e-64
Match length	129
% identity	91
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	200644
Seq. ID	LIB3048-005-Q1-L1-E12
Method	BLASTX
NCBI GI	g1345979
BLAST score	257
E value	3.0e-22
Match length	116
% identity	47
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No.	200645
Seq. ID	LIB3048-005-Q1-L1-E2
Method	BLASTX
NCBI GI	g3915037
BLAST score	593
E value	1.0e-61
Match length	135
% identity	85
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	200646
Seq. ID	LIB3048-005-Q1-L1-E6
Method	BLASTX
NCBI GI	g4262162
BLAST score	388
E value	1.0e-37
Match length	117
% identity	64
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	200647
Seq. ID	LIB3048-005-Q1-L1-E7
Method	BLASTX
NCBI GI	g1546696
BLAST score	187
E value	1.0e-14
Match length	56
% identity	61
NCBI Description	(X98807) peroxidase ATP21a [Arabidopsis thaliana]

Seq. No.	200648
Seq. ID	LIB3048-005-Q1-L1-E8
Method	BLASTX
NCBI GI	g4406818
BLAST score	427
E value	3.0e-42
Match length	101
% identity	73
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	200649
Seq. ID	LIB3048-005-Q1-L1-E9
Method	BLASTX
NCBI GI	g4519507
BLAST score	612
E value	7.0e-64
Match length	129
% identity	89
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No.	200650
Seq. ID	LIB3048-005-Q1-L1-F10
Method	BLASTX
NCBI GI	g872116
BLAST score	597
E value	4.0e-62
Match length	134
% identity	39
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	200651
Seq. ID	LIB3048-005-Q1-L1-F2
Method	BLASTX

NCBI GI	g3335351
BLAST score	379
E value	9.0e-37
Match length	92
% identity	9
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	200652
Seq. ID	LIB3048-005-Q1-L1-F4
Method	BLASTX
NCBI GI	g1407705
BLAST score	387
E value	1.0e-37
Match length	122
% identity	69
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	200653
Seq. ID	LIB3048-005-Q1-L1-F6
Method	BLASTX
NCBI GI	g4433048
BLAST score	392
E value	4.0e-38
Match length	123
% identity	62
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	200654
Seq. ID	LIB3048-005-Q1-L1-F7
Method	BLASTX
NCBI GI	g1747296
BLAST score	544
E value	6.0e-56
Match length	127
% identity	85
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	200655
Seq. ID	LIB3048-005-Q1-L1-F8
Method	BLASTX
NCBI GI	g2244792
BLAST score	508
E value	1.0e-51
Match length	124
% identity	72
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	200656
Seq. ID	LIB3048-005-Q1-L1-F9
Method	BLASTX
NCBI GI	g3608155
BLAST score	305
E value	7.0e-28
Match length	133

% identity	46
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	200657
Seq. ID	LIB3048-005-Q1-L1-G1
Method	BLASTX
NCBI GI	g3935168
BLAST score	300
E value	2.0e-27
Match length	72
% identity	82
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	200658
Seq. ID	LIB3048-005-Q1-L1-G10
Method	BLASTX
NCBI GI	g3334147
BLAST score	363
E value	2.0e-67
Match length	136
% identity	90
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	200659
Seq. ID	LIB3048-005-Q1-L1-G12
Method	BLASTX
NCBI GI	g2146797
BLAST score	578
E value	7.0e-60
Match length	134
% identity	80
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	200660
Seq. ID	LIB3048-005-Q1-L1-G3
Method	BLASTX
NCBI GI	g1350986
BLAST score	249
E value	8.0e-25
Match length	113
% identity	56
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No.	200661
Seq. ID	LIB3048-005-Q1-L1-G7
Method	BLASTX
NCBI GI	g3882211
BLAST score	363
E value	1.0e-34
Match length	134
% identity	55
NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]

Seq. No.	200662
Seq. ID	LIB3048-005-Q1-L1-H10
Method	BLASTX
NCBI GI	g4432859
BLAST score	205
E value	3.0e-16
Match length	126
% identity	44
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	200663
Seq. ID	LIB3048-005-Q1-L1-H11
Method	BLASTX
NCBI GI	g2317729
BLAST score	408
E value	5.0e-40
Match length	92
% identity	85
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	200664
Seq. ID	LIB3048-005-Q1-L1-H5
Method	BLASTX
NCBI GI	g2760347
BLAST score	616
E value	2.0e-64
Match length	124
% identity	18
NCBI Description	(U84968) ubiquitin [Arabidopsis thaliana]

Seq. No.	200665
Seq. ID	LIB3048-005-Q1-L1-H6
Method	BLASTX
NCBI GI	g3044212
BLAST score	420
E value	1.0e-41
Match length	87
% identity	90
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	200666
Seq. ID	LIB3048-005-Q1-L1-H7
Method	BLASTX
NCBI GI	g113742
BLAST score	283
E value	3.0e-25
Match length	133
% identity	44
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	200667
Seq. ID	LIB3048-006-Q1-L1-A1
Method	BLASTX
NCBI GI	g2980770
BLAST score	354
E value	9.0e-34
Match length	80
% identity	81
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	200668
Seq. ID	LIB3048-006-Q1-L1-A12
Method	BLASTX
NCBI GI	g2244759
BLAST score	458
E value	6.0e-46
Match length	116
% identity	69
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	200669
Seq. ID	LIB3048-006-Q1-L1-A2
Method	BLASTX
NCBI GI	g3122914
BLAST score	542
E value	1.0e-55
Match length	125
% identity	79
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	200670
Seq. ID	LIB3048-006-Q1-L1-A3
Method	BLASTX
NCBI GI	g1346387
BLAST score	620
E value	9.0e-65
Match length	134
% identity	89
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	200671
Seq. ID	LIB3048-006-Q1-L1-A6
Method	BLASTX
NCBI GI	g1061420
BLAST score	426
E value	3.0e-42
Match length	93
% identity	86
NCBI Description	(U38965) p-type H+-ATPase [Vicia faba]

Seq. No.	200672

Seq. ID	LIB3048-006-Q1-L1-A7
Method	BLASTX
NCBI GI	g464846
BLAST score	379
E value	1.0e-36
Match length	76
% identity	91
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	200673
Seq. ID	LIB3048-006-Q1-L1-A9
Method	BLASTX
NCBI GI	g4100123
BLAST score	220
E value	5.0e-18
Match length	115
% identity	41
NCBI Description	(U94347) elongation factor EF-1alpha [Pyrobaculum aerophilum]

Seq. No.	200674
Seq. ID	LIB3048-006-Q1-L1-B1
Method	BLASTX
NCBI GI	g3334320
BLAST score	591
E value	2.0e-61
Match length	115
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	200675
Seq. ID	LIB3048-006-Q1-L1-B4
Method	BLASTX
NCBI GI	g2102691
BLAST score	179
E value	3.0e-13
Match length	86
% identity	47
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	200676
Seq. ID	LIB3048-006-Q1-L1-B5
Method	BLASTX
NCBI GI	g2851455
BLAST score	248
E value	1.0e-21
Match length	71
% identity	70
NCBI Description	DYNAMIN-LIKE PROTEIN >gi_2267213 (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana]

Seq. No.	200677
Seq. ID	LIB3048-006-Q1-L1-B7
Method	BLASTX

NCBI GI	g1658193
BLAST score	175
E value	3.0e-13
Match length	69
% identity	54
NCBI Description	(U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum bicolor]

Seq. No.	200678
Seq. ID	LIB3048-006-Q1-L1-B8
Method	BLASTX
NCBI GI	g3142303
BLAST score	252
E value	1.0e-21
Match length	108
% identity	45
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	200679
Seq. ID	LIB3048-006-Q1-L1-B9
Method	BLASTX
NCBI GI	g1856971
BLAST score	473
E value	1.0e-47
Match length	103
% identity	87
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	200680
Seq. ID	LIB3048-006-Q1-L1-C1
Method	BLASTX
NCBI GI	g232024
BLAST score	186
E value	3.0e-14
Match length	79
% identity	53
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	200681
Seq. ID	LIB3048-006-Q1-L1-C4
Method	BLASTX
NCBI GI	g1346180
BLAST score	385
E value	3.0e-37
Match length	89
% identity	83
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374) homology with RNA-binding proteins in meristematic tissue

[Sinapis alba]

Seq. No.	200682
Seq. ID	LIB3048-006-Q1-L1-C8
Method	BLASTX
NCBI GI	g1709804
BLAST score	446
E value	2.0e-44
Match length	118
% identity	72
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	200683
Seq. ID	LIB3048-006-Q1-L1-D1
Method	BLASTX
NCBI GI	g2642158
BLAST score	465
E value	1.0e-46
Match length	129
% identity	70
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200684
Seq. ID	LIB3048-006-Q1-L1-D3
Method	BLASTX
NCBI GI	g4335751
BLAST score	403
E value	2.0e-39
Match length	114
% identity	61
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	200685
Seq. ID	LIB3048-006-Q1-L1-D5
Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200686
Seq. ID	LIB3048-006-Q1-L1-D6
Method	BLASTX
NCBI GI	g549010
BLAST score	300
E value	2.0e-27
Match length	103
% identity	65
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)

>gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	200687
Seq. ID	LIB3048-006-Q1-L1-D7
Method	BLASTX
NCBI GI	g1155261
BLAST score	227
E value	6.0e-19
Match length	91
% identity	56
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	200688
Seq. ID	LIB3048-006-Q1-L1-D8
Method	BLASTX
NCBI GI	g1856971
BLAST score	511
E value	5.0e-52
Match length	109
% identity	89
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	200689
Seq. ID	LIB3048-006-Q1-L1-D9
Method	BLASTX
NCBI GI	g1407705
BLAST score	593
E value	1.0e-61
Match length	130
% identity	84
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	200690
Seq. ID	LIB3048-006-Q1-L1-E1
Method	BLASTX
NCBI GI	g2281115
BLAST score	618
E value	1.0e-64
Match length	131
% identity	89
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	200691
Seq. ID	LIB3048-006-Q1-L1-E12
Method	BLASTX
NCBI GI	g2088647

BLAST score	337
E value	9.0e-32
Match length	86
% identity	76
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	200692
Seq. ID	LIB3048-006-Q1-L1-E2
Method	BLASTX
NCBI GI	g1345979
BLAST score	214
E value	3.0e-17
Match length	102
% identity	45
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No.	200693
Seq. ID	LIB3048-006-Q1-L1-E3
Method	BLASTX
NCBI GI	g4455225
BLAST score	310
E value	1.0e-28
Match length	88
% identity	67
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	200694
Seq. ID	LIB3048-006-Q1-L1-E5
Method	BLASTX
NCBI GI	g4539330
BLAST score	240
E value	3.0e-20
Match length	97
% identity	48
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	200695
Seq. ID	LIB3048-006-Q1-L1-E6
Method	BLASTX
NCBI GI	g4490732
BLAST score	174
E value	2.0e-12
Match length	71
% identity	55
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	200696
Seq. ID	LIB3048-006-Q1-L1-E7
Method	BLASTX
NCBI GI	g1407705
BLAST score	232

E value	2.0e-19
Match length	61
% identity	69
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	200697
Seq. ID	LIB3048-006-Q1-L1-E8
Method	BLASTX
NCBI GI	g3367591
BLAST score	259
E value	1.0e-22
Match length	101
% identity	46
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	200698
Seq. ID	LIB3048-006-Q1-L1-F1
Method	BLASTX
NCBI GI	g4468986
BLAST score	177
E value	7.0e-13
Match length	80
% identity	46
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	200699
Seq. ID	LIB3048-006-Q1-L1-F11
Method	BLASTX
NCBI GI	g3108075
BLAST score	156
E value	1.0e-10
Match length	94
% identity	39
NCBI Description	(AF060797) putative beta-ureidopropionase [Manduca sexta]

Seq. No.	200700
Seq. ID	LIB3048-006-Q1-L1-F12
Method	BLASTN
NCBI GI	g13192
BLAST score	150
E value	6.0e-79
Match length	233
% identity	92
NCBI Description	Oenothera berteriana mitDNA with part of plastid rRNA operon

Seq. No.	200701
Seq. ID	LIB3048-006-Q1-L1-F2
Method	BLASTX
NCBI GI	g1589913
BLAST score	163
E value	8.0e-12
Match length	60
% identity	57
NCBI Description	(U69694) ATP-sulfurylase precursor [Brassica oleracea]

Seq. No.	200702

Seq. ID LIB3048-006-Q1-L1-F6
Method BLASTX
NCBI GI g1155261
BLAST score 356
E value 8.0e-34
Match length 99
% identity 73
NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No. 200703
Seq. ID LIB3048-006-Q1-L1-F7
Method BLASTX
NCBI GI g3402693
BLAST score 157
E value 1.0e-10
Match length 88
% identity 44
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 200704
Seq. ID LIB3048-006-Q1-L1-G1
Method BLASTX
NCBI GI g3935168
BLAST score 370
E value 2.0e-35
Match length 137
% identity 60
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 200705
Seq. ID LIB3048-006-Q1-L1-G10
Method BLASTX
NCBI GI g2499819
BLAST score 353
E value 1.0e-33
Match length 97
% identity 68
NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No. 200706
Seq. ID LIB3048-006-Q1-L1-G12
Method BLASTX
NCBI GI g2463509
BLAST score 545
E value 5.0e-56
Match length 132
% identity 76
NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 200707
Seq. ID LIB3048-006-Q1-L1-G2
Method BLASTX

NCBI GI	g2369714
BLAST score	455
E value	1.0e-45
Match length	101
% identity	82
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	200708
Seq. ID	LIB3048-006-Q1-L1-G5
Method	BLASTX
NCBI GI	g3184082
BLAST score	195
E value	4.0e-15
Match length	91
% identity	44
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	200709
Seq. ID	LIB3048-006-Q1-L1-G7
Method	BLASTX
NCBI GI	g2462762
BLAST score	404
E value	2.0e-39
Match length	102
% identity	74
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	200710
Seq. ID	LIB3048-006-Q1-L1-G8
Method	BLASTX
NCBI GI	g2833386
BLAST score	150
E value	1.0e-09
Match length	91
% identity	44
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf__2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	200711
Seq. ID	LIB3048-006-Q1-L1-H12
Method	BLASTX
NCBI GI	g2129597
BLAST score	392
E value	3.0e-38
Match length	81
% identity	91
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1

[Arabidopsis thaliana]

Seq. No.	200712
Seq. ID	LIB3048-006-Q1-L1-H2
Method	BLASTX
NCBI GI	g3493367
BLAST score	302
E value	7.0e-28
Match length	62
% identity	92
NCBI Description	(AB017159) citrate synthase [Daucus carota]

Seq. No.	200713
Seq. ID	LIB3048-006-Q1-L1-H3
Method	BLASTX
NCBI GI	g1363325
BLAST score	314
E value	5.0e-29
Match length	108
% identity	60
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	200714
Seq. ID	LIB3048-006-Q1-L1-H5
Method	BLASTX
NCBI GI	g136640
BLAST score	473
E value	1.0e-47
Match length	92
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum]

Seq. No.	200715
Seq. ID	LIB3048-006-Q1-L1-H8
Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200716
Seq. ID	LIB3048-006-Q1-L1-H9
Method	BLASTX
NCBI GI	g2102691
BLAST score	277
E value	1.0e-24
Match length	102
% identity	57
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	200717
Seq. ID	LIB3048-007-Q1-L1-A1

Method	BLASTX
NCBI GI	g282881
BLAST score	193
E value	8.0e-15
Match length	120
% identity	38
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	200718
Seq. ID	LIB3048-007-Q1-L1-A2
Method	BLASTX
NCBI GI	g2909781
BLAST score	489
E value	2.0e-49
Match length	118
% identity	81
NCBI Description	(AF020288) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	200719
Seq. ID	LIB3048-007-Q1-L1-A3
Method	BLASTX
NCBI GI	g2340166
BLAST score	230
E value	1.0e-19
Match length	72
% identity	69
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	200720
Seq. ID	LIB3048-007-Q1-L1-A5
Method	BLASTX
NCBI GI	g2497538
BLAST score	224
E value	2.0e-18
Match length	70
% identity	64
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	200721
Seq. ID	LIB3048-007-Q1-L1-A6
Method	BLASTX
NCBI GI	g1778370
BLAST score	546
E value	3.0e-56
Match length	106
% identity	93
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	200722
Seq. ID	LIB3048-007-Q1-L1-A7

Method	BLASTX
NCBI GI	g1703200
BLAST score	549
E value	1.0e-56
Match length	115
% identity	92
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	200723
Seq. ID	LIB3048-007-Q1-L1-A9
Method	BLASTX
NCBI GI	g1076511
BLAST score	528
E value	4.0e-54
Match length	114
% identity	88
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	200724
Seq. ID	LIB3048-007-Q1-L1-B1
Method	BLASTX
NCBI GI	g1169782
BLAST score	470
E value	2.0e-47
Match length	112
% identity	76
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	200725
Seq. ID	LIB3048-007-Q1-L1-B10
Method	BLASTX
NCBI GI	g2443329
BLAST score	217
E value	5.0e-18
Match length	76
% identity	59
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	200726
Seq. ID	LIB3048-007-Q1-L1-B2
Method	BLASTX
NCBI GI	g3882081
BLAST score	533
E value	1.0e-54
Match length	108
% identity	37
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	200727
Seq. ID	LIB3048-007-Q1-L1-B3

Method	BLASTX
NCBI GI	g1362010
BLAST score	171
E value	2.0e-12
Match length	93
% identity	12
NCBI Description	ubiquitin-like protein 9 - Arabidopsis thaliana

Seq. No.	200728
Seq. ID	LIB3048-007-Q1-L1-B4
Method	BLASTX
NCBI GI	g2463509
BLAST score	566
E value	2.0e-58
Match length	132
% identity	82
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	200729
Seq. ID	LIB3048-007-Q1-L1-B5
Method	BLASTX
NCBI GI	g1709498
BLAST score	394
E value	2.0e-38
Match length	117
% identity	67
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	200730
Seq. ID	LIB3048-007-Q1-L1-B6
Method	BLASTX
NCBI GI	g1174592
BLAST score	705
E value	9.0e-75
Match length	132
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	200731
Seq. ID	LIB3048-007-Q1-L1-B7
Method	BLASTX
NCBI GI	g3334147
BLAST score	584
E value	1.0e-60
Match length	120
% identity	87
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	200732
Seq. ID	LIB3048-007-Q1-L1-B9
Method	BLASTX

NCBI GI	g282881
BLAST score	136
E value	1.0e-08
Match length	65
% identity	45
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	200733
Seq. ID	LIB3048-007-Q1-L1-C1
Method	BLASTX
NCBI GI	g2739381
BLAST score	297
E value	6.0e-27
Match length	102
% identity	59
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	200734
Seq. ID	LIB3048-007-Q1-L1-C10
Method	BLASTX
NCBI GI	g4468046
BLAST score	277
E value	1.0e-24
Match length	110
% identity	55
NCBI Description	(X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No.	200735
Seq. ID	LIB3048-007-Q1-L1-C12
Method	BLASTX
NCBI GI	g2833388
BLAST score	482
E value	1.0e-48
Match length	112
% identity	81
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	200736
Seq. ID	LIB3048-007-Q1-L1-C3
Method	BLASTX
NCBI GI	g4544454
BLAST score	324
E value	4.0e-30
Match length	129
% identity	55
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	200737
Seq. ID	LIB3048-007-Q1-L1-C4
Method	BLASTX
NCBI GI	g3096935

BLAST score	158
E value	1.0e-10
Match length	80
% identity	40
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	200738
Seq. ID	LIB3048-007-Q1-L1-C5
Method	BLASTX
NCBI GI	g3329294
BLAST score	151
E value	7.0e-10
Match length	115
% identity	30
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	200739
Seq. ID	LIB3048-007-Q1-L1-C6
Method	BLASTX
NCBI GI	g1142619
BLAST score	327
E value	2.0e-30
Match length	124
% identity	56
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	200740
Seq. ID	LIB3048-007-Q1-L1-C7
Method	BLASTX
NCBI GI	g3329294
BLAST score	149
E value	1.0e-09
Match length	115
% identity	30
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	200741
Seq. ID	LIB3048-007-Q1-L1-C8
Method	BLASTX
NCBI GI	g529353
BLAST score	415
E value	9.0e-41
Match length	113
% identity	64
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	200742
Seq. ID	LIB3048-007-Q1-L1-C9
Method	BLASTX
NCBI GI	g3096935
BLAST score	143
E value	6.0e-09
Match length	69
% identity	42

NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]
Seq. No.	200743
Seq. ID	LIB3048-007-Q1-L1-D1
Method	BLASTX
NCBI GI	g3924597
BLAST score	166
E value	1.0e-11
Match length	72
% identity	43
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.	200744
Seq. ID	LIB3048-007-Q1-L1-D12
Method	BLASTX
NCBI GI	g4558547
BLAST score	282
E value	3.0e-25
Match length	109
% identity	51
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]
Seq. No.	200745
Seq. ID	LIB3048-007-Q1-L1-D8
Method	BLASTX
NCBI GI	g2462762
BLAST score	436
E value	3.0e-43
Match length	111
% identity	73
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.	200746
Seq. ID	LIB3048-007-Q1-L1-D9
Method	BLASTX
NCBI GI	g4519507
BLAST score	605
E value	5.0e-63
Match length	132
% identity	86
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]
Seq. No.	200747
Seq. ID	LIB3048-007-Q1-L1-E1
Method	BLASTX
NCBI GI	g3334147
BLAST score	392
E value	4.0e-38
Match length	106
% identity	71
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]
Seq. No.	200748
Seq. ID	LIB3048-007-Q1-L1-E2

Method	BLASTX
NCBI GI	g3335351
BLAST score	395
E value	2.0e-38
Match length	117
% identity	11
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	200749
Seq. ID	LIB3048-007-Q1-L1-E3
Method	BLASTX
NCBI GI	g3548802
BLAST score	306
E value	5.0e-28
Match length	128
% identity	47
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	200750
Seq. ID	LIB3048-007-Q1-L1-E6
Method	BLASTX
NCBI GI	g603074
BLAST score	416
E value	6.0e-41
Match length	129
% identity	58
NCBI Description	(U18197) ATP:citrate lyase [Homo sapiens]

Seq. No.	200751
Seq. ID	LIB3048-007-Q1-L1-E9
Method	BLASTX
NCBI GI	g477819
BLAST score	551
E value	1.0e-56
Match length	134
% identity	77
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	200752
Seq. ID	LIB3048-007-Q1-L1-F1
Method	BLASTX
NCBI GI	g4262250
BLAST score	412
E value	2.0e-40
Match length	121
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	200753

Seq. ID	LIB3048-007-Q1-L1-F10
Method	BLASTX
NCBI GI	g4558547
BLAST score	193
E value	4.0e-15
Match length	61
% identity	59
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200754
Seq. ID	LIB3048-007-Q1-L1-F11
Method	BLASTX
NCBI GI	g3335351
BLAST score	453
E value	3.0e-45
Match length	135
% identity	17
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	200755
Seq. ID	LIB3048-007-Q1-L1-F12
Method	BLASTX
NCBI GI	g3062801
BLAST score	304
E value	6.0e-28
Match length	96
% identity	61
NCBI Description	(AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No.	200756
Seq. ID	LIB3048-007-Q1-L1-F4
Method	BLASTX
NCBI GI	g2739279
BLAST score	351
E value	3.0e-33
Match length	123
% identity	58
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	200757
Seq. ID	LIB3048-007-Q1-L1-F7
Method	BLASTX
NCBI GI	g1171978
BLAST score	420
E value	2.0e-41
Match length	113
% identity	22
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	200758

Seq. ID	LIB3048-007-Q1-L1-F8
Method	BLASTX
NCBI GI	g4530126
BLAST score	345
E value	1.0e-32
Match length	98
% identity	68
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	200759
Seq. ID	LIB3048-007-Q1-L1-F9
Method	BLASTX
NCBI GI	g2996096
BLAST score	593
E value	1.0e-61
Match length	122
% identity	94
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	200760
Seq. ID	LIB3048-007-Q1-L1-G1
Method	BLASTX
NCBI GI	g2129956
BLAST score	330
E value	8.0e-31
Match length	114
% identity	52
NCBI Description	photoassimilate-responsive protein PAR-1c precursor - common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]

Seq. No.	200761
Seq. ID	LIB3048-007-Q1-L1-G11
Method	BLASTX
NCBI GI	g2766452
BLAST score	222
E value	4.0e-18
Match length	73
% identity	58
NCBI Description	(AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No.	200762
Seq. ID	LIB3048-007-Q1-L1-G2
Method	BLASTX
NCBI GI	g2497538
BLAST score	224
E value	2.0e-18
Match length	70
% identity	64
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	200763
Seq. ID	LIB3048-007-Q1-L1-G3

Method	BLASTX
NCBI GI	g2262173
BLAST score	349
E value	4.0e-33
Match length	115
% identity	62
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	200764
Seq. ID	LIB3048-007-Q1-L1-G4
Method	BLASTX
NCBI GI	g3334659
BLAST score	248
E value	3.0e-21
Match length	124
% identity	42
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	200765
Seq. ID	LIB3048-007-Q1-L1-G9
Method	BLASTX
NCBI GI	g3831455
BLAST score	175
E value	1.0e-12
Match length	43
% identity	81
NCBI Description	(AC005700) putative ubiquitin activating enzyme [Arabidopsis thaliana]

Seq. No.	200766
Seq. ID	LIB3048-007-Q1-L1-H1
Method	BLASTX
NCBI GI	g2827551
BLAST score	299
E value	3.0e-27
Match length	111
% identity	59
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	200767
Seq. ID	LIB3048-007-Q1-L1-H10
Method	BLASTX
NCBI GI	g1172903
BLAST score	148
E value	1.0e-09
Match length	58
% identity	47
NCBI Description	GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi_1073884_pir__D64062 ATP--GTP 3'-pyrophosphotransferase (relA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573303 (U32718) GTP pyrophosphokinase (relA) [Haemophilus influenzae Rd]

Seq. No.	200768
Seq. ID	LIB3048-007-Q1-L1-H3
Method	BLASTX

NCBI GI	g3132696
BLAST score	585
E value	1.0e-60
Match length	130
% identity	86
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	200769
Seq. ID	LIB3048-007-Q1-L1-H4
Method	BLASTX
NCBI GI	g3377797
BLAST score	347
E value	4.0e-33
Match length	78
% identity	87
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	200770
Seq. ID	LIB3048-007-Q1-L1-H7
Method	BLASTX
NCBI GI	g1572819
BLAST score	236
E value	8.0e-20
Match length	98
% identity	49
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	200771
Seq. ID	LIB3048-007-Q1-L1-H8
Method	BLASTX
NCBI GI	g4468046
BLAST score	264
E value	4.0e-23
Match length	106
% identity	56
NCBI Description	(X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No.	200772
Seq. ID	LIB3048-008-Q1-L1-A1
Method	BLASTX
NCBI GI	g2146797
BLAST score	346
E value	9.0e-33
Match length	104
% identity	37
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	200773
Seq. ID	LIB3048-008-Q1-L1-A12

Method	BLASTX
NCBI GI	g3785986
BLAST score	161
E value	5.0e-11
Match length	67
% identity	54
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	200774
Seq. ID	LIB3048-008-Q1-L1-A2
Method	BLASTX
NCBI GI	g3549670
BLAST score	511
E value	4.0e-52
Match length	118
% identity	81
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	200775
Seq. ID	LIB3048-008-Q1-L1-A4
Method	BLASTX
NCBI GI	g4101626
BLAST score	481
E value	1.0e-48
Match length	124
% identity	73
NCBI Description	(AF005096) desaturase/cytochrome b5 protein [Ricinus communis]

Seq. No.	200776
Seq. ID	LIB3048-008-Q1-L1-A5
Method	BLASTX
NCBI GI	g2569938
BLAST score	176
E value	9.0e-13
Match length	68
% identity	54
NCBI Description	(Y15193) GAI [Arabidopsis thaliana]

Seq. No.	200777
Seq. ID	LIB3048-008-Q1-L1-A6
Method	BLASTX
NCBI GI	g3641836
BLAST score	526
E value	7.0e-54
Match length	122
% identity	83
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	200778
Seq. ID	LIB3048-008-Q1-L1-A7
Method	BLASTX
NCBI GI	g1361983
BLAST score	484
E value	7.0e-49
Match length	130

% identity	75
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	200779
Seq. ID	LIB3048-008-Q1-L1-A8
Method	BLASTX
NCBI GI	g2642450
BLAST score	563
E value	3.0e-58
Match length	123
% identity	88
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	200780
Seq. ID	LIB3048-008-Q1-L1-B1
Method	BLASTX
NCBI GI	g1556429
BLAST score	365
E value	5.0e-35
Match length	100
% identity	72
NCBI Description	(X84226) citrate synthase [Nicotiana tabacum]

Seq. No.	200781
Seq. ID	LIB3048-008-Q1-L1-B11
Method	BLASTX
NCBI GI	g1402912
BLAST score	477
E value	5.0e-48
Match length	128
% identity	71
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	200782
Seq. ID	LIB3048-008-Q1-L1-B12
Method	BLASTX
NCBI GI	g2462826
BLAST score	229
E value	3.0e-28
Match length	130
% identity	52
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	200783
Seq. ID	LIB3048-008-Q1-L1-B2
Method	BLASTX
NCBI GI	g2388580
BLAST score	270
E value	7.0e-24
Match length	62
% identity	71
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	200784
Seq. ID	LIB3048-008-Q1-L1-B3
Method	BLASTX
NCBI GI	g2827711
BLAST score	424
E value	6.0e-42
Match length	117
% identity	68
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	200785
Seq. ID	LIB3048-008-Q1-L1-B4
Method	BLASTX
NCBI GI	g2995953
BLAST score	157
E value	1.0e-10
Match length	46
% identity	72
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	200786
Seq. ID	LIB3048-008-Q1-L1-B5
Method	BLASTN
NCBI GI	g1017801
BLAST score	34
E value	9.0e-10
Match length	58
% identity	90
NCBI Description	Shuttle expression vector pBKCMV

Seq. No.	200787
Seq. ID	LIB3048-008-Q1-L1-B6
Method	BLASTX
NCBI GI	g2462746
BLAST score	410
E value	3.0e-40
Match length	99
% identity	79
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	200788
Seq. ID	LIB3048-008-Q1-L1-B8
Method	BLASTX
NCBI GI	g2465923
BLAST score	142
E value	9.0e-09
Match length	116
% identity	34
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	200789
Seq. ID	LIB3048-008-Q1-L1-B9
Method	BLASTX
NCBI GI	g3881138

BLAST score 161
E value 5.0e-11
Match length 51
% identity 55
NCBI Description (AL023846) Y52B11C.1 [Caenorhabditis elegans]

Seq. No. 200790
Seq. ID LIB3048-008-Q1-L1-C1
Method BLASTX
NCBI GI g2245064
BLAST score 208
E value 2.0e-16
Match length 88
% identity 51
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 200791
Seq. ID LIB3048-008-Q1-L1-C10
Method BLASTX
NCBI GI g1170031
BLAST score 650
E value 3.0e-68
Match length 137
% identity 89
NCBI Description GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_541940_pir__JQ2263 glutamate 1-semialdehyde aminotransferase (EC 2.6.1.-) precursor - soybean >gi_310567 (L12453) glutamate 1-semialdehyde aminotransferase [Glycine max] >gi_747968 (U20260) glutamate 1-semialdehyde aminotransferase [Glycine max]

Seq. No. 200792
Seq. ID LIB3048-008-Q1-L1-C11
Method BLASTX
NCBI GI g3065814
BLAST score 176
E value 1.0e-12
Match length 126
% identity 40
NCBI Description (AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus norvegicus] >gi_3168585_dbj_BAA28609_ (AB001321) sodium-dependent dicarboxylate transporter [Rattus norvegicus]

Seq. No. 200793
Seq. ID LIB3048-008-Q1-L1-C12
Method BLASTX
NCBI GI g2462822
BLAST score 284
E value 2.0e-25
Match length 137
% identity 49
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 200794
Seq. ID LIB3048-008-Q1-L1-C2

Method	BLASTX
NCBI GI	g3450842
BLAST score	244
E value	9.0e-21
Match length	92
% identity	55
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	200795
Seq. ID	LIB3048-008-Q1-L1-C4
Method	BLASTX
NCBI GI	g2827561
BLAST score	169
E value	5.0e-12
Match length	102
% identity	36
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292809_emb_CAA19799_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	200796
Seq. ID	LIB3048-008-Q1-L1-C9
Method	BLASTX
NCBI GI	g1363325
BLAST score	321
E value	9.0e-30
Match length	108
% identity	61
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	200797
Seq. ID	LIB3048-008-Q1-L1-D10
Method	BLASTX
NCBI GI	g1495251
BLAST score	312
E value	1.0e-28
Match length	137
% identity	49
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	200798
Seq. ID	LIB3048-008-Q1-L1-D2
Method	BLASTX
NCBI GI	g3287683
BLAST score	303
E value	8.0e-28
Match length	117
% identity	14
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb_D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	200799
Seq. ID	LIB3048-008-Q1-L1-D3
Method	BLASTX
NCBI GI	g3107931

BLAST score	171
E value	3.0e-25
Match length	86
% identity	76
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	200800
Seq. ID	LIB3048-008-Q1-L1-D4
Method	BLASTX
NCBI GI	g3641836
BLAST score	579
E value	5.0e-60
Match length	132
% identity	84
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	200801
Seq. ID	LIB3048-008-Q1-L1-D6
Method	BLASTX
NCBI GI	g3319355
BLAST score	539
E value	2.0e-55
Match length	115
% identity	88
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	200802
Seq. ID	LIB3048-008-Q1-L1-D7
Method	BLASTX
NCBI GI	g4105798
BLAST score	574
E value	2.0e-59
Match length	132
% identity	67
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	200803
Seq. ID	LIB3048-008-Q1-L1-D9
Method	BLASTX
NCBI GI	g4204265
BLAST score	229
E value	6.0e-19
Match length	121
% identity	45
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	200804
Seq. ID	LIB3048-008-Q1-L1-E10
Method	BLASTX
NCBI GI	g2369714
BLAST score	671
E value	9.0e-71
Match length	136
% identity	95
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	200805
Seq. ID	LIB3048-008-Q1-L1-E12
Method	BLASTX
NCBI GI	g4455225
BLAST score	611
E value	9.0e-64
Match length	131
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	200806
Seq. ID	LIB3048-008-Q1-L1-E4
Method	BLASTX
NCBI GI	g3335351
BLAST score	490
E value	1.0e-49
Match length	127
% identity	10
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	200807
Seq. ID	LIB3048-008-Q1-L1-E6
Method	BLASTX
NCBI GI	g2134102
BLAST score	246
E value	5.0e-21
Match length	110
% identity	55
NCBI Description	kinesin-like protein 1 - African clawed frog >gi_562793_emb_CAA57539_ (X82012) kinesin-like protein 1 [Xenopus laevis]

Seq. No.	200808
Seq. ID	LIB3048-008-Q1-L1-E7
Method	BLASTX
NCBI GI	g1345655
BLAST score	231
E value	6.0e-29
Match length	97
% identity	68
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	200809
Seq. ID	LIB3048-008-Q1-L1-E8
Method	BLASTX
NCBI GI	g2911059
BLAST score	517
E value	8.0e-53
Match length	123
% identity	85
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	200810
Seq. ID	LIB3048-008-Q1-L1-E9
Method	BLASTX
NCBI GI	g2244987
BLAST score	230
E value	4.0e-19
Match length	98
% identity	48
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No.	200811
Seq. ID	LIB3048-008-Q1-L1-F1
Method	BLASTX
NCBI GI	g3602981
BLAST score	204
E value	5.0e-16
Match length	86
% identity	52
NCBI Description	(AF041468) acetohydroxyacid synthetase small subunit [Guillardia theta]

Seq. No.	200812
Seq. ID	LIB3048-008-Q1-L1-F11
Method	BLASTX
NCBI GI	g417073
BLAST score	261
E value	1.0e-36
Match length	95
% identity	74
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	200813
Seq. ID	LIB3048-008-Q1-L1-F12
Method	BLASTX
NCBI GI	g4262174
BLAST score	554
E value	5.0e-57
Match length	137
% identity	70
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	200814
Seq. ID	LIB3048-008-Q1-L1-F3
Method	BLASTX
NCBI GI	g2833381
BLAST score	234
E value	2.0e-31
Match length	123
% identity	56
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_1172159 (U44126) starch synthase [Ipomoea batatas]

Seq. No. 200815

Seq. ID LIB3048-008-Q1-L1-F5
Method BLASTX
NCBI GI g1332579
BLAST score 546
E value 3.0e-56
Match length 111
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 200816
Seq. ID LIB3048-008-Q1-L1-F6
Method BLASTX
NCBI GI g1706323
BLAST score 391
E value 5.0e-38
Match length 114
% identity 65
NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No. 200817
Seq. ID LIB3048-008-Q1-L1-F7
Method BLASTX
NCBI GI g1142619
BLAST score 330
E value 7.0e-31
Match length 124
% identity 56
NCBI Description (U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No. 200818
Seq. ID LIB3048-008-Q1-L1-F9
Method BLASTX
NCBI GI g4519507
BLAST score 559
E value 1.0e-57
Match length 118
% identity 89
NCBI Description (D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No. 200819
Seq. ID LIB3048-008-Q1-L1-G1
Method BLASTX
NCBI GI g3176708
BLAST score 265
E value 3.0e-23
Match length 88
% identity 58
NCBI Description (AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No. 200820
Seq. ID LIB3048-008-Q1-L1-G10

Method	BLASTX
NCBI GI	g2597826
BLAST score	322
E value	7.0e-30
Match length	109
% identity	61
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	200821
Seq. ID	LIB3048-008-Q1-L1-G12
Method	BLASTX
NCBI GI	g2462826
BLAST score	386
E value	2.0e-37
Match length	135
% identity	54
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	200822
Seq. ID	LIB3048-008-Q1-L1-G2
Method	BLASTX
NCBI GI	g3047082
BLAST score	423
E value	6.0e-42
Match length	101
% identity	77
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	200823
Seq. ID	LIB3048-008-Q1-L1-G3
Method	BLASTX
NCBI GI	g1155261
BLAST score	530
E value	3.0e-54
Match length	123
% identity	85
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	200824
Seq. ID	LIB3048-008-Q1-L1-G5
Method	BLASTX
NCBI GI	g1332579
BLAST score	535
E value	6.0e-55
Match length	109
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	200825
Seq. ID	LIB3048-008-Q1-L1-G6
Method	BLASTX
NCBI GI	g2935298
BLAST score	440
E value	9.0e-44
Match length	123

% identity	74
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	200826
Seq. ID	LIB3048-008-Q1-L1-G9
Method	BLASTX
NCBI GI	g2326372
BLAST score	524
E value	1.0e-53
Match length	137
% identity	69
NCBI Description	(Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No.	200827
Seq. ID	LIB3048-008-Q1-L1-H1
Method	BLASTX
NCBI GI	g2498706
BLAST score	150
E value	9.0e-10
Match length	42
% identity	67
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	200828
Seq. ID	LIB3048-008-Q1-L1-H10
Method	BLASTX
NCBI GI	g3287683
BLAST score	379
E value	1.0e-36
Match length	135
% identity	16
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb_D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	200829
Seq. ID	LIB3048-008-Q1-L1-H11
Method	BLASTX
NCBI GI	g3602981
BLAST score	195
E value	6.0e-15
Match length	87
% identity	51
NCBI Description	(AF041468) acetohydroxyacid synthetase small subunit [Guillardia theta]

Seq. No.	200830
Seq. ID	LIB3048-008-Q1-L1-H12
Method	BLASTX
NCBI GI	g3426048
BLAST score	283
E value	1.0e-28
Match length	130
% identity	77

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No. 200831
Seq. ID LIB3048-008-Q1-L1-H2
Method BLASTX
NCBI GI g2780192
BLAST score 226
E value 7.0e-19
Match length 94
% identity 51
NCBI Description (AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No. 200832
Seq. ID LIB3048-008-Q1-L1-H3
Method BLASTX
NCBI GI g1619300
BLAST score 176
E value 9.0e-13
Match length 44
% identity 77
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 200833
Seq. ID LIB3048-008-Q1-L1-H4
Method BLASTX
NCBI GI g3152609
BLAST score 345
E value 9.0e-33
Match length 103
% identity 60
NCBI Description (AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No. 200834
Seq. ID LIB3048-008-Q1-L1-H6
Method BLASTX
NCBI GI g1644427
BLAST score 466
E value 9.0e-47
Match length 112
% identity 81
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 200835
Seq. ID LIB3048-008-Q1-L1-H7
Method BLASTX
NCBI GI g1777312
BLAST score 325
E value 3.0e-30
Match length 91
% identity 68
NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 200836
Seq. ID LIB3048-008-Q1-L1-H8

Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200837
Seq. ID	LIB3048-008-Q1-L1-H9
Method	BLASTX
NCBI GI	g4204265
BLAST score	230
E value	4.0e-19
Match length	121
% identity	45
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	200838
Seq. ID	LIB3048-009-Q1-L1-A12
Method	BLASTX
NCBI GI	g4558664
BLAST score	261
E value	9.0e-23
Match length	128
% identity	9
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200839
Seq. ID	LIB3048-009-Q1-L1-A4
Method	BLASTX
NCBI GI	g1066163
BLAST score	185
E value	6.0e-14
Match length	117
% identity	40
NCBI Description	(X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica napus]

Seq. No.	200840
Seq. ID	LIB3048-009-Q1-L1-B10
Method	BLASTX
NCBI GI	g3063699
BLAST score	329
E value	1.0e-30
Match length	129
% identity	50
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	200841
Seq. ID	LIB3048-009-Q1-L1-B11
Method	BLASTX
NCBI GI	g1729760
BLAST score	381
E value	5.0e-37
Match length	84
% identity	82

NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	200842
Seq. ID	LIB3048-009-Q1-L1-B2
Method	BLASTX
NCBI GI	g1729760
BLAST score	624
E value	2.0e-65
Match length	109
% identity	99
NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	200843
Seq. ID	LIB3048-009-Q1-L1-B3
Method	BLASTX
NCBI GI	g3123515
BLAST score	533
E value	1.0e-54
Match length	112
% identity	91
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	200844
Seq. ID	LIB3048-009-Q1-L1-B9
Method	BLASTN
NCBI GI	g3869068
BLAST score	78
E value	7.0e-36
Match length	248
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	200845
Seq. ID	LIB3048-009-Q1-L1-C10
Method	BLASTX
NCBI GI	g3935168
BLAST score	336
E value	2.0e-31
Match length	129
% identity	58
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	200846
Seq. ID	LIB3048-009-Q1-L1-C12
Method	BLASTX
NCBI GI	g3643611
BLAST score	471
E value	2.0e-47
Match length	124
% identity	73
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	200847
Seq. ID	LIB3048-009-Q1-L1-C7
Method	BLASTX
NCBI GI	g4100433

BLAST score	171
E value	9.0e-14
Match length	71
% identity	56
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	200848
Seq. ID	LIB3048-009-Q1-L1-D10
Method	BLASTX
NCBI GI	g3075394
BLAST score	476
E value	5.0e-48
Match length	123
% identity	78
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	200849
Seq. ID	LIB3048-009-Q1-L1-D12
Method	BLASTX
NCBI GI	g417073
BLAST score	465
E value	1.0e-46
Match length	124
% identity	73
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	200850
Seq. ID	LIB3048-009-Q1-L1-D4
Method	BLASTX
NCBI GI	g3033377
BLAST score	210
E value	7.0e-17
Match length	106
% identity	43
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	200851
Seq. ID	LIB3048-009-Q1-L1-D6
Method	BLASTX
NCBI GI	g2462746
BLAST score	365
E value	5.0e-35
Match length	93
% identity	75
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	200852
Seq. ID	LIB3048-009-Q1-L1-D9
Method	BLASTX
NCBI GI	g2760347

BLAST score	620
E value	7.0e-65
Match length	126
% identity	18
NCBI Description	(U84968) ubiquitin [Arabidopsis thaliana]

Seq. No.	200853
Seq. ID	LIB3048-009-Q1-L1-E10
Method	BLASTX
NCBI GI	g4490747
BLAST score	462
E value	2.0e-46
Match length	122
% identity	74
NCBI Description	(AL035708) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	200854
Seq. ID	LIB3048-009-Q1-L1-E2
Method	BLASTX
NCBI GI	g4539383
BLAST score	410
E value	3.0e-40
Match length	115
% identity	67
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	200855
Seq. ID	LIB3048-009-Q1-L1-E5
Method	BLASTX
NCBI GI	g584861
BLAST score	226
E value	1.0e-18
Match length	81
% identity	51
NCBI Description	CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4) >gi_480396_pir__S36806 cytochrome P450 71A2 - eggplant >gi_408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome P-450EG4 [Solanum melongena]

Seq. No.	200856
Seq. ID	LIB3048-009-Q1-L1-F1
Method	BLASTX
NCBI GI	g3482930
BLAST score	148
E value	1.0e-09
Match length	42
% identity	64
NCBI Description	(AC003970) Similar to pectinacetylesterase [Arabidopsis thaliana]

Seq. No.	200857
Seq. ID	LIB3048-009-Q1-L1-F10
Method	BLASTX
NCBI GI	g2443329
BLAST score	406

E value	9.0e-40
Match length	126
% identity	67
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	200858
Seq. ID	LIB3048-009-Q1-L1-F2
Method	BLASTX
NCBI GI	g100490
BLAST score	539
E value	2.0e-55
Match length	114
% identity	24
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	200859
Seq. ID	LIB3048-009-Q1-L1-F3
Method	BLASTX
NCBI GI	g3212865
BLAST score	492
E value	7.0e-50
Match length	120
% identity	82
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	200860
Seq. ID	LIB3048-009-Q1-L1-F4
Method	BLASTX
NCBI GI	g1086252
BLAST score	241
E value	2.0e-20
Match length	87
% identity	60
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	200861
Seq. ID	LIB3048-009-Q1-L1-F5
Method	BLASTX
NCBI GI	g3548802
BLAST score	244
E value	7.0e-21
Match length	111
% identity	46
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	200862
Seq. ID	LIB3048-009-Q1-L1-F9
Method	BLASTX
NCBI GI	g4218535
BLAST score	434

E value	5.0e-43
Match length	114
% identity	67
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	200863
Seq. ID	LIB3048-009-Q1-L1-G1
Method	BLASTX
NCBI GI	g1531758
BLAST score	605
E value	4.0e-63
Match length	119
% identity	91
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	200864
Seq. ID	LIB3048-009-Q1-L1-G12
Method	BLASTX
NCBI GI	g2832642
BLAST score	302
E value	1.0e-27
Match length	124
% identity	30
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	200865
Seq. ID	LIB3048-009-Q1-L1-G3
Method	BLASTX
NCBI GI	g3297827
BLAST score	394
E value	2.0e-38
Match length	95
% identity	82
NCBI Description	(AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	200866
Seq. ID	LIB3048-009-Q1-L1-G4
Method	BLASTX
NCBI GI	g2996096
BLAST score	602
E value	8.0e-63
Match length	117
% identity	97
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	200867
Seq. ID	LIB3048-009-Q1-L1-G5
Method	BLASTX
NCBI GI	g4335773
BLAST score	160
E value	7.0e-11
Match length	87
% identity	43
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	200868
Seq. ID	LIB3048-009-Q1-L1-G8
Method	BLASTX
NCBI GI	g1620009
BLAST score	182
E value	2.0e-13
Match length	150
% identity	29
NCBI Description	(D85184) flavonoid 3',5'-hydroxylase [Gentiana triflora]

Seq. No.	200869
Seq. ID	LIB3048-009-Q1-L1-H1
Method	BLASTX
NCBI GI	g133940
BLAST score	461
E value	3.0e-46
Match length	106
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	200870
Seq. ID	LIB3048-009-Q1-L1-H11
Method	BLASTX
NCBI GI	g3461814
BLAST score	435
E value	4.0e-43
Match length	128
% identity	66
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200871
Seq. ID	LIB3048-009-Q1-L1-H12
Method	BLASTX
NCBI GI	g1777386
BLAST score	181
E value	1.0e-13
Match length	88
% identity	40
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	200872
Seq. ID	LIB3048-009-Q1-L1-H4
Method	BLASTX
NCBI GI	g2632105
BLAST score	291
E value	3.0e-26
Match length	84
% identity	69
NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	200873

Seq. ID	LIB3048-010-Q1-L1-A12
Method	BLASTX
NCBI GI	g2827546
BLAST score	320
E value	1.0e-29
Match length	128
% identity	46
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	200874
Seq. ID	LIB3048-010-Q1-L1-A3
Method	BLASTX
NCBI GI	g2102691
BLAST score	283
E value	3.0e-25
Match length	102
% identity	58
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	200875
Seq. ID	LIB3048-010-Q1-L1-A4
Method	BLASTX
NCBI GI	g548488
BLAST score	361
E value	1.0e-34
Match length	102
% identity	62
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	200876
Seq. ID	LIB3048-010-Q1-L1-A5
Method	BLASTX
NCBI GI	g1364161
BLAST score	631
E value	5.0e-66
Match length	135
% identity	90
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	200877
Seq. ID	LIB3048-010-Q1-L1-A7
Method	BLASTX
NCBI GI	g2129622
BLAST score	556
E value	3.0e-57
Match length	130
% identity	80
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	200878
Seq. ID	LIB3048-010-Q1-L1-A8
Method	BLASTX
NCBI GI	g4432844
BLAST score	194

E value	8.0e-15
Match length	84
% identity	51
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	200879
Seq. ID	LIB3048-010-Q1-L1-A9
Method	BLASTX
NCBI GI	g3687223
BLAST score	143
E value	5.0e-09
Match length	110
% identity	33
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200880
Seq. ID	LIB3048-010-Q1-L1-B10
Method	BLASTX
NCBI GI	g3894383
BLAST score	199
E value	2.0e-15
Match length	126
% identity	3
NCBI Description	(AF053993) disease resistance protein [Lycopersicon esculentum]

Seq. No.	200881
Seq. ID	LIB3048-010-Q1-L1-B11
Method	BLASTX
NCBI GI	g2129825
BLAST score	490
E value	1.0e-49
Match length	116
% identity	81
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	200882
Seq. ID	LIB3048-010-Q1-L1-B12
Method	BLASTN
NCBI GI	g4165340
BLAST score	38
E value	6.0e-12
Match length	167
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	200883
Seq. ID	LIB3048-010-Q1-L1-B2
Method	BLASTX
NCBI GI	g1169782
BLAST score	304
E value	9.0e-28
Match length	74
% identity	76
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis

thaliana]

Seq. No. 200884
Seq. ID LIB3048-010-Q1-L1-B3
Method BLASTX
NCBI GI g3080401
BLAST score 388
E value 9.0e-38
Match length 106
% identity 71
NCBI Description (AL022603) putative protein [Arabidopsis thaliana] >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 200885
Seq. ID LIB3048-010-Q1-L1-B6
Method BLASTX
NCBI GI g3493172
BLAST score 347
E value 4.0e-33
Match length 79
% identity 87
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. No. 200886
Seq. ID LIB3048-010-Q1-L1-B9
Method BLASTX
NCBI GI g1364161
BLAST score 589
E value 3.0e-61
Match length 127
% identity 88
NCBI Description thiolase precursor, peroxisomal - ripe mango

Seq. No. 200887
Seq. ID LIB3048-010-Q1-L1-C1
Method BLASTX
NCBI GI g3287693
BLAST score 680
E value 8.0e-72
Match length 137
% identity 92
NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No. 200888
Seq. ID LIB3048-010-Q1-L1-C10
Method BLASTX
NCBI GI g4105798
BLAST score 482
E value 1.0e-48
Match length 101
% identity 75
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 200889

Seq. ID	LIB3048-010-Q1-L1-C11
Method	BLASTX
NCBI GI	g4262250
BLAST score	446
E value	2.0e-44
Match length	125
% identity	76
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	200890
Seq. ID	LIB3048-010-Q1-L1-C12
Method	BLASTX
NCBI GI	g4455223
BLAST score	431
E value	1.0e-42
Match length	127
% identity	25
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	200891
Seq. ID	LIB3048-010-Q1-L1-C2
Method	BLASTX
NCBI GI	g2129597
BLAST score	540
E value	2.0e-55
Match length	107
% identity	95
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	200892
Seq. ID	LIB3048-010-Q1-L1-C3
Method	BLASTX
NCBI GI	g2440035
BLAST score	392
E value	3.0e-38
Match length	112
% identity	54
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	200893
Seq. ID	LIB3048-010-Q1-L1-C4
Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200894
Seq. ID	LIB3048-010-Q1-L1-C6
Method	BLASTX
NCBI GI	g4432844

BLAST score 194
E value 8.0e-15
Match length 84
% identity 51
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 200895
Seq. ID LIB3048-010-Q1-L1-C7
Method BLASTX
NCBI GI g3549691
BLAST score 594
E value 9.0e-62
Match length 134
% identity 76
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No. 200896
Seq. ID LIB3048-010-Q1-L1-D10
Method BLASTX
NCBI GI g4539423
BLAST score 370
E value 2.0e-35
Match length 97
% identity 73
NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No. 200897
Seq. ID LIB3048-010-Q1-L1-D12
Method BLASTX
NCBI GI g542200
BLAST score 337
E value 1.0e-31
Match length 123
% identity 50
NCBI Description hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No. 200898
Seq. ID LIB3048-010-Q1-L1-D4
Method BLASTX
NCBI GI g1706323
BLAST score 361
E value 2.0e-34
Match length 122
% identity 61
NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No. 200899
Seq. ID LIB3048-010-Q1-L1-D5
Method BLASTN
NCBI GI g12262
BLAST score 37

E value	2.0e-11
Match length	127
% identity	67
NCBI Description	Spinach plastid genes infA, rps 11 and rpoA for initiation factor IF-1, ribosomal protein S11 and RNA polymerase alpha subunit

Seq. No.	200900
Seq. ID	LIB3048-010-Q1-L1-D6
Method	BLASTX
NCBI GI	g4539423
BLAST score	522
E value	2.0e-53
Match length	120
% identity	82
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	200901
Seq. ID	LIB3048-010-Q1-L1-D9
Method	BLASTX
NCBI GI	g3336903
BLAST score	401
E value	4.0e-39
Match length	113
% identity	69
NCBI Description	(Y10809) bZIP DNA-binding protein [Petroselinum crispum]

Seq. No.	200902
Seq. ID	LIB3048-010-Q1-L1-E10
Method	BLASTX
NCBI GI	g100487
BLAST score	143
E value	7.0e-09
Match length	63
% identity	52
NCBI Description	TNP1 protein - garden snapdragon >gi_16057_emb_CAA40554_ (X57297) TNP1 [Antirrhinum majus]

Seq. No.	200903
Seq. ID	LIB3048-010-Q1-L1-E11
Method	BLASTX
NCBI GI	g1488521
BLAST score	485
E value	5.0e-49
Match length	124
% identity	77
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	200904
Seq. ID	LIB3048-010-Q1-L1-E12
Method	BLASTX
NCBI GI	g2088651
BLAST score	297
E value	6.0e-27
Match length	111
% identity	51

NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	200905
Seq. ID	LIB3048-010-Q1-L1-E2
Method	BLASTX
NCBI GI	g4432860
BLAST score	277
E value	8.0e-25
Match length	98
% identity	15
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	200906
Seq. ID	LIB3048-010-Q1-L1-E5
Method	BLASTX
NCBI GI	g2529703
BLAST score	362
E value	7.0e-35
Match length	90
% identity	78
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	200907
Seq. ID	LIB3048-010-Q1-L1-F1
Method	BLASTX
NCBI GI	g2369714
BLAST score	445
E value	2.0e-44
Match length	125
% identity	72
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	200908
Seq. ID	LIB3048-010-Q1-L1-F10
Method	BLASTX
NCBI GI	g1572819
BLAST score	172
E value	2.0e-12
Match length	97
% identity	42
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	200909
Seq. ID	LIB3048-010-Q1-L1-F11
Method	BLASTX
NCBI GI	g2353183
BLAST score	155
E value	3.0e-10
Match length	125
% identity	31
NCBI Description	(AF015566) CtrA [Dictyostelium discoideum]

Seq. No.	200910

Seq. ID	LIB3048-010-Q1-L1-F2
Method	BLASTX
NCBI GI	g2230757
BLAST score	179
E value	1.0e-13
Match length	58
% identity	59
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	200911
Seq. ID	LIB3048-010-Q1-L1-F6
Method	BLASTX
NCBI GI	g3582328
BLAST score	284
E value	2.0e-25
Match length	109
% identity	50
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200912
Seq. ID	LIB3048-010-Q1-L1-F7
Method	BLASTX
NCBI GI	g1346387
BLAST score	603
E value	8.0e-63
Match length	131
% identity	89
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	200913
Seq. ID	LIB3048-010-Q1-L1-F8
Method	BLASTX
NCBI GI	g267146
BLAST score	295
E value	7.0e-27
Match length	70
% identity	74
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	200914
Seq. ID	LIB3048-010-Q1-L1-F9
Method	BLASTX
NCBI GI	g543867
BLAST score	372
E value	9.0e-36
Match length	101
% identity	80
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato

>gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	200915
Seq. ID	LIB3048-010-Q1-L1-G1
Method	BLASTX
NCBI GI	g136739
BLAST score	233
E value	7.0e-20
Match length	72
% identity	64
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	200916
Seq. ID	LIB3048-010-Q1-L1-G10
Method	BLASTX
NCBI GI	g1176658
BLAST score	154
E value	3.0e-10
Match length	60
% identity	52
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	200917
Seq. ID	LIB3048-010-Q1-L1-G11
Method	BLASTX
NCBI GI	g2623299
BLAST score	282
E value	3.0e-25
Match length	97
% identity	55
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200918
Seq. ID	LIB3048-010-Q1-L1-G2
Method	BLASTX
NCBI GI	g3184082
BLAST score	230
E value	3.0e-19
Match length	99
% identity	44
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	200919
Seq. ID	LIB3048-010-Q1-L1-G4
Method	BLASTX
NCBI GI	g2827546
BLAST score	172
E value	7.0e-13
Match length	61

% identity	57
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	200920
Seq. ID	LIB3048-010-Q1-L1-G7
Method	BLASTX
NCBI GI	g2959781
BLAST score	586
E value	7.0e-61
Match length	129
% identity	84
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	200921
Seq. ID	LIB3048-010-Q1-L1-G8
Method	BLASTX
NCBI GI	g2809326
BLAST score	294
E value	1.0e-26
Match length	79
% identity	73
NCBI Description	(U72663) uricase II [Phaseolus vulgaris]

Seq. No.	200922
Seq. ID	LIB3048-010-Q1-L1-G9
Method	BLASTX
NCBI GI	g4539423
BLAST score	555
E value	3.0e-57
Match length	123
% identity	87
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	200923
Seq. ID	LIB3048-010-Q1-L1-H1
Method	BLASTX
NCBI GI	g2129769
BLAST score	274
E value	1.0e-26
Match length	86
% identity	73
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	200924
Seq. ID	LIB3048-010-Q1-L1-H11
Method	BLASTX
NCBI GI	g1076386
BLAST score	643
E value	2.0e-67
Match length	129
% identity	93
NCBI Description	protein kinase ADK1 - Arabidopsis thaliana >gi_1216484 (U48779) dual specificity kinase 1 [Arabidopsis thaliana]

Seq. No.	200925
Seq. ID	LIB3048-010-Q1-L1-H3
Method	BLASTX
NCBI GI	g3775985
BLAST score	392
E value	4.0e-38
Match length	90
% identity	83
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	200926
Seq. ID	LIB3048-010-Q1-L1-H6
Method	BLASTX
NCBI GI	g4539315
BLAST score	276
E value	2.0e-24
Match length	145
% identity	46
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	200927
Seq. ID	LIB3048-011-Q1-L1-A10
Method	BLASTX
NCBI GI	g3142303
BLAST score	277
E value	1.0e-24
Match length	138
% identity	41
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	200928
Seq. ID	LIB3048-011-Q1-L1-A11
Method	BLASTX
NCBI GI	g529353
BLAST score	226
E value	1.0e-18
Match length	76
% identity	55
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	200929
Seq. ID	LIB3048-011-Q1-L1-A12
Method	BLASTX
NCBI GI	g2213534
BLAST score	236
E value	8.0e-20
Match length	71
% identity	66
NCBI Description	(X98739) DNA-binding PD1-like protein [Pisum sativum]

Seq. No.	200930
Seq. ID	LIB3048-011-Q1-L1-A2

Method	BLASTN
NCBI GI	g2829205
BLAST score	143
E value	1.0e-74
Match length	396
% identity	20
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	200931
Seq. ID	LIB3048-011-Q1-L1-A3
Method	BLASTX
NCBI GI	g116923
BLAST score	258
E value	2.0e-22
Match length	105
% identity	57
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	200932
Seq. ID	LIB3048-011-Q1-L1-A4
Method	BLASTX
NCBI GI	g4455340
BLAST score	325
E value	3.0e-32
Match length	103
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	200933
Seq. ID	LIB3048-011-Q1-L1-A5
Method	BLASTX
NCBI GI	g4539400
BLAST score	409
E value	3.0e-42
Match length	107
% identity	72
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	200934
Seq. ID	LIB3048-011-Q1-L1-A6
Method	BLASTX
NCBI GI	g2369714
BLAST score	614
E value	4.0e-64
Match length	124
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	200935
Seq. ID	LIB3048-011-Q1-L1-A8
Method	BLASTX
NCBI GI	g1255951
BLAST score	499

E value 8.0e-61
Match length 134
% identity 78
NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 200936
Seq. ID LIB3048-011-Q1-L1-A9
Method BLASTX
NCBI GI g1361983
BLAST score 486
E value 4.0e-49
Match length 136
% identity 73
NCBI Description ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 200937
Seq. ID LIB3048-011-Q1-L1-B10
Method BLASTX
NCBI GI g2369714
BLAST score 366
E value 2.0e-35
Match length 83
% identity 87
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 200938
Seq. ID LIB3048-011-Q1-L1-B11
Method BLASTX
NCBI GI g3152603
BLAST score 293
E value 2.0e-26
Match length 93
% identity 57
NCBI Description (AC004482) unknown protein [Arabidopsis thaliana]

Seq. No. 200939
Seq. ID LIB3048-011-Q1-L1-B2
Method BLASTX
NCBI GI g2146797
BLAST score 565
E value 2.0e-58
Match length 131
% identity 80
NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No. 200940
Seq. ID LIB3048-011-Q1-L1-B4
Method BLASTX
NCBI GI g3334138
BLAST score 435
E value 4.0e-43
Match length 93
% identity 84

NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	200941
Seq. ID	LIB3048-011-Q1-L1-B5
Method	BLASTX
NCBI GI	g3158376
BLAST score	215
E value	8.0e-18
Match length	59
% identity	71
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	200942
Seq. ID	LIB3048-011-Q1-L1-B8
Method	BLASTN
NCBI GI	g4388705
BLAST score	39
E value	2.0e-12
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	200943
Seq. ID	LIB3048-011-Q1-L1-B9
Method	BLASTX
NCBI GI	g3775985
BLAST score	418
E value	4.0e-41
Match length	96
% identity	83
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	200944
Seq. ID	LIB3048-011-Q1-L1-C1
Method	BLASTX
NCBI GI	g133940
BLAST score	492
E value	8.0e-50
Match length	114
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	200945
Seq. ID	LIB3048-011-Q1-L1-C10
Method	BLASTX
NCBI GI	g3204134
BLAST score	339
E value	2.0e-32
Match length	68
% identity	85
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	200946
Seq. ID	LIB3048-011-Q1-L1-C12
Method	BLASTX
NCBI GI	g167367
BLAST score	377
E value	1.0e-36
Match length	88
% identity	85
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	200947
Seq. ID	LIB3048-011-Q1-L1-C2
Method	BLASTX
NCBI GI	g480297
BLAST score	342
E value	2.0e-32
Match length	92
% identity	70
NCBI Description	glycoprotein EP1 - carrot >gi_349437 (L16983) N-glycosylation sites: (130..138), (244..252), (352..360), (734..742), (748..756), (865..873) [Daucus carota]

Seq. No.	200948
Seq. ID	LIB3048-011-Q1-L1-C5
Method	BLASTX
NCBI GI	g3924598
BLAST score	147
E value	2.0e-09
Match length	78
% identity	35
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	200949
Seq. ID	LIB3048-011-Q1-L1-C6
Method	BLASTX
NCBI GI	g2290683
BLAST score	258
E value	1.0e-22
Match length	60
% identity	78
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	200950
Seq. ID	LIB3048-011-Q1-L1-C8
Method	BLASTX
NCBI GI	g1495251
BLAST score	252
E value	7.0e-22
Match length	101
% identity	52
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	200951
Seq. ID	LIB3048-011-Q1-L1-C9
Method	BLASTX
NCBI GI	g4185136
BLAST score	472

E value	2.0e-47
Match length	136
% identity	63
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	200952
Seq. ID	LIB3048-011-Q1-L1-D10
Method	BLASTX
NCBI GI	g2956783
BLAST score	315
E value	5.0e-29
Match length	137
% identity	49
NCBI Description	(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq. No.	200953
Seq. ID	LIB3048-011-Q1-L1-D11
Method	BLASTX
NCBI GI	g4263792
BLAST score	431
E value	3.0e-43
Match length	116
% identity	78
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	200954
Seq. ID	LIB3048-011-Q1-L1-D2
Method	BLASTX
NCBI GI	g606942
BLAST score	180
E value	4.0e-13
Match length	79
% identity	54
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	200955
Seq. ID	LIB3048-011-Q1-L1-D5
Method	BLASTX
NCBI GI	g1709498
BLAST score	582
E value	2.0e-60
Match length	122
% identity	82
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	200956
Seq. ID	LIB3048-011-Q1-L1-D7
Method	BLASTX
NCBI GI	g2827715
BLAST score	429
E value	2.0e-42
Match length	110

% identity	10
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	200957
Seq. ID	LIB3048-011-Q1-L1-D8
Method	BLASTX
NCBI GI	g1723119
BLAST score	152
E value	4.0e-10
Match length	91
% identity	31
NCBI Description	HYPOTHETICAL PROTEIN KIAA0174 >gi_1136408_dbj_BAA11491_ (D79996) KIAA0174 [Homo sapiens]

Seq. No.	200958
Seq. ID	LIB3048-011-Q1-L1-E1
Method	BLASTX
NCBI GI	g421929
BLAST score	382
E value	4.0e-37
Match length	99
% identity	12
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	200959
Seq. ID	LIB3048-011-Q1-L1-E10
Method	BLASTX
NCBI GI	g3393062
BLAST score	307
E value	2.0e-28
Match length	83
% identity	61
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	200960
Seq. ID	LIB3048-011-Q1-L1-E11
Method	BLASTX
NCBI GI	g3158376
BLAST score	457
E value	1.0e-45
Match length	123
% identity	74
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	200961
Seq. ID	LIB3048-011-Q1-L1-E12
Method	BLASTX
NCBI GI	g3687235
BLAST score	296
E value	8.0e-27
Match length	103
% identity	61
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	200962
Seq. ID	LIB3048-011-Q1-L1-E2
Method	BLASTX
NCBI GI	g3402693
BLAST score	140
E value	1.0e-08
Match length	84
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	200963
Seq. ID	LIB3048-011-Q1-L1-E4
Method	BLASTX
NCBI GI	g1407705
BLAST score	551
E value	1.0e-56
Match length	127
% identity	82
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	200964
Seq. ID	LIB3048-011-Q1-L1-E6
Method	BLASTX
NCBI GI	g3419681
BLAST score	331
E value	6.0e-31
Match length	124
% identity	48
NCBI Description	(U37371) chaperonin [Candida albicans]

Seq. No.	200965
Seq. ID	LIB3048-011-Q1-L1-E7
Method	BLASTX
NCBI GI	g3204134
BLAST score	474
E value	9.0e-48
Match length	121
% identity	62
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	200966
Seq. ID	LIB3048-011-Q1-L1-E8
Method	BLASTX
NCBI GI	g4262174
BLAST score	420
E value	1.0e-41
Match length	103
% identity	71
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	200967
Seq. ID	LIB3048-011-Q1-L1-F11
Method	BLASTX
NCBI GI	g130582
BLAST score	249
E value	3.0e-21
Match length	130

% identity	38
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	200968
Seq. ID	LIB3048-011-Q1-L1-F3
Method	BLASTX
NCBI GI	g2462746
BLAST score	462
E value	3.0e-46
Match length	109
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	200969
Seq. ID	LIB3048-011-Q1-L1-F4
Method	BLASTN
NCBI GI	g1841463
BLAST score	38
E value	5.0e-12
Match length	62
% identity	90
NCBI Description	N.tabacum mRNA for LIM-domain protein

Seq. No.	200970
Seq. ID	LIB3048-011-Q1-L1-F6
Method	BLASTX
NCBI GI	g483057
BLAST score	174
E value	1.0e-12
Match length	68
% identity	49
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	200971
Seq. ID	LIB3048-011-Q1-L1-F7
Method	BLASTX
NCBI GI	g2465923
BLAST score	556
E value	3.0e-57
Match length	135
% identity	75
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	200972
Seq. ID	LIB3048-011-Q1-L1-F8
Method	BLASTX
NCBI GI	g2129921
BLAST score	150
E value	6.0e-10

Match length	43
% identity	70
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	200973
Seq. ID	LIB3048-011-Q1-L1-F9
Method	BLASTX
NCBI GI	g2398521
BLAST score	340
E value	6.0e-32
Match length	116
% identity	60
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	200974
Seq. ID	LIB3048-011-Q1-L1-G1
Method	BLASTX
NCBI GI	g3834309
BLAST score	203
E value	5.0e-16
Match length	63
% identity	56
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	200975
Seq. ID	LIB3048-011-Q1-L1-G10
Method	BLASTX
NCBI GI	g4539423
BLAST score	587
E value	6.0e-61
Match length	133
% identity	85
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	200976
Seq. ID	LIB3048-011-Q1-L1-G2
Method	BLASTX
NCBI GI	g3249105
BLAST score	145
E value	4.0e-09
Match length	72
% identity	54
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	200977
Seq. ID	LIB3048-011-Q1-L1-G5
Method	BLASTX
NCBI GI	g1169782
BLAST score	504
E value	8.0e-52
Match length	142

% identity	73
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	200978
Seq. ID	LIB3048-011-Q1-L1-G7
Method	BLASTX
NCBI GI	g1706918
BLAST score	315
E value	5.0e-29
Match length	126
% identity	48
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	200979
Seq. ID	LIB3048-011-Q1-L1-G8
Method	BLASTX
NCBI GI	g2597826
BLAST score	271
E value	7.0e-24
Match length	93
% identity	57
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	200980
Seq. ID	LIB3048-011-Q1-L1-G9
Method	BLASTX
NCBI GI	g3947733
BLAST score	283
E value	2.0e-25
Match length	113
% identity	51
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	200981
Seq. ID	LIB3048-011-Q1-L1-H10
Method	BLASTX
NCBI GI	g3935165
BLAST score	190
E value	2.0e-14
Match length	83
% identity	58
NCBI Description	(AC004557) F17L21.8 [Arabidopsis thaliana]

Seq. No.	200982
Seq. ID	LIB3048-011-Q1-L1-H12
Method	BLASTX
NCBI GI	g2506139
BLAST score	285
E value	2.0e-25
Match length	73
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	200983
Seq. ID	LIB3048-011-Q1-L1-H2
Method	BLASTX
NCBI GI	g1364161
BLAST score	568
E value	9.0e-59
Match length	122
% identity	89
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	200984
Seq. ID	LIB3048-011-Q1-L1-H3
Method	BLASTX
NCBI GI	g3608171
BLAST score	609
E value	2.0e-63
Match length	133
% identity	89
NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No.	200985
Seq. ID	LIB3048-011-Q1-L1-H7
Method	BLASTX
NCBI GI	g3183247
BLAST score	207
E value	1.0e-16
Match length	61
% identity	61
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB

Seq. No.	200986
Seq. ID	LIB3048-011-Q1-L1-H9
Method	BLASTX
NCBI GI	g4106061
BLAST score	209
E value	1.0e-16
Match length	61
% identity	64
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	200987
Seq. ID	LIB3048-012-Q1-L1-A1
Method	BLASTX
NCBI GI	g82131
BLAST score	434
E value	6.0e-43
Match length	133
% identity	67
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	200988
Seq. ID	LIB3048-012-Q1-L1-A10
Method	BLASTX
NCBI GI	g3775985
BLAST score	412
E value	2.0e-40
Match length	96
% identity	82
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	200989
Seq. ID	LIB3048-012-Q1-L1-A11
Method	BLASTX
NCBI GI	g2244841
BLAST score	156
E value	2.0e-10
Match length	40
% identity	65
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200990
Seq. ID	LIB3048-012-Q1-L1-A2
Method	BLASTX
NCBI GI	g3393062
BLAST score	411
E value	3.0e-40
Match length	140
% identity	54
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	200991
Seq. ID	LIB3048-012-Q1-L1-A4
Method	BLASTX
NCBI GI	g3687223
BLAST score	277
E value	6.0e-25
Match length	82
% identity	73
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	200992
Seq. ID	LIB3048-012-Q1-L1-A5
Method	BLASTX
NCBI GI	g2462746
BLAST score	536
E value	6.0e-55
Match length	124
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	200993
Seq. ID	LIB3048-012-Q1-L1-A9
Method	BLASTX
NCBI GI	g2811066
BLAST score	324

E value	4.0e-30
Match length	130
% identity	45
NCBI Description	PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN MULTIPLE ADVANCED CANCERS 1) >gi_1916330 (U92437) MMAC1 [Mus musculus]

Seq. No.	200994
Seq. ID	LIB3048-012-Q1-L1-B1
Method	BLASTN
NCBI GI	g4097011
BLAST score	41
E value	3.0e-14
Match length	89
% identity	87
NCBI Description	Cloning vector pRcCMV-luc luciferase gene, complete cds

Seq. No.	200995
Seq. ID	LIB3048-012-Q1-L1-B10
Method	BLASTX
NCBI GI	g3738257
BLAST score	216
E value	2.0e-17
Match length	50
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	200996
Seq. ID	LIB3048-012-Q1-L1-B11
Method	BLASTX
NCBI GI	g1245182
BLAST score	199
E value	1.0e-15
Match length	40
% identity	85
NCBI Description	(U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.	200997
Seq. ID	LIB3048-012-Q1-L1-B12
Method	BLASTX
NCBI GI	g2529703
BLAST score	327
E value	1.0e-30
Match length	114
% identity	60
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	200998
Seq. ID	LIB3048-012-Q1-L1-B2
Method	BLASTX
NCBI GI	g2996096
BLAST score	743
E value	3.0e-79
Match length	144
% identity	99

NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	200999
Seq. ID	LIB3048-012-Q1-L1-B3
Method	BLASTX
NCBI GI	g3924598
BLAST score	141
E value	1.0e-08
Match length	82
% identity	35
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	201000
Seq. ID	LIB3048-012-Q1-L1-B5
Method	BLASTX
NCBI GI	g2290683
BLAST score	223
E value	1.0e-18
Match length	52
% identity	77
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	201001
Seq. ID	LIB3048-012-Q1-L1-B6
Method	BLASTX
NCBI GI	g2570164
BLAST score	461
E value	4.0e-46
Match length	137
% identity	61
NCBI Description	(D45183) chitinase [Chenopodium amaranticolor]

Seq. No.	201002
Seq. ID	LIB3048-012-Q1-L1-B7
Method	BLASTX
NCBI GI	g483057
BLAST score	159
E value	9.0e-11
Match length	106
% identity	37
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	201003
Seq. ID	LIB3048-012-Q1-L1-C11
Method	BLASTX
NCBI GI	g3882211
BLAST score	363
E value	1.0e-34
Match length	133
% identity	55
NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]

Seq. No.	201004
Seq. ID	LIB3048-012-Q1-L1-C12

Method	BLASTX
NCBI GI	g3687235
BLAST score	175
E value	8.0e-16
Match length	110
% identity	57
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	201005
Seq. ID	LIB3048-012-Q1-L1-C2
Method	BLASTX
NCBI GI	g4510348
BLAST score	147
E value	2.0e-09
Match length	98
% identity	32
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	201006
Seq. ID	LIB3048-012-Q1-L1-C3
Method	BLASTX
NCBI GI	g167367
BLAST score	537
E value	4.0e-55
Match length	121
% identity	86
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	201007
Seq. ID	LIB3048-012-Q1-L1-C6
Method	BLASTX
NCBI GI	g3834323
BLAST score	254
E value	7.0e-22
Match length	145
% identity	39
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	201008
Seq. ID	LIB3048-012-Q1-L1-C7
Method	BLASTX
NCBI GI	g3123745
BLAST score	249
E value	3.0e-21
Match length	68
% identity	71
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	201009
Seq. ID	LIB3048-012-Q1-L1-C9
Method	BLASTX
NCBI GI	g4454464
BLAST score	300
E value	3.0e-27
Match length	121
% identity	51

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 201010
Seq. ID LIB3048-012-Q1-L1-D11
Method BLASTX
NCBI GI g3668089
BLAST score 182
E value 2.0e-13
Match length 89
% identity 42
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 201011
Seq. ID LIB3048-012-Q1-L1-D12
Method BLASTX
NCBI GI g3608412
BLAST score 411
E value 2.0e-40
Match length 129
% identity 60
NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No. 201012
Seq. ID LIB3048-012-Q1-L1-D4
Method BLASTX
NCBI GI g3790102
BLAST score 485
E value 6.0e-49
Match length 102
% identity 85
NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No. 201013
Seq. ID LIB3048-012-Q1-L1-D5
Method BLASTX
NCBI GI g2500378
BLAST score 437
E value 3.0e-43
Match length 94
% identity 84
NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 201014
Seq. ID LIB3048-012-Q1-L1-D6
Method BLASTX
NCBI GI g3894159
BLAST score 172
E value 3.0e-12
Match length 80
% identity 41
NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201015
Seq. ID LIB3048-012-Q1-L1-D7
Method BLASTX

NCBI GI	g3548802
BLAST score	372
E value	1.0e-35
Match length	142
% identity	50
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	201016
Seq. ID	LIB3048-012-Q1-L1-D8
Method	BLASTX
NCBI GI	g2894558
BLAST score	214
E value	3.0e-17
Match length	71
% identity	63
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	201017
Seq. ID	LIB3048-012-Q1-L1-D9
Method	BLASTX
NCBI GI	g1076511
BLAST score	544
E value	7.0e-56
Match length	134
% identity	80
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	201018
Seq. ID	LIB3048-012-Q1-L1-E1
Method	BLASTX
NCBI GI	g464365
BLAST score	190
E value	1.0e-29
Match length	103
% identity	69
NCBI Description	PEROXIDASE P7 >gi_66306_pir__OPNB7 peroxidase (EC 1.11.1.7) - turnip

Seq. No.	201019
Seq. ID	LIB3048-012-Q1-L1-E10
Method	BLASTX
NCBI GI	g1107526
BLAST score	536
E value	6.0e-55
Match length	131
% identity	79
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	201020
Seq. ID	LIB3048-012-Q1-L1-E11
Method	BLASTX
NCBI GI	g4508073
BLAST score	380

E value	1.0e-36
Match length	98
% identity	69
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	201021
Seq. ID	LIB3048-012-Q1-L1-E2
Method	BLASTX
NCBI GI	g1698548
BLAST score	672
E value	7.0e-71
Match length	148
% identity	83
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	201022
Seq. ID	LIB3048-012-Q1-L1-E5
Method	BLASTX
NCBI GI	g4185136
BLAST score	505
E value	3.0e-51
Match length	141
% identity	65
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	201023
Seq. ID	LIB3048-012-Q1-L1-E6
Method	BLASTX
NCBI GI	g417073
BLAST score	686
E value	2.0e-72
Match length	147
% identity	87
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	201024
Seq. ID	LIB3048-012-Q1-L1-E7
Method	BLASTX
NCBI GI	g2281093
BLAST score	729
E value	1.0e-77
Match length	146
% identity	53
NCBI Description	(AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No.	201025
Seq. ID	LIB3048-012-Q1-L1-E9
Method	BLASTN
NCBI GI	g2829205
BLAST score	145
E value	8.0e-76
Match length	382
% identity	21

NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	201026
Seq. ID	LIB3048-012-Q1-L1-F1
Method	BLASTX
NCBI GI	g3540180
BLAST score	351
E value	3.0e-33
Match length	144
% identity	56
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	201027
Seq. ID	LIB3048-012-Q1-L1-F11
Method	BLASTX
NCBI GI	g1708236
BLAST score	445
E value	3.0e-44
Match length	96
% identity	91
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	201028
Seq. ID	LIB3048-012-Q1-L1-F12
Method	BLASTX
NCBI GI	g1129145
BLAST score	647
E value	6.0e-68
Match length	140
% identity	89
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	201029
Seq. ID	LIB3048-012-Q1-L1-F2
Method	BLASTX
NCBI GI	g1364161
BLAST score	632
E value	3.0e-66
Match length	138
% identity	88
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	201030
Seq. ID	LIB3048-012-Q1-L1-F3
Method	BLASTN
NCBI GI	g3241927
BLAST score	44
E value	2.0e-15
Match length	214

% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	201031
Seq. ID	LIB3048-012-Q1-L1-F4
Method	BLASTX
NCBI GI	g2129597
BLAST score	361
E value	1.0e-34
Match length	72
% identity	96
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201032
Seq. ID	LIB3048-012-Q1-L1-F7
Method	BLASTX
NCBI GI	g4138647
BLAST score	207
E value	2.0e-20
Match length	95
% identity	60
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	201033
Seq. ID	LIB3048-012-Q1-L1-F8
Method	BLASTN
NCBI GI	g1777727
BLAST score	92
E value	3.0e-44
Match length	272
% identity	83
NCBI Description	Gossypium hirsutum 18S ribosomal RNA gene, partial sequence

Seq. No.	201034
Seq. ID	LIB3048-012-Q1-L1-G10
Method	BLASTX
NCBI GI	g4580531
BLAST score	247
E value	4.0e-21
Match length	125
% identity	47
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	201035
Seq. ID	LIB3048-012-Q1-L1-G11
Method	BLASTX
NCBI GI	g3860319
BLAST score	565
E value	2.0e-58
Match length	134
% identity	84
NCBI Description	(AJ012686) nucleolar protein [Cicer arietinum]

Seq. No.	201036
Seq. ID	LIB3048-012-Q1-L1-G2
Method	BLASTX
NCBI GI	g1657621
BLAST score	674
E value	4.0e-71
Match length	150
% identity	83
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	201037
Seq. ID	LIB3048-012-Q1-L1-G3
Method	BLASTX
NCBI GI	g4580531
BLAST score	222
E value	4.0e-18
Match length	115
% identity	46
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	201038
Seq. ID	LIB3048-012-Q1-L1-G4
Method	BLASTX
NCBI GI	g765203
BLAST score	317
E value	3.0e-29
Match length	93
% identity	67
NCBI Description	(S73865) linoleate:oxygen oxidoreductase, lipoxygenase, LOX {EC 1.13.11.12} [Solanum tuberosum, cv. Desiree, roots, Peptide, 857 aa] [Solanum tuberosum]

Seq. No.	201039
Seq. ID	LIB3048-012-Q1-L1-G5
Method	BLASTX
NCBI GI	g3608485
BLAST score	602
E value	1.0e-62
Match length	135
% identity	93
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No.	201040
Seq. ID	LIB3048-012-Q1-L1-G6
Method	BLASTX
NCBI GI	g2088648
BLAST score	152
E value	6.0e-10
Match length	110
% identity	36
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201041
Seq. ID	LIB3048-012-Q1-L1-G7
Method	BLASTX
NCBI GI	g3132696

BLAST score	602
E value	1.0e-62
Match length	137
% identity	84
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201042
Seq. ID	LIB3048-012-Q1-L1-G8
Method	BLASTX
NCBI GI	g4115371
BLAST score	349
E value	4.0e-33
Match length	110
% identity	64
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	201043
Seq. ID	LIB3048-012-Q1-L1-G9
Method	BLASTX
NCBI GI	g2911044
BLAST score	479
E value	3.0e-48
Match length	124
% identity	74
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201044
Seq. ID	LIB3048-012-Q1-L1-H1
Method	BLASTX
NCBI GI	g3132696
BLAST score	642
E value	2.0e-67
Match length	145
% identity	85
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201045
Seq. ID	LIB3048-012-Q1-L1-H10
Method	BLASTX
NCBI GI	g1407705
BLAST score	614
E value	4.0e-64
Match length	137
% identity	83
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	201046
Seq. ID	LIB3048-012-Q1-L1-H11
Method	BLASTX
NCBI GI	g2129597
BLAST score	554
E value	4.0e-57
Match length	109
% identity	95
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1

[Arabidopsis thaliana]

Seq. No.	201047
Seq. ID	LIB3048-012-Q1-L1-H2
Method	BLASTX
NCBI GI	g3641837
BLAST score	524
E value	2.0e-53
Match length	151
% identity	72
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	201048
Seq. ID	LIB3048-012-Q1-L1-H3
Method	BLASTX
NCBI GI	g3450842
BLAST score	497
E value	2.0e-50
Match length	135
% identity	70
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	201049
Seq. ID	LIB3048-012-Q1-L1-H4
Method	BLASTX
NCBI GI	g3450842
BLAST score	487
E value	4.0e-49
Match length	131
% identity	71
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	201050
Seq. ID	LIB3048-012-Q1-L1-H5
Method	BLASTX
NCBI GI	g3242720
BLAST score	374
E value	6.0e-36
Match length	139
% identity	49
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	201051
Seq. ID	LIB3048-012-Q1-L1-H7
Method	BLASTX
NCBI GI	g3461820
BLAST score	171
E value	4.0e-12
Match length	52
% identity	60
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 201052

Seq. ID	LIB3048-012-Q1-L1-H8
Method	BLASTX
NCBI GI	g1346180
BLAST score	386
E value	2.0e-37
Match length	86
% identity	85
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	201053
Seq. ID	LIB3048-013-Q1-L1-A1
Method	BLASTX
NCBI GI	g1617272
BLAST score	574
E value	2.0e-59
Match length	131
% identity	80
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	201054
Seq. ID	LIB3048-013-Q1-L1-A11
Method	BLASTX
NCBI GI	g3264771
BLAST score	205
E value	2.0e-16
Match length	94
% identity	44
NCBI Description	(AF071895) turgor-responsive-like protein [Prunus armeniaca]

Seq. No.	201055
Seq. ID	LIB3048-013-Q1-L1-A3
Method	BLASTX
NCBI GI	g2317906
BLAST score	566
E value	2.0e-58
Match length	112
% identity	96
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	201056
Seq. ID	LIB3048-013-Q1-L1-A8
Method	BLASTX
NCBI GI	g2245036
BLAST score	148
E value	2.0e-09
Match length	43
% identity	63
NCBI Description	(Z97342) triacylglycerol lipase homolog [Arabidopsis thaliana]

Seq. No.	201057
Seq. ID	LIB3048-013-Q1-L1-B1
Method	BLASTX
NCBI GI	g4580460

BLAST score	469
E value	3.0e-54
Match length	138
% identity	79
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	201058
Seq. ID	LIB3048-013-Q1-L1-B10
Method	BLASTX
NCBI GI	g3738257
BLAST score	535
E value	8.0e-55
Match length	115
% identity	90
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	201059
Seq. ID	LIB3048-013-Q1-L1-B12
Method	BLASTX
NCBI GI	g3063392
BLAST score	440
E value	1.0e-43
Match length	117
% identity	76
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	201060
Seq. ID	LIB3048-013-Q1-L1-B2
Method	BLASTX
NCBI GI	g4580460
BLAST score	155
E value	2.0e-16
Match length	86
% identity	54
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	201061
Seq. ID	LIB3048-013-Q1-L1-B6
Method	BLASTX
NCBI GI	g2506139
BLAST score	234
E value	1.0e-19
Match length	60
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	201062
Seq. ID	LIB3048-013-Q1-L1-B7
Method	BLASTX
NCBI GI	g4249382
BLAST score	187
E value	2.0e-14

Match length	83
% identity	51
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	201063
Seq. ID	LIB3048-013-Q1-L1-B8
Method	BLASTX
NCBI GI	g2827546
BLAST score	325
E value	3.0e-30
Match length	131
% identity	47
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	201064
Seq. ID	LIB3048-013-Q1-L1-B9
Method	BLASTX
NCBI GI	g4432860
BLAST score	173
E value	2.0e-12
Match length	81
% identity	20
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	201065
Seq. ID	LIB3048-013-Q1-L1-C10
Method	BLASTX
NCBI GI	g2739376
BLAST score	341
E value	4.0e-34
Match length	100
% identity	77
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	201066
Seq. ID	LIB3048-013-Q1-L1-C12
Method	BLASTX
NCBI GI	g4539423
BLAST score	584
E value	1.0e-60
Match length	132
% identity	86
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	201067
Seq. ID	LIB3048-013-Q1-L1-C2
Method	BLASTX
NCBI GI	g2129550
BLAST score	555
E value	3.0e-57
Match length	125
% identity	83

NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	201068
Seq. ID	LIB3048-013-Q1-L1-C3
Method	BLASTX
NCBI GI	g2462746
BLAST score	493
E value	7.0e-50
Match length	122
% identity	76
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	201069
Seq. ID	LIB3048-013-Q1-L1-C5
Method	BLASTX
NCBI GI	g1172995
BLAST score	258
E value	2.0e-22
Match length	102
% identity	55
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	201070
Seq. ID	LIB3048-013-Q1-L1-C6
Method	BLASTX
NCBI GI	g1617272
BLAST score	542
E value	1.0e-55
Match length	131
% identity	76
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	201071
Seq. ID	LIB3048-013-Q1-L1-C7
Method	BLASTX
NCBI GI	g544250
BLAST score	503
E value	5.0e-51
Match length	126
% identity	75
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	201072

Seq. ID	LIB3048-013-Q1-L1-C9
Method	BLASTX
NCBI GI	g3212859
BLAST score	581
E value	3.0e-60
Match length	134
% identity	46
NCBI Description	(AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201073
Seq. ID	LIB3048-013-Q1-L1-D1
Method	BLASTX
NCBI GI	g3044212
BLAST score	657
E value	4.0e-69
Match length	142
% identity	89
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	201074
Seq. ID	LIB3048-013-Q1-L1-D12
Method	BLASTX
NCBI GI	g3688181
BLAST score	286
E value	1.0e-25
Match length	94
% identity	66
NCBI Description	(AL031804) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	201075
Seq. ID	LIB3048-013-Q1-L1-D5
Method	BLASTX
NCBI GI	g4098129
BLAST score	543
E value	2.0e-58
Match length	123
% identity	84
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	201076
Seq. ID	LIB3048-013-Q1-L1-D6
Method	BLASTX
NCBI GI	g1142619
BLAST score	384
E value	4.0e-37
Match length	140
% identity	59
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	201077
Seq. ID	LIB3048-013-Q1-L1-D8
Method	BLASTX
NCBI GI	g4539423
BLAST score	597
E value	4.0e-62

Match length	136
% identity	85
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	201078
Seq. ID	LIB3048-013-Q1-L1-E10
Method	BLASTX
NCBI GI	g100487
BLAST score	143
E value	7.0e-09
Match length	63
% identity	52
NCBI Description	TNP1 protein - garden snapdragon >gi_16057_emb_CAA40554_ (X57297) TNP1 [Antirrhinum majus]

Seq. No.	201079
Seq. ID	LIB3048-013-Q1-L1-E12
Method	BLASTX
NCBI GI	g2281115
BLAST score	575
E value	2.0e-59
Match length	135
% identity	83
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201080
Seq. ID	LIB3048-013-Q1-L1-E2
Method	BLASTX
NCBI GI	g2137603
BLAST score	184
E value	1.0e-13
Match length	87
% identity	40
NCBI Description	nuclear receptor co-repressor N-CoR - mouse >gi_1022718 (U35312) nuclear receptor co-repressor [Mus musculus] >gi_1583865_prf__2121436A thyroid hormone receptor co-repressor [Mus musculus]

Seq. No.	201081
Seq. ID	LIB3048-013-Q1-L1-E4
Method	BLASTX
NCBI GI	g1709498
BLAST score	419
E value	2.0e-41
Match length	98
% identity	79
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201082
Seq. ID	LIB3048-013-Q1-L1-E5
Method	BLASTX
NCBI GI	g2739381

BLAST score	321
E value	1.0e-29
Match length	114
% identity	59
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	201083
Seq. ID	LIB3048-013-Q1-L1-E6
Method	BLASTX
NCBI GI	g2541876
BLAST score	293
E value	2.0e-26
Match length	120
% identity	49
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	201084
Seq. ID	LIB3048-013-Q1-L1-E7
Method	BLASTX
NCBI GI	g4100433
BLAST score	423
E value	1.0e-41
Match length	120
% identity	69
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	201085
Seq. ID	LIB3048-013-Q1-L1-E8
Method	BLASTX
NCBI GI	g479386
BLAST score	607
E value	3.0e-63
Match length	128
% identity	93
NCBI Description	isocitrate dehydrogenase - soybean

Seq. No.	201086
Seq. ID	LIB3048-013-Q1-L1-E9
Method	BLASTX
NCBI GI	g1808656
BLAST score	601
E value	1.0e-62
Match length	135
% identity	85
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	201087
Seq. ID	LIB3048-013-Q1-L1-F10
Method	BLASTX
NCBI GI	g2398521
BLAST score	341
E value	4.0e-32
Match length	108
% identity	63
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	201088
Seq. ID	LIB3048-013-Q1-L1-F2
Method	BLASTX
NCBI GI	g1076511
BLAST score	569
E value	8.0e-59
Match length	141
% identity	79
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	201089
Seq. ID	LIB3048-013-Q1-L1-F3
Method	BLASTX
NCBI GI	g4309698
BLAST score	548
E value	2.0e-56
Match length	125
% identity	89
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	201090
Seq. ID	LIB3048-013-Q1-L1-F5
Method	BLASTX
NCBI GI	g480450
BLAST score	658
E value	3.0e-69
Match length	141
% identity	91
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	201091
Seq. ID	LIB3048-013-Q1-L1-F6
Method	BLASTX
NCBI GI	g2494113
BLAST score	673
E value	5.0e-71
Match length	140
% identity	84
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	201092
Seq. ID	LIB3048-013-Q1-L1-F7
Method	BLASTX
NCBI GI	g2499946
BLAST score	616
E value	3.0e-64
Match length	131
% identity	89
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	201093
Seq. ID	LIB3048-013-Q1-L1-G1
Method	BLASTX
NCBI GI	g4567267
BLAST score	177
E value	8.0e-13
Match length	38
% identity	45
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	201094
Seq. ID	LIB3048-013-Q1-L1-G10
Method	BLASTX
NCBI GI	g3775985
BLAST score	444
E value	4.0e-44
Match length	102
% identity	84
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	201095
Seq. ID	LIB3048-013-Q1-L1-G12
Method	BLASTX
NCBI GI	g3860319
BLAST score	247
E value	3.0e-21
Match length	102
% identity	55
NCBI Description	(AJ012686) nucleolar protein [Cicer arietinum]

Seq. No.	201096
Seq. ID	LIB3048-013-Q1-L1-G3
Method	BLASTX
NCBI GI	g4539399
BLAST score	365
E value	7.0e-35
Match length	75
% identity	96
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	201097
Seq. ID	LIB3048-013-Q1-L1-G5
Method	BLASTX
NCBI GI	g3582021
BLAST score	169
E value	6.0e-12
Match length	116
% identity	34
NCBI Description	(Y09423) cytochrome P450 [Nepeta racemosa]

Seq. No.	201098
Seq. ID	LIB3048-013-Q1-L1-G6

Method	BLASTX
NCBI GI	g3461833
BLAST score	699
E value	5.0e-74
Match length	140
% identity	86
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]

Seq. No.	201099
Seq. ID	LIB3048-013-Q1-L1-G7
Method	BLASTX
NCBI GI	g4455180
BLAST score	377
E value	3.0e-36
Match length	127
% identity	67
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	201100
Seq. ID	LIB3048-013-Q1-L1-H1
Method	BLASTX
NCBI GI	g2827548
BLAST score	230
E value	2.0e-19
Match length	94
% identity	49
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201101
Seq. ID	LIB3048-013-Q1-L1-H11
Method	BLASTX
NCBI GI	g3775985
BLAST score	368
E value	3.0e-35
Match length	97
% identity	76
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	201102
Seq. ID	LIB3048-013-Q1-L1-H3
Method	BLASTX
NCBI GI	g3759184
BLAST score	258
E value	2.0e-22
Match length	143
% identity	43
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	201103
Seq. ID	LIB3048-013-Q1-L1-H5
Method	BLASTX
NCBI GI	g2827555
BLAST score	418
E value	4.0e-41
Match length	140
% identity	64

NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	201104
Seq. ID	LIB3048-013-Q1-L1-H6
Method	BLASTX
NCBI GI	g2827555
BLAST score	384
E value	4.0e-37
Match length	137
% identity	61
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	201105
Seq. ID	LIB3048-013-Q1-L1-H7
Method	BLASTX
NCBI GI	g3785974
BLAST score	248
E value	3.0e-21
Match length	102
% identity	51
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	201106
Seq. ID	LIB3048-013-Q1-L1-H8
Method	BLASTX
NCBI GI	g4455155
BLAST score	340
E value	5.0e-32
Match length	69
% identity	90
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	201107
Seq. ID	LIB3048-013-Q1-L1-H9
Method	BLASTX
NCBI GI	g1407705
BLAST score	365
E value	5.0e-35
Match length	111
% identity	60
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	201108
Seq. ID	LIB3048-014-Q1-L1-A11
Method	BLASTX
NCBI GI	g1684857
BLAST score	663
E value	8.0e-70
Match length	139
% identity	39
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	201109
Seq. ID	LIB3048-014-Q1-L1-A12

Method	BLASTX
NCBI GI	g3132696
BLAST score	463
E value	2.0e-46
Match length	123
% identity	75
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201110
Seq. ID	LIB3048-014-Q1-L1-A4
Method	BLASTX
NCBI GI	g2708750
BLAST score	236
E value	5.0e-20
Match length	96
% identity	54
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	201111
Seq. ID	LIB3048-014-Q1-L1-A7
Method	BLASTX
NCBI GI	g2660664
BLAST score	243
E value	7.0e-21
Match length	78
% identity	63
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	201112
Seq. ID	LIB3048-014-Q1-L1-A8
Method	BLASTX
NCBI GI	g3287834
BLAST score	239
E value	2.0e-20
Match length	70
% identity	70
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE SYNTHASE) >gi_2147016_pir__S68366 (+)-delta-cadinene synthase isozyme XC14 - Gossypium arboreum >gi_1045314 (U23205) (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]

Seq. No.	201113
Seq. ID	LIB3048-014-Q1-L1-A9
Method	BLASTX
NCBI GI	g4519507
BLAST score	239
E value	4.0e-20
Match length	117
% identity	45
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No.	201114
Seq. ID	LIB3048-014-Q1-L1-B1
Method	BLASTX

NCBI GI g2911052
BLAST score 344
E value 1.0e-32
Match length 97
% identity 71
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 201115
Seq. ID LIB3048-014-Q1-L1-B11
Method BLASTX
NCBI GI g3492803
BLAST score 259
E value 2.0e-22
Match length 124
% identity 47
NCBI Description (AJ002479) ENBP1 [Medicago truncatula]

Seq. No. 201116
Seq. ID LIB3048-014-Q1-L1-B12
Method BLASTX
NCBI GI g2245060
BLAST score 226
E value 3.0e-19
Match length 66
% identity 64
NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 201117
Seq. ID LIB3048-014-Q1-L1-B2
Method BLASTX
NCBI GI g100287
BLAST score 240
E value 2.0e-20
Match length 64
% identity 73
NCBI Description glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) - tobacco

Seq. No. 201118
Seq. ID LIB3048-014-Q1-L1-B6
Method BLASTX
NCBI GI g4455365
BLAST score 264
E value 5.0e-23
Match length 57
% identity 79
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 201119
Seq. ID LIB3048-014-Q1-L1-C10
Method BLASTX
NCBI GI g4325324
BLAST score 608
E value 2.0e-63
Match length 133
% identity 86
NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	201120
Seq. ID	LIB3048-014-Q1-L1-C11
Method	BLASTX
NCBI GI	g2996096
BLAST score	708
E value	4.0e-75
Match length	136
% identity	99
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	201121
Seq. ID	LIB3048-014-Q1-L1-C2
Method	BLASTX
NCBI GI	g3080400
BLAST score	275
E value	9.0e-25
Match length	70
% identity	76
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	201122
Seq. ID	LIB3048-014-Q1-L1-C8
Method	BLASTX
NCBI GI	g4558664
BLAST score	284
E value	2.0e-25
Match length	144
% identity	11
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201123
Seq. ID	LIB3048-014-Q1-L1-D11
Method	BLASTX
NCBI GI	g3641837
BLAST score	478
E value	3.0e-48
Match length	137
% identity	72
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	201124
Seq. ID	LIB3048-014-Q1-L1-D6
Method	BLASTX
NCBI GI	g2367431
BLAST score	154
E value	2.0e-10
Match length	68
% identity	43
NCBI Description	(AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No.	201125
Seq. ID	LIB3048-014-Q1-L1-D8

Method	BLASTN
NCBI GI	g499359
BLAST score	53
E value	1.0e-21
Match length	61
% identity	97
NCBI Description	Drimys winteri 18S ribosomal RNA (18S rRNA), ca. bp 911 to 1124 in mature rRNA

Seq. No.	201126
Seq. ID	LIB3048-014-Q1-L1-D9
Method	BLASTX
NCBI GI	g132944
BLAST score	624
E value	3.0e-65
Match length	124
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	201127
Seq. ID	LIB3048-014-Q1-L1-E1
Method	BLASTX
NCBI GI	g1777386
BLAST score	165
E value	5.0e-12
Match length	63
% identity	51
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	201128
Seq. ID	LIB3048-014-Q1-L1-E7
Method	BLASTX
NCBI GI	g1762148
BLAST score	276
E value	1.0e-24
Match length	71
% identity	79
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]

Seq. No.	201129
Seq. ID	LIB3048-014-Q1-L1-E8
Method	BLASTX
NCBI GI	g2911052
BLAST score	206
E value	8.0e-17
Match length	56
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201130
Seq. ID	LIB3048-014-Q1-L1-E9
Method	BLASTX
NCBI GI	g3024756
BLAST score	230
E value	5.0e-19

Match length	136
% identity	35
NCBI Description	TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi_1926403_emb_CAA71604_ (Y10582) type II DNA topoisomerase subunit B [Sulfolobus shibatae]

Seq. No.	201131
Seq. ID	LIB3048-014-Q1-L1-F12
Method	BLASTX
NCBI GI	g4239845
BLAST score	153
E value	4.0e-10
Match length	43
% identity	70
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	201132
Seq. ID	LIB3048-014-Q1-L1-F5
Method	BLASTX
NCBI GI	g1143322
BLAST score	626
E value	2.0e-65
Match length	141
% identity	81
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	201133
Seq. ID	LIB3048-014-Q1-L1-F7
Method	BLASTN
NCBI GI	g3869068
BLAST score	45
E value	1.0e-16
Match length	137
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	201134
Seq. ID	LIB3048-014-Q1-L1-F9
Method	BLASTX
NCBI GI	g2129597
BLAST score	554
E value	4.0e-57
Match length	109
% identity	95
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201135
Seq. ID	LIB3048-014-Q1-L1-G11
Method	BLASTX
NCBI GI	g2462762
BLAST score	444
E value	4.0e-44
Match length	112

% identity	73
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	201136
Seq. ID	LIB3048-014-Q1-L1-G12
Method	BLASTX
NCBI GI	g1710838
BLAST score	309
E value	2.0e-28
Match length	117
% identity	57
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	201137
Seq. ID	LIB3048-014-Q1-L1-G2
Method	BLASTX
NCBI GI	g1944216
BLAST score	381
E value	5.0e-37
Match length	82
% identity	87
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	201138
Seq. ID	LIB3048-014-Q1-L1-G7
Method	BLASTX
NCBI GI	g2739279
BLAST score	355
E value	1.0e-33
Match length	126
% identity	57
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	201139
Seq. ID	LIB3048-014-Q1-L1-G9
Method	BLASTX
NCBI GI	g2924781
BLAST score	432
E value	9.0e-43
Match length	137
% identity	62
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	201140
Seq. ID	LIB3048-014-Q1-L1-H1
Method	BLASTX
NCBI GI	g119354
BLAST score	289
E value	3.0e-26
Match length	73
% identity	82

NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]
Seq. No.	201141
Seq. ID	LIB3048-014-Q1-L1-H12
Method	BLASTX
NCBI GI	g2462826
BLAST score	356
E value	6.0e-34
Match length	123
% identity	54
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]
Seq. No.	201142
Seq. ID	LIB3048-014-Q1-L1-H5
Method	BLASTX
NCBI GI	g1256509
BLAST score	311
E value	8.0e-29
Match length	71
% identity	77
NCBI Description	(X92943) pectate lyase [Musa acuminata]
Seq. No.	201143
Seq. ID	LIB3048-014-Q1-L1-H9
Method	BLASTX
NCBI GI	g1009232
BLAST score	204
E value	5.0e-16
Match length	73
% identity	60
NCBI Description	(L38828) EF-1-alpha-related GTP-binding protein [Nicotiana tabacum]
Seq. No.	201144
Seq. ID	LIB3048-015-Q1-L1-A10
Method	BLASTN
NCBI GI	g2829205
BLAST score	116
E value	2.0e-58
Match length	399
% identity	25
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds
Seq. No.	201145
Seq. ID	LIB3048-015-Q1-L1-A11
Method	BLASTX
NCBI GI	g2342724
BLAST score	256
E value	4.0e-22
Match length	103
% identity	75
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	201146
Seq. ID	LIB3048-015-Q1-L1-A12
Method	BLASTX
NCBI GI	g2492490
BLAST score	231
E value	2.0e-24
Match length	94
% identity	70
NCBI Description	14-3-3-LIKE PROTEIN >gi_913214_bbs_163396 (S76737) T14-3-3=ADP ribosyltransferase activator [Nicotiana tabacum=tobacco, var. Wisconsin, S-25 cells, Peptide, 251 aa] [Nicotiana tabacum]

Seq. No.	201147
Seq. ID	LIB3048-015-Q1-L1-A2
Method	BLASTX
NCBI GI	g4544387
BLAST score	403
E value	2.0e-39
Match length	103
% identity	73
NCBI Description	(AC007047) putative purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	201148
Seq. ID	LIB3048-015-Q1-L1-A7
Method	BLASTX
NCBI GI	g3122288
BLAST score	536
E value	4.0e-55
Match length	116
% identity	51
NCBI Description	IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA) >gi_1568635 (U69533) AtKAP alpha [Arabidopsis thaliana]

Seq. No.	201149
Seq. ID	LIB3048-015-Q1-L1-A8
Method	BLASTX
NCBI GI	g1709498
BLAST score	455
E value	2.0e-45
Match length	104
% identity	80
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201150
Seq. ID	LIB3048-015-Q1-L1-A9
Method	BLASTX
NCBI GI	g4490732
BLAST score	154
E value	3.0e-10
Match length	59

% identity	56
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	201151
Seq. ID	LIB3048-015-Q1-L1-B1
Method	BLASTX
NCBI GI	g3123515
BLAST score	499
E value	1.0e-50
Match length	106
% identity	90
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	201152
Seq. ID	LIB3048-015-Q1-L1-B11
Method	BLASTX
NCBI GI	g4336426
BLAST score	406
E value	9.0e-40
Match length	129
% identity	62
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	201153
Seq. ID	LIB3048-015-Q1-L1-B12
Method	BLASTX
NCBI GI	g4539400
BLAST score	469
E value	4.0e-47
Match length	127
% identity	71
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	201154
Seq. ID	LIB3048-015-Q1-L1-B2
Method	BLASTX
NCBI GI	g1403522
BLAST score	273
E value	2.0e-24
Match length	82
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	201155
Seq. ID	LIB3048-015-Q1-L1-B3
Method	BLASTX
NCBI GI	g2351380
BLAST score	196
E value	2.0e-15
Match length	85
% identity	45
NCBI Description	(U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN

Seq. No.	201156

Seq. ID	LIB3048-015-Q1-L1-B5
Method	BLASTX
NCBI GI	g2130051
BLAST score	459
E value	4.0e-46
Match length	97
% identity	81
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	201157
Seq. ID	LIB3048-015-Q1-L1-B7
Method	BLASTX
NCBI GI	g3402693
BLAST score	154
E value	3.0e-10
Match length	88
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	201158
Seq. ID	LIB3048-015-Q1-L1-C10
Method	BLASTX
NCBI GI	g2499945
BLAST score	506
E value	2.0e-51
Match length	127
% identity	76
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No.	201159
Seq. ID	LIB3048-015-Q1-L1-C11
Method	BLASTX
NCBI GI	g119640
BLAST score	293
E value	2.0e-26
Match length	107
% identity	51
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir__S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	201160
Seq. ID	LIB3048-015-Q1-L1-C12
Method	BLASTX
NCBI GI	g603473
BLAST score	170
E value	1.0e-12

Match length	41
% identity	78
NCBI Description	(D28582) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	201161
Seq. ID	LIB3048-015-Q1-L1-C2
Method	BLASTX
NCBI GI	g3077640
BLAST score	283
E value	2.0e-25
Match length	105
% identity	56
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No.	201162
Seq. ID	LIB3048-015-Q1-L1-C3
Method	BLASTX
NCBI GI	g82131
BLAST score	309
E value	2.0e-28
Match length	93
% identity	67
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	201163
Seq. ID	LIB3048-015-Q1-L1-C4
Method	BLASTX
NCBI GI	g1076678
BLAST score	310
E value	5.0e-29
Match length	68
% identity	93
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	201164
Seq. ID	LIB3048-015-Q1-L1-C8
Method	BLASTX
NCBI GI	g2444178
BLAST score	476
E value	6.0e-48
Match length	135
% identity	74
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	201165
Seq. ID	LIB3048-015-Q1-L1-C9
Method	BLASTX
NCBI GI	g627468
BLAST score	268
E value	1.0e-23
Match length	120
% identity	49
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	201166
Seq. ID	LIB3048-015-Q1-L1-D1
Method	BLASTX
NCBI GI	g2642158
BLAST score	523
E value	1.0e-53
Match length	113
% identity	81
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201167
Seq. ID	LIB3048-015-Q1-L1-D11
Method	BLASTX
NCBI GI	g627468
BLAST score	250
E value	2.0e-21
Match length	124
% identity	47
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	201168
Seq. ID	LIB3048-015-Q1-L1-D2
Method	BLASTX
NCBI GI	g3075392
BLAST score	502
E value	5.0e-51
Match length	122
% identity	76
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	201169
Seq. ID	LIB3048-015-Q1-L1-D3
Method	BLASTX
NCBI GI	g902584
BLAST score	419
E value	2.0e-41
Match length	96
% identity	13
NCBI Description	(U29159) polyubiquitin containing 7 ubiquitin monomers [Zea mays]

Seq. No.	201170
Seq. ID	LIB3048-015-Q1-L1-D4
Method	BLASTX
NCBI GI	g1729760
BLAST score	528
E value	5.0e-54
Match length	100
% identity	97
NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	201171
Seq. ID	LIB3048-015-Q1-L1-D5
Method	BLASTX

NCBI GI	g2275204
BLAST score	329
E value	8.0e-31
Match length	82
% identity	73
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	201172
Seq. ID	LIB3048-015-Q1-L1-D6
Method	BLASTX
NCBI GI	g167367
BLAST score	746
E value	1.0e-79
Match length	143
% identity	97
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	201173
Seq. ID	LIB3048-015-Q1-L1-D7
Method	BLASTX
NCBI GI	g4105798
BLAST score	352
E value	9.0e-34
Match length	85
% identity	65
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	201174
Seq. ID	LIB3048-015-Q1-L1-E1
Method	BLASTX
NCBI GI	g2983447
BLAST score	141
E value	8.0e-09
Match length	102
% identity	40
NCBI Description	(AE000714) large subunit of isopropylmalate isomerase [Aquifex aeolicus]

Seq. No.	201175
Seq. ID	LIB3048-015-Q1-L1-E10
Method	BLASTX
NCBI GI	g2632254
BLAST score	405
E value	1.0e-39
Match length	117
% identity	66
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	201176
Seq. ID	LIB3048-015-Q1-L1-E11
Method	BLASTX
NCBI GI	g1200205
BLAST score	230
E value	4.0e-19
Match length	94
% identity	56

NCBI Description	(X95753) DAG [Antirrhinum majus]
Seq. No.	201177
Seq. ID	LIB3048-015-Q1-L1-E3
Method	BLASTX
NCBI GI	g2062169
BLAST score	448
E value	8.0e-45
Match length	100
% identity	48
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]
Seq. No.	201178
Seq. ID	LIB3048-015-Q1-L1-E6
Method	BLASTX
NCBI GI	g2829918
BLAST score	410
E value	3.0e-49
Match length	144
% identity	73
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]
Seq. No.	201179
Seq. ID	LIB3048-015-Q1-L1-E8
Method	BLASTX
NCBI GI	g2252868
BLAST score	200
E value	9.0e-16
Match length	95
% identity	49
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]
Seq. No.	201180
Seq. ID	LIB3048-015-Q1-L1-E9
Method	BLASTX
NCBI GI	g1076515
BLAST score	354
E value	1.0e-33
Match length	114
% identity	60
NCBI Description	pectinesterase precursor - kidney bean >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus vulgaris]
Seq. No.	201181
Seq. ID	LIB3048-015-Q1-L1-F10
Method	BLASTX
NCBI GI	g4539296
BLAST score	190
E value	2.0e-14
Match length	95
% identity	42
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]

Seq. No.	201182
Seq. ID	LIB3048-015-Q1-L1-F12
Method	BLASTX
NCBI GI	g1871182
BLAST score	173
E value	1.0e-24
Match length	105
% identity	63
NCBI Description	(U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No.	201183
Seq. ID	LIB3048-015-Q1-L1-F2
Method	BLASTX
NCBI GI	g400972
BLAST score	201
E value	6.0e-18
Match length	107
% identity	50
NCBI Description	RETICULINE OXIDASE PRECURSOR (BERBERINE-BRIDGE-FORMING ENZYME) (BBE) (TETRAHYDROPROTOBERBERINE SYNTHASE) >gi_99506_pir__A41533 reticuline oxidase (EC 1.5.3.9) precursor - California poppy >gi_239110_bbs_65555 (S65550) (S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming), berberine bridge enzyme {EC 1.5.3.9} [Eschscholtzia californica, Peptide, 538 aa] [Eschscholzia californica] >gi_2897944 (AF005655) berberine bridge enzyme [Eschscholzia californica]

Seq. No.	201184
Seq. ID	LIB3048-015-Q1-L1-F4
Method	BLASTX
NCBI GI	g417745
BLAST score	464
E value	9.0e-47
Match length	96
% identity	93
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No.	201185
Seq. ID	LIB3048-015-Q1-L1-F5
Method	BLASTX
NCBI GI	g282994
BLAST score	380
E value	6.0e-37
Match length	86
% identity	79
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	201186
Seq. ID	LIB3048-015-Q1-L1-F7
Method	BLASTX
NCBI GI	g3559805
BLAST score	584
E value	1.0e-60

Match length	132
% identity	78
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	201187
Seq. ID	LIB3048-015-Q1-L1-F8
Method	BLASTX
NCBI GI	g2264373
BLAST score	156
E value	2.0e-10
Match length	62
% identity	48
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Seq. No.	201188
Seq. ID	LIB3048-015-Q1-L1-F9
Method	BLASTX
NCBI GI	g4262234
BLAST score	289
E value	5.0e-26
Match length	128
% identity	50
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	201189
Seq. ID	LIB3048-015-Q1-L1-G11
Method	BLASTX
NCBI GI	g476936
BLAST score	334
E value	3.0e-31
Match length	72
% identity	85
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - mung bean

Seq. No.	201190
Seq. ID	LIB3048-015-Q1-L1-G12
Method	BLASTX
NCBI GI	g4406759
BLAST score	169
E value	6.0e-12
Match length	73
% identity	48
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201191
Seq. ID	LIB3048-015-Q1-L1-G5
Method	BLASTX
NCBI GI	g3204134
BLAST score	436
E value	2.0e-43
Match length	109
% identity	73
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	201192

Seq. ID	LIB3048-015-Q1-L1-G6
Method	BLASTX
NCBI GI	g2288988
BLAST score	141
E value	1.0e-08
Match length	129
% identity	32
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201193
Seq. ID	LIB3048-015-Q1-L1-G7
Method	BLASTX
NCBI GI	g1085595
BLAST score	372
E value	6.0e-36
Match length	87
% identity	89
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase - Prunus persica >gi_452671_emb_CAA54449_ (X77232) 1-aminocyclopropane-1-carboxylate oxidase [Prunus persica] >gi_3510500 (AF026793) 1-aminocyclopropane-1-carboxylate oxidase; ACC oxidase [Prunus armeniaca]

Seq. No.	201194
Seq. ID	LIB3048-015-Q1-L1-H12
Method	BLASTX
NCBI GI	g4098129
BLAST score	607
E value	3.0e-63
Match length	128
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	201195
Seq. ID	LIB3048-015-Q1-L1-H3
Method	BLASTX
NCBI GI	g3413511
BLAST score	493
E value	4.0e-50
Match length	104
% identity	88
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	201196
Seq. ID	LIB3048-015-Q1-L1-H5
Method	BLASTX
NCBI GI	g4558659
BLAST score	199
E value	8.0e-17
Match length	102
% identity	49
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	201197
Seq. ID	LIB3048-015-Q1-L1-H6
Method	BLASTX

NCBI GI g4107343
BLAST score 224
E value 2.0e-21
Match length 105
% identity 54
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq. No. 201198
Seq. ID LIB3048-016-Q1-L1-A11
Method BLASTX
NCBI GI g464775
BLAST score 556
E value 2.0e-57
Match length 128
% identity 84
NCBI Description SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No. 201199
Seq. ID LIB3048-016-Q1-L1-A12
Method BLASTX
NCBI GI g627468
BLAST score 226
E value 8.0e-19
Match length 101
% identity 49
NCBI Description hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No. 201200
Seq. ID LIB3048-016-Q1-L1-A3
Method BLASTX
NCBI GI g2995990
BLAST score 214
E value 2.0e-17
Match length 87
% identity 56
NCBI Description (AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No. 201201
Seq. ID LIB3048-016-Q1-L1-A6
Method BLASTX
NCBI GI g2811025
BLAST score 416
E value 5.0e-41
Match length 106
% identity 72
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 201202
Seq. ID LIB3048-016-Q1-L1-A7
Method BLASTN
NCBI GI g1777727

BLAST score	226
E value	1.0e-124
Match length	230
% identity	100
NCBI Description	Gossypium hirsutum 18S ribosomal RNA gene, partial sequence

Seq. No.	201203
Seq. ID	LIB3048-016-Q1-L1-A8
Method	BLASTX
NCBI GI	g548488
BLAST score	430
E value	1.0e-42
Match length	118
% identity	64
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	201204
Seq. ID	LIB3048-016-Q1-L1-B12
Method	BLASTX
NCBI GI	g2462745
BLAST score	261
E value	9.0e-23
Match length	121
% identity	39
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	201205
Seq. ID	LIB3048-016-Q1-L1-B2
Method	BLASTX
NCBI GI	g2244792
BLAST score	554
E value	4.0e-57
Match length	119
% identity	82
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	201206
Seq. ID	LIB3048-016-Q1-L1-B6
Method	BLASTX
NCBI GI	g3132696
BLAST score	508
E value	8.0e-52
Match length	116
% identity	84
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201207
Seq. ID	LIB3048-016-Q1-L1-B7
Method	BLASTN
NCBI GI	g2995991
BLAST score	32
E value	6.0e-09
Match length	68
% identity	87
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	201208
Seq. ID	LIB3048-016-Q1-L1-B8
Method	BLASTX
NCBI GI	g3046703
BLAST score	618
E value	1.0e-64
Match length	121
% identity	95
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No.	201209
Seq. ID	LIB3048-016-Q1-L1-B9
Method	BLASTX
NCBI GI	g1084349
BLAST score	582
E value	2.0e-60
Match length	124
% identity	90
NCBI Description	aldehyde dehydrogenase homolog btg-26 - rape >gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No.	201210
Seq. ID	LIB3048-016-Q1-L1-C10
Method	BLASTX
NCBI GI	g584929
BLAST score	178
E value	1.0e-13
Match length	39
% identity	69
NCBI Description	BASIC ENDOCHITINASE CHB4 PRECURSOR >gi_17799_emb_CAA43708_ (X61488) chitinase [Brassica napus]

Seq. No.	201211
Seq. ID	LIB3048-016-Q1-L1-C12
Method	BLASTX
NCBI GI	g1518540
BLAST score	410
E value	3.0e-40
Match length	118
% identity	70
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	201212
Seq. ID	LIB3048-016-Q1-L1-C2
Method	BLASTX
NCBI GI	g1332579
BLAST score	493
E value	5.0e-50
Match length	101
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	201213

Seq. ID	LIB3048-016-Q1-L1-C4
Method	BLASTX
NCBI GI	g3393062
BLAST score	145
E value	3.0e-09
Match length	94
% identity	37
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	201214
Seq. ID	LIB3048-016-Q1-L1-C6
Method	BLASTX
NCBI GI	g1169586
BLAST score	370
E value	1.0e-35
Match length	81
% identity	86
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946) fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No.	201215
Seq. ID	LIB3048-016-Q1-L1-C8
Method	BLASTX
NCBI GI	g3047084
BLAST score	387
E value	1.0e-37
Match length	122
% identity	66
NCBI Description	(AF058914) similar to aminoacyl-tRNA synthetases [Arabidopsis thaliana]

Seq. No.	201216
Seq. ID	LIB3048-016-Q1-L1-D1
Method	BLASTX
NCBI GI	g4567260
BLAST score	181
E value	7.0e-14
Match length	52
% identity	62
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	201217
Seq. ID	LIB3048-016-Q1-L1-D11
Method	BLASTX
NCBI GI	g2462745
BLAST score	231
E value	3.0e-19
Match length	121
% identity	36
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	201218
Seq. ID	LIB3048-016-Q1-L1-D3

Method	BLASTX
NCBI GI	g116908
BLAST score	159
E value	4.0e-11
Match length	71
% identity	54
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_166420 (M63853) S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase [Medicago sativa]

Seq. No.	201219
Seq. ID	LIB3048-016-Q1-L1-D6
Method	BLASTX
NCBI GI	g4098244
BLAST score	429
E value	1.0e-42
Match length	106
% identity	79
NCBI Description	(U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No.	201220
Seq. ID	LIB3048-016-Q1-L1-E1
Method	BLASTX
NCBI GI	g3377810
BLAST score	260
E value	1.0e-22
Match length	104
% identity	50
NCBI Description	(AF076275) contains similarity to glutaredoxins [Arabidopsis thaliana]

Seq. No.	201221
Seq. ID	LIB3048-016-Q1-L1-E12
Method	BLASTX
NCBI GI	g629669
BLAST score	203
E value	6.0e-16
Match length	114
% identity	37
NCBI Description	hypothetical protein - tomato

Seq. No.	201222
Seq. ID	LIB3048-016-Q1-L1-E2
Method	BLASTX
NCBI GI	g2244898
BLAST score	477
E value	4.0e-48
Match length	115
% identity	77
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	201223
Seq. ID	LIB3048-016-Q1-L1-E3
Method	BLASTX

09650100.120201

NCBI GI	g2494320
BLAST score	170
E value	3.0e-12
Match length	71
% identity	55
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	201224
Seq. ID	LIB3048-016-Q1-L1-E6
Method	BLASTX
NCBI GI	g1364161
BLAST score	553
E value	5.0e-57
Match length	119
% identity	89
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	201225
Seq. ID	LIB3048-016-Q1-L1-E8
Method	BLASTX
NCBI GI	g1877497
BLAST score	532
E value	2.0e-54
Match length	126
% identity	77
NCBI Description	(U88971) 1-aminocyclopropane-1-carboxylate synthase [Pelargonium x hortorum]

Seq. No.	201226
Seq. ID	LIB3048-016-Q1-L1-E9
Method	BLASTX
NCBI GI	g1326165
BLAST score	306
E value	3.0e-28
Match length	97
% identity	63
NCBI Description	(U55032) aspartic protease [Brassica napus]

Seq. No.	201227
Seq. ID	LIB3048-016-Q1-L1-F11
Method	BLASTN
NCBI GI	g167346
BLAST score	53
E value	6.0e-21
Match length	171
% identity	87
NCBI Description	Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds

Seq. No.	201228
Seq. ID	LIB3048-016-Q1-L1-F3
Method	BLASTX
NCBI GI	g1518540
BLAST score	219
E value	9.0e-21

Match length	69
% identity	75
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	201229
Seq. ID	LIB3048-016-Q1-L1-F4
Method	BLASTX
NCBI GI	g1488521
BLAST score	416
E value	3.0e-41
Match length	121
% identity	73
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	201230
Seq. ID	LIB3048-016-Q1-L1-F9
Method	BLASTX
NCBI GI	g1326165
BLAST score	284
E value	2.0e-25
Match length	120
% identity	44
NCBI Description	(U55032) aspartic protease [Brassica napus]

Seq. No.	201231
Seq. ID	LIB3048-016-Q1-L1-G1
Method	BLASTX
NCBI GI	g542200
BLAST score	308
E value	3.0e-28
Match length	106
% identity	51
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	201232
Seq. ID	LIB3048-016-Q1-L1-G10
Method	BLASTX
NCBI GI	g1723239
BLAST score	348
E value	5.0e-33
Match length	116
% identity	59
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	201233
Seq. ID	LIB3048-016-Q1-L1-G11
Method	BLASTX
NCBI GI	g2622920
BLAST score	150
E value	3.0e-10
Match length	71
% identity	42
NCBI Description	(AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium

thermoautotrophicum]

Seq. No.	201234
Seq. ID	LIB3048-016-Q1-L1-G3
Method	BLASTX
NCBI GI	g285741
BLAST score	288
E value	4.0e-26
Match length	102
% identity	60
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	201235
Seq. ID	LIB3048-016-Q1-L1-G4
Method	BLASTX
NCBI GI	g3892055
BLAST score	519
E value	5.0e-53
Match length	121
% identity	79
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	201236
Seq. ID	LIB3048-016-Q1-L1-G5
Method	BLASTX
NCBI GI	g3288883
BLAST score	354
E value	9.0e-34
Match length	99
% identity	72
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	201237
Seq. ID	LIB3048-016-Q1-L1-G6
Method	BLASTX
NCBI GI	g2507422
BLAST score	321
E value	7.0e-30
Match length	94
% identity	74
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201238
Seq. ID	LIB3048-016-Q1-L1-G7
Method	BLASTX
NCBI GI	g2369766
BLAST score	284
E value	1.0e-25
Match length	76
% identity	68
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 201239

Seq. ID	LIB3048-016-Q1-L1-G8
Method	BLASTX
NCBI GI	g2407790
BLAST score	307
E value	2.0e-28
Match length	98
% identity	19
NCBI Description	(AF019910) grr1 [Glycine max]

Seq. No.	201240
Seq. ID	LIB3048-016-Q1-L1-H10
Method	BLASTX
NCBI GI	g3914019
BLAST score	471
E value	2.0e-47
Match length	114
% identity	81
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014 (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa acuminata]

Seq. No.	201241
Seq. ID	LIB3048-016-Q1-L1-H12
Method	BLASTX
NCBI GI	g2622920
BLAST score	263
E value	5.0e-23
Match length	119
% identity	43
NCBI Description	(AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium thermoautotrophicum]

Seq. No.	201242
Seq. ID	LIB3048-016-Q1-L1-H4
Method	BLASTX
NCBI GI	g3096919
BLAST score	165
E value	6.0e-12
Match length	40
% identity	72
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	201243
Seq. ID	LIB3048-016-Q1-L1-H5
Method	BLASTX
NCBI GI	g3603456
BLAST score	514
E value	2.0e-52
Match length	114
% identity	28
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	201244
Seq. ID	LIB3048-016-Q1-L1-H6
Method	BLASTX

NCBI GI	g3831456
BLAST score	180
E value	2.0e-16
Match length	116
% identity	46
NCBI Description	(AC005700) putative ion channel protein [Arabidopsis thaliana]

Seq. No.	201245
Seq. ID	LIB3048-016-Q1-L1-H7
Method	BLASTX
NCBI GI	g1654140
BLAST score	529
E value	3.0e-54
Match length	122
% identity	83
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	201246
Seq. ID	LIB3048-016-Q1-L1-H9
Method	BLASTX
NCBI GI	g3264771
BLAST score	163
E value	8.0e-12
Match length	45
% identity	64
NCBI Description	(AF071895) turgor-responsive-like protein [Prunus armeniaca]

Seq. No.	201247
Seq. ID	LIB3048-017-Q1-L1-A10
Method	BLASTX
NCBI GI	g2244905
BLAST score	356
E value	6.0e-34
Match length	110
% identity	56
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	201248
Seq. ID	LIB3048-017-Q1-L1-A11
Method	BLASTX
NCBI GI	g3746059
BLAST score	510
E value	7.0e-52
Match length	138
% identity	66
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201249
Seq. ID	LIB3048-017-Q1-L1-A12
Method	BLASTX
NCBI GI	g126770
BLAST score	591

E value	3.0e-63
Match length	123
% identity	98
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate synthase (EC 4.1.3.2) - upland cotton >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567) [Gossypium hirsutum]

Seq. No.	201250
Seq. ID	LIB3048-017-Q1-L1-A3
Method	BLASTX
NCBI GI	g3913431
BLAST score	249
E value	1.0e-21
Match length	96
% identity	53
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C >gi_2661607_emb_CAA15715_ (AL009197) hypothetical mrna splicibg factor [Schizosaccharomyces pombe]

Seq. No.	201251
Seq. ID	LIB3048-017-Q1-L1-A4
Method	BLASTX
NCBI GI	g2827548
BLAST score	180
E value	3.0e-13
Match length	83
% identity	47
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201252
Seq. ID	LIB3048-017-Q1-L1-A5
Method	BLASTX
NCBI GI	g3249105
BLAST score	425
E value	5.0e-42
Match length	120
% identity	65
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	201253
Seq. ID	LIB3048-017-Q1-L1-A6
Method	BLASTX
NCBI GI	g4455210
BLAST score	205
E value	3.0e-16
Match length	107
% identity	43
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	201254
Seq. ID	LIB3048-017-Q1-L1-A8
Method	BLASTX

NCBI GI	g1495251
BLAST score	330
E value	7.0e-31
Match length	126
% identity	54
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	201255
Seq. ID	LIB3048-017-Q1-L1-A9
Method	BLASTX
NCBI GI	g125606
BLAST score	227
E value	8.0e-19
Match length	76
% identity	58
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	201256
Seq. ID	LIB3048-017-Q1-L1-B1
Method	BLASTX
NCBI GI	g633110
BLAST score	526
E value	6.0e-54
Match length	110
% identity	92
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	201257
Seq. ID	LIB3048-017-Q1-L1-B10
Method	BLASTN
NCBI GI	g3849811
BLAST score	35
E value	1.0e-10
Match length	91
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	201258
Seq. ID	LIB3048-017-Q1-L1-B3
Method	BLASTX
NCBI GI	g421855
BLAST score	389
E value	8.0e-38
Match length	112
% identity	70
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No.	201259
Seq. ID	LIB3048-017-Q1-L1-B4
Method	BLASTX
NCBI GI	g1856971
BLAST score	465

E value	1.0e-46
Match length	98
% identity	90
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	201260
Seq. ID	LIB3048-017-Q1-L1-B6
Method	BLASTX
NCBI GI	g3450842
BLAST score	231
E value	3.0e-19
Match length	87
% identity	56
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	201261
Seq. ID	LIB3048-017-Q1-L1-B7
Method	BLASTX
NCBI GI	g2369714
BLAST score	493
E value	4.0e-50
Match length	104
% identity	92
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	201262
Seq. ID	LIB3048-017-Q1-L1-B8
Method	BLASTX
NCBI GI	g1531674
BLAST score	572
E value	2.0e-59
Match length	111
% identity	95
NCBI Description	(U68462) actin [Striga asiatica]

Seq. No.	201263
Seq. ID	LIB3048-017-Q1-L1-B9
Method	BLASTX
NCBI GI	g4558664
BLAST score	262
E value	7.0e-23
Match length	126
% identity	11
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201264
Seq. ID	LIB3048-017-Q1-L1-C1
Method	BLASTX
NCBI GI	g2507426
BLAST score	474
E value	1.0e-47
Match length	128
% identity	73
NCBI Description	ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR

(ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_ (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No.	201265
Seq. ID	LIB3048-017-Q1-L1-C10
Method	BLASTX
NCBI GI	g2244792
BLAST score	582
E value	2.0e-60
Match length	127
% identity	80
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	201266
Seq. ID	LIB3048-017-Q1-L1-C11
Method	BLASTX
NCBI GI	g119010
BLAST score	202
E value	2.0e-16
Match length	46
% identity	85
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM GGIB50 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE, BASIC) (GLUCANASE GLA) >gi_100329_pir__A38257 glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) basic precursor (clone ggIb50) - common tobacco (cv. Samsun NN)

Seq. No.	201267
Seq. ID	LIB3048-017-Q1-L1-C12
Method	BLASTX
NCBI GI	g1076668
BLAST score	364
E value	7.0e-35
Match length	111
% identity	63
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	201268
Seq. ID	LIB3048-017-Q1-L1-C2
Method	BLASTX
NCBI GI	g1769887
BLAST score	454
E value	2.0e-45
Match length	106
% identity	78
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	201269
Seq. ID	LIB3048-017-Q1-L1-C3
Method	BLASTX
NCBI GI	g2529703
BLAST score	494
E value	4.0e-50

Match length	118
% identity	82
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	201270
Seq. ID	LIB3048-017-Q1-L1-C5
Method	BLASTX
NCBI GI	g2642648
BLAST score	381
E value	8.0e-51
Match length	139
% identity	78
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	201271
Seq. ID	LIB3048-017-Q1-L1-C9
Method	BLASTX
NCBI GI	g1488521
BLAST score	453
E value	3.0e-45
Match length	126
% identity	70
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	201272
Seq. ID	LIB3048-017-Q1-L1-D11
Method	BLASTX
NCBI GI	g2832642
BLAST score	314
E value	6.0e-30
Match length	124
% identity	25
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	201273
Seq. ID	LIB3048-017-Q1-L1-D4
Method	BLASTX
NCBI GI	g4432866
BLAST score	252
E value	1.0e-21
Match length	117
% identity	37
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	201274
Seq. ID	LIB3048-017-Q1-L1-D5
Method	BLASTX
NCBI GI	g4567251
BLAST score	287
E value	3.0e-26
Match length	70
% identity	76

NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	201275
Seq. ID	LIB3048-017-Q1-L1-D7
Method	BLASTX
NCBI GI	g1483230
BLAST score	399
E value	6.0e-39
Match length	106
% identity	80
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	201276
Seq. ID	LIB3048-017-Q1-L1-E1
Method	BLASTX
NCBI GI	g1084349
BLAST score	431
E value	1.0e-42
Match length	122
% identity	75
NCBI Description	aldehyde dehydrogenase homolog btg-26 - rape >gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No.	201277
Seq. ID	LIB3048-017-Q1-L1-E12
Method	BLASTX
NCBI GI	g4539400
BLAST score	489
E value	2.0e-49
Match length	125
% identity	75
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	201278
Seq. ID	LIB3048-017-Q1-L1-E2
Method	BLASTX
NCBI GI	g2129597
BLAST score	546
E value	4.0e-56
Match length	109
% identity	94
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201279
Seq. ID	LIB3048-017-Q1-L1-E4
Method	BLASTX
NCBI GI	g1272410
BLAST score	343
E value	7.0e-47
Match length	117
% identity	74
NCBI Description	(U52045) immunophilin precursor [Vicia faba]

Seq. No.	201280
Seq. ID	LIB3048-017-Q1-L1-E7
Method	BLASTX
NCBI GI	g4325338
BLAST score	630
E value	6.0e-66
Match length	128
% identity	88
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	201281
Seq. ID	LIB3048-017-Q1-L1-E9
Method	BLASTX
NCBI GI	g3746059
BLAST score	534
E value	1.0e-54
Match length	135
% identity	69
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201282
Seq. ID	LIB3048-017-Q1-L1-F1
Method	BLASTX
NCBI GI	g2244792
BLAST score	577
E value	8.0e-60
Match length	127
% identity	80
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	201283
Seq. ID	LIB3048-017-Q1-L1-F10
Method	BLASTX
NCBI GI	g1107526
BLAST score	523
E value	2.0e-53
Match length	127
% identity	77
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	201284
Seq. ID	LIB3048-017-Q1-L1-F12
Method	BLASTX
NCBI GI	g2772934
BLAST score	465
E value	1.0e-46
Match length	112
% identity	76
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	201285
Seq. ID	LIB3048-017-Q1-L1-F2
Method	BLASTX

NCBI GI g2244792
BLAST score 277
E value 8.0e-25
Match length 101
% identity 56
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 201286
Seq. ID LIB3048-017-Q1-L1-F3
Method BLASTX
NCBI GI g4558664
BLAST score 228
E value 7.0e-19
Match length 118
% identity 7
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201287
Seq. ID LIB3048-017-Q1-L1-F4
Method BLASTX
NCBI GI g4337046
BLAST score 240
E value 3.0e-20
Match length 126
% identity 45
NCBI Description (AF124162) molybdopterin synthase sulphurylase [Nicotiana plumbaginifolia]

Seq. No. 201288
Seq. ID LIB3048-017-Q1-L1-F6
Method BLASTX
NCBI GI g633110
BLAST score 482
E value 7.0e-49
Match length 96
% identity 94
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No. 201289
Seq. ID LIB3048-017-Q1-L1-F7
Method BLASTX
NCBI GI g4262142
BLAST score 268
E value 1.0e-23
Match length 87
% identity 56
NCBI Description (AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 201290
Seq. ID LIB3048-017-Q1-L1-F8
Method BLASTX
NCBI GI g1848212
BLAST score 428
E value 2.0e-42
Match length 83
% identity 45

NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No.	201291
Seq. ID	LIB3048-017-Q1-L1-G3
Method	BLASTX
NCBI GI	g4544454
BLAST score	474
E value	9.0e-48
Match length	122
% identity	74
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	201292
Seq. ID	LIB3048-017-Q1-L1-G4
Method	BLASTX
NCBI GI	g2827715
BLAST score	503
E value	4.0e-51
Match length	125
% identity	9
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	201293
Seq. ID	LIB3048-017-Q1-L1-H2
Method	BLASTX
NCBI GI	g4164161
BLAST score	478
E value	3.0e-48
Match length	118
% identity	74
NCBI Description	(AB015497) ethylene response sensor [Passiflora edulis]

Seq. No.	201294
Seq. ID	LIB3048-017-Q1-L1-H3
Method	BLASTN
NCBI GI	g3869068
BLAST score	78
E value	8.0e-36
Match length	248
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	201295
Seq. ID	LIB3048-017-Q1-L1-H4
Method	BLASTX
NCBI GI	g3643611
BLAST score	455
E value	2.0e-45
Match length	122
% identity	72
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	201296
Seq. ID	LIB3048-017-Q1-L1-H6

Method	BLASTX
NCBI GI	g1335862
BLAST score	641
E value	3.0e-67
Match length	136
% identity	92
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	201297
Seq. ID	LIB3048-017-Q1-L1-H8
Method	BLASTX
NCBI GI	g3643611
BLAST score	189
E value	2.0e-15
Match length	81
% identity	57
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	201298
Seq. ID	LIB3048-018-Q1-L1-A1
Method	BLASTX
NCBI GI	g548774
BLAST score	273
E value	2.0e-24
Match length	78
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	201299
Seq. ID	LIB3048-018-Q1-L1-A11
Method	BLASTX
NCBI GI	g2398679
BLAST score	594
E value	7.0e-62
Match length	118
% identity	95
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	201300
Seq. ID	LIB3048-018-Q1-L1-A12
Method	BLASTX
NCBI GI	g3426051
BLAST score	315
E value	4.0e-29
Match length	122
% identity	53
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201301
Seq. ID	LIB3048-018-Q1-L1-A6
Method	BLASTX
NCBI GI	g119354
BLAST score	214
E value	1.0e-17

Match length	54
% identity	81
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	201302
Seq. ID	LIB3048-018-Q1-L1-A8
Method	BLASTX
NCBI GI	g4539335
BLAST score	272
E value	5.0e-24
Match length	133
% identity	40
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	201303
Seq. ID	LIB3048-018-Q1-L1-B1
Method	BLASTX
NCBI GI	g120673
BLAST score	374
E value	3.0e-36
Match length	93
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No.	201304
Seq. ID	LIB3048-018-Q1-L1-B10
Method	BLASTX
NCBI GI	g4539422
BLAST score	236
E value	5.0e-20
Match length	84
% identity	58
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	201305
Seq. ID	LIB3048-018-Q1-L1-B12
Method	BLASTX
NCBI GI	g2813966
BLAST score	154
E value	3.0e-10
Match length	100
% identity	38
NCBI Description	(Z97053) placental protein Diff33 [Homo sapiens] >gi_4545219_gb_AAD22448.1_ (AF112227) TDE homolog [Homo sapiens]

Seq. No.	201306
Seq. ID	LIB3048-018-Q1-L1-B3
Method	BLASTX

NCBI GI	g136739
BLAST score	229
E value	8.0e-32
Match length	109
% identity	64
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	201307
Seq. ID	LIB3048-018-Q1-L1-B4
Method	BLASTX
NCBI GI	g1709498
BLAST score	543
E value	9.0e-56
Match length	122
% identity	80
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201308
Seq. ID	LIB3048-018-Q1-L1-B6
Method	BLASTX
NCBI GI	g2213852
BLAST score	139
E value	1.0e-08
Match length	65
% identity	48
NCBI Description	(AF003007) VVTL1 [Vitis vinifera]

Seq. No.	201309
Seq. ID	LIB3048-018-Q1-L1-B8
Method	BLASTX
NCBI GI	g1174592
BLAST score	499
E value	1.0e-61
Match length	141
% identity	83
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	201310
Seq. ID	LIB3048-018-Q1-L1-B9
Method	BLASTX
NCBI GI	g3850588
BLAST score	277
E value	5.0e-25
Match length	73
% identity	77
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No.	201311
Seq. ID	LIB3048-018-Q1-L1-C10
Method	BLASTX
NCBI GI	g4508073
BLAST score	384
E value	4.0e-37
Match length	99
% identity	70
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	201312
Seq. ID	LIB3048-018-Q1-L1-C11
Method	BLASTX
NCBI GI	g3811007
BLAST score	563
E value	4.0e-58
Match length	113
% identity	95
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	201313
Seq. ID	LIB3048-018-Q1-L1-C12
Method	BLASTX
NCBI GI	g3421090
BLAST score	197
E value	3.0e-15
Match length	43
% identity	93
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	201314
Seq. ID	LIB3048-018-Q1-L1-C3
Method	BLASTX
NCBI GI	g3115374
BLAST score	173
E value	1.0e-12
Match length	76
% identity	53
NCBI Description	(AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

Seq. No.	201315
Seq. ID	LIB3048-018-Q1-L1-C4
Method	BLASTX
NCBI GI	g3115374
BLAST score	451
E value	5.0e-45
Match length	124
% identity	70
NCBI Description	(AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

Seq. No.	201316
Seq. ID	LIB3048-018-Q1-L1-C8
Method	BLASTX

NCBI GI	g3044212
BLAST score	213
E value	1.0e-17
Match length	50
% identity	84
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	201317
Seq. ID	LIB3048-018-Q1-L1-C9
Method	BLASTX
NCBI GI	g3122263
BLAST score	179
E value	1.0e-13
Match length	44
% identity	77
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_2209274 (U62044) eukaryotic initiation factor (iso)-4F p28 subunit [Arabidopsis thaliana]

Seq. No.	201318
Seq. ID	LIB3048-018-Q1-L1-D1
Method	BLASTX
NCBI GI	g2129597
BLAST score	356
E value	4.0e-34
Match length	73
% identity	93
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201319
Seq. ID	LIB3048-018-Q1-L1-D10
Method	BLASTX
NCBI GI	g3935168
BLAST score	345
E value	1.0e-32
Match length	136
% identity	57
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	201320
Seq. ID	LIB3048-018-Q1-L1-D12
Method	BLASTX
NCBI GI	g119354
BLAST score	483
E value	3.0e-58
Match length	127
% identity	86
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	201321
Seq. ID	LIB3048-018-Q1-L1-D3
Method	BLASTN
NCBI GI	g758693
BLAST score	102
E value	3.0e-50
Match length	130
% identity	95
NCBI Description	Catharanthus roseus S-adenosyl-L-methionine decarboxylase proenzyme mRNA, complete cds

Seq. No.	201322
Seq. ID	LIB3048-018-Q1-L1-D4
Method	BLASTX
NCBI GI	g2117624
BLAST score	498
E value	1.0e-50
Match length	120
% identity	78
NCBI Description	peroxidase (EC 1.11.1.7) 2 - alfalfa >gi_971564_emb_CAA62228_ (X90695) peroxidase2 [Medicago sativa]

Seq. No.	201323
Seq. ID	LIB3048-018-Q1-L1-D5
Method	BLASTX
NCBI GI	g1361983
BLAST score	176
E value	2.0e-13
Match length	56
% identity	66
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	201324
Seq. ID	LIB3048-018-Q1-L1-D6
Method	BLASTX
NCBI GI	g2511574
BLAST score	375
E value	2.0e-36
Match length	80
% identity	95
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	201325
Seq. ID	LIB3048-018-Q1-L1-D8
Method	BLASTX
NCBI GI	g2290683
BLAST score	276
E value	9.0e-25
Match length	65
% identity	77
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	201326
Seq. ID	LIB3048-018-Q1-L1-E1
Method	BLASTX
NCBI GI	g2864624
BLAST score	192
E value	6.0e-15
Match length	86
% identity	44
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	201327
Seq. ID	LIB3048-018-Q1-L1-E10
Method	BLASTX
NCBI GI	g3402693
BLAST score	143
E value	7.0e-09
Match length	86
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	201328
Seq. ID	LIB3048-018-Q1-L1-E5
Method	BLASTX
NCBI GI	g3892057
BLAST score	212
E value	5.0e-17
Match length	58
% identity	76
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201329
Seq. ID	LIB3048-018-Q1-L1-F1
Method	BLASTX
NCBI GI	g3264771
BLAST score	215
E value	6.0e-18
Match length	59
% identity	66
NCBI Description	(AF071895) turgor-responsive-like protein [Prunus armeniaca]

Seq. No.	201330
Seq. ID	LIB3048-018-Q1-L1-F11
Method	BLASTX
NCBI GI	g3335351
BLAST score	476
E value	6.0e-48
Match length	136
% identity	10
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	201331
Seq. ID	LIB3048-018-Q1-L1-F12
Method	BLASTX
NCBI GI	g1399275

BLAST score	647
E value	6.0e-68
Match length	134
% identity	90
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	201332
Seq. ID	LIB3048-018-Q1-L1-F5
Method	BLASTX
NCBI GI	g4185599
BLAST score	158
E value	6.0e-11
Match length	83
% identity	48
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	201333
Seq. ID	LIB3048-018-Q1-L1-F8
Method	BLASTX
NCBI GI	g1173256
BLAST score	450
E value	6.0e-45
Match length	108
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	201334
Seq. ID	LIB3048-018-Q1-L1-G1
Method	BLASTX
NCBI GI	g4100433
BLAST score	185
E value	3.0e-14
Match length	55
% identity	58
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	201335
Seq. ID	LIB3048-018-Q1-L1-G10
Method	BLASTX
NCBI GI	g3461820
BLAST score	214
E value	3.0e-17
Match length	57
% identity	61
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	201336
Seq. ID	LIB3048-018-Q1-L1-G12
Method	BLASTX
NCBI GI	g132944

BLAST score	601
E value	1.0e-62
Match length	120
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	201337
Seq. ID	LIB3048-018-Q1-L1-G4
Method	BLASTX
NCBI GI	g4235430
BLAST score	367
E value	3.0e-35
Match length	90
% identity	79
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	201338
Seq. ID	LIB3048-018-Q1-L1-G5
Method	BLASTX
NCBI GI	g1364161
BLAST score	605
E value	5.0e-63
Match length	132
% identity	87
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	201339
Seq. ID	LIB3048-018-Q1-L1-G9
Method	BLASTX
NCBI GI	g3642014
BLAST score	184
E value	1.0e-13
Match length	85
% identity	42
NCBI Description	(AL031620) similar to Zinc finger, C3HC4 type (RING finger) [Caenorhabditis elegans]

Seq. No.	201340
Seq. ID	LIB3048-018-Q1-L1-H1
Method	BLASTX
NCBI GI	g1143322
BLAST score	357
E value	2.0e-34
Match length	82
% identity	79
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	201341
Seq. ID	LIB3048-018-Q1-L1-H12
Method	BLASTN
NCBI GI	g2605910
BLAST score	65
E value	2.0e-28
Match length	168
% identity	85

NCBI Description	Kosteletzkya virginica clone KVATP3 plasma membrane H+-ATPase mRNA, partial cds

Seq. No.	201342
Seq. ID	LIB3048-018-Q1-L1-H4
Method	BLASTX
NCBI GI	g3335363
BLAST score	337
E value	1.0e-31
Match length	119
% identity	32
NCBI Description	(AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201343
Seq. ID	LIB3048-018-Q1-L1-H6
Method	BLASTX
NCBI GI	g4580460
BLAST score	331
E value	3.0e-31
Match length	81
% identity	81
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	201344
Seq. ID	LIB3048-019-Q1-L1-A1
Method	BLASTX
NCBI GI	g2281115
BLAST score	614
E value	5.0e-64
Match length	145
% identity	81
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201345
Seq. ID	LIB3048-019-Q1-L1-A11
Method	BLASTX
NCBI GI	g486993
BLAST score	154
E value	9.0e-11
Match length	66
% identity	53
NCBI Description	translation elongation factor eEF-1 alpha chain (clone 50-1.5) - slime mold (Dictyostelium discoideum) (fragment) >gi_7277_emb_CAA39442_ (X55972) elongation factor 1 alpha [Dictyostelium discoideum]

Seq. No.	201346
Seq. ID	LIB3048-019-Q1-L1-A12
Method	BLASTX
NCBI GI	g70644
BLAST score	654
E value	9.0e-69
Match length	137
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	201347
Seq. ID	LIB3048-019-Q1-L1-A3
Method	BLASTX
NCBI GI	g3608155
BLAST score	336
E value	2.0e-31
Match length	146
% identity	48
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	201348
Seq. ID	LIB3048-019-Q1-L1-A9
Method	BLASTX
NCBI GI	g1174592
BLAST score	599
E value	2.0e-62
Match length	113
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	201349
Seq. ID	LIB3048-019-Q1-L1-B1
Method	BLASTX
NCBI GI	g4417304
BLAST score	518
E value	8.0e-53
Match length	146
% identity	62
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	201350
Seq. ID	LIB3048-019-Q1-L1-B10
Method	BLASTX
NCBI GI	g4006829
BLAST score	610
E value	1.0e-63
Match length	136
% identity	86
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	201351
Seq. ID	LIB3048-019-Q1-L1-B12
Method	BLASTX
NCBI GI	g1346180
BLAST score	382
E value	6.0e-37
Match length	85
% identity	85
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	201352
Seq. ID	LIB3048-019-Q1-L1-B4
Method	BLASTX
NCBI GI	g544250
BLAST score	540
E value	2.0e-55
Match length	134
% identity	76
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	201353
Seq. ID	LIB3048-019-Q1-L1-B7
Method	BLASTX
NCBI GI	g4510406
BLAST score	389
E value	1.0e-37
Match length	114
% identity	66
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	201354
Seq. ID	LIB3048-019-Q1-L1-B8
Method	BLASTX
NCBI GI	g2258418
BLAST score	341
E value	5.0e-32
Match length	101
% identity	61
NCBI Description	(AF007875) dolichol monophosphate mannose synthase [Homo sapiens]

Seq. No.	201355
Seq. ID	LIB3048-019-Q1-L1-B9
Method	BLASTX
NCBI GI	g2618699
BLAST score	149
E value	2.0e-09
Match length	50
% identity	60
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	201356
Seq. ID	LIB3048-019-Q1-L1-C10
Method	BLASTX
NCBI GI	g4468046
BLAST score	298
E value	5.0e-27
Match length	115
% identity	57
NCBI Description	(X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No.	201357
Seq. ID	LIB3048-019-Q1-L1-C11
Method	BLASTX
NCBI GI	g3249064

BLAST score	461
E value	4.0e-46
Match length	139
% identity	64
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	201358
Seq. ID	LIB3048-019-Q1-L1-C2
Method	BLASTX
NCBI GI	g2673917
BLAST score	520
E value	4.0e-53
Match length	131
% identity	50
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	201359
Seq. ID	LIB3048-019-Q1-L1-C6
Method	BLASTX
NCBI GI	g2462745
BLAST score	250
E value	2.0e-21
Match length	121
% identity	37
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	201360
Seq. ID	LIB3048-019-Q1-L1-C8
Method	BLASTX
NCBI GI	g267146
BLAST score	554
E value	5.0e-57
Match length	151
% identity	66
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	201361
Seq. ID	LIB3048-019-Q1-L1-C9
Method	BLASTX
NCBI GI	g4468817
BLAST score	302
E value	1.0e-27
Match length	70
% identity	49
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	201362
Seq. ID	LIB3048-019-Q1-L1-D1
Method	BLASTX
NCBI GI	g4432866

BLAST score 398
E value 1.0e-38
Match length 145
% identity 50
NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 201363
Seq. ID LIB3048-019-Q1-L1-D10
Method BLASTX
NCBI GI g629562
BLAST score 574
E value 2.0e-59
Match length 139
% identity 77
NCBI Description sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No. 201364
Seq. ID LIB3048-019-Q1-L1-D11
Method BLASTX
NCBI GI g1769901
BLAST score 422
E value 1.0e-41
Match length 140
% identity 59
NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No. 201365
Seq. ID LIB3048-019-Q1-L1-D12
Method BLASTX
NCBI GI g421929
BLAST score 480
E value 2.0e-48
Match length 147
% identity 9
NCBI Description ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No. 201366
Seq. ID LIB3048-019-Q1-L1-D5
Method BLASTX
NCBI GI g3763933
BLAST score 378
E value 2.0e-36
Match length 133
% identity 73
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	201367
Seq. ID	LIB3048-019-Q1-L1-D6
Method	BLASTX
NCBI GI	g2894612
BLAST score	602
E value	2.0e-63
Match length	142
% identity	85
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	201368
Seq. ID	LIB3048-019-Q1-L1-E1
Method	BLASTX
NCBI GI	g629602
BLAST score	352
E value	2.0e-33
Match length	119
% identity	59
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	201369
Seq. ID	LIB3048-019-Q1-L1-E10
Method	BLASTX
NCBI GI	g1769901
BLAST score	272
E value	1.0e-34
Match length	133
% identity	57
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No.	201370
Seq. ID	LIB3048-019-Q1-L1-E12
Method	BLASTX
NCBI GI	g2245070
BLAST score	402
E value	3.0e-39
Match length	94
% identity	77
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201371
Seq. ID	LIB3048-019-Q1-L1-E2
Method	BLASTX
NCBI GI	g4530126
BLAST score	422
E value	1.0e-41
Match length	116
% identity	71
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	201372

Seq. ID	LIB3048-019-Q1-L1-E5
Method	BLASTX
NCBI GI	g2924781
BLAST score	418
E value	4.0e-41
Match length	136
% identity	62
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	201373
Seq. ID	LIB3048-019-Q1-L1-E6
Method	BLASTX
NCBI GI	g3894159
BLAST score	161
E value	6.0e-11
Match length	80
% identity	40
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201374
Seq. ID	LIB3048-019-Q1-L1-E8
Method	BLASTX
NCBI GI	g1399275
BLAST score	695
E value	1.0e-73
Match length	145
% identity	90
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	201375
Seq. ID	LIB3048-019-Q1-L1-E9
Method	BLASTX
NCBI GI	g2129597
BLAST score	554
E value	4.0e-57
Match length	109
% identity	95
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201376
Seq. ID	LIB3048-019-Q1-L1-F1
Method	BLASTX
NCBI GI	g3335375
BLAST score	592
E value	2.0e-61
Match length	132
% identity	86
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	201377

Seq. ID	LIB3048-019-Q1-L1-F10
Method	BLASTX
NCBI GI	g4262174
BLAST score	571
E value	5.0e-59
Match length	139
% identity	71
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	201378
Seq. ID	LIB3048-019-Q1-L1-F11
Method	BLASTX
NCBI GI	g3121739
BLAST score	204
E value	6.0e-16
Match length	100
% identity	23
NCBI Description	ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759_pir__I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens] >gi_4557229_ref_NP_001078.1_pAAMP_ angio-associated, migratory cell protein

Seq. No.	201379
Seq. ID	LIB3048-019-Q1-L1-F12
Method	BLASTX
NCBI GI	g4335752
BLAST score	250
E value	2.0e-21
Match length	124
% identity	43
NCBI Description	(AC006284) putative myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	201380
Seq. ID	LIB3048-019-Q1-L1-F3
Method	BLASTX
NCBI GI	g3329294
BLAST score	149
E value	2.0e-09
Match length	129
% identity	29
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	201381
Seq. ID	LIB3048-019-Q1-L1-F4
Method	BLASTX
NCBI GI	g3746059
BLAST score	472
E value	2.0e-47
Match length	140
% identity	62
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201382
Seq. ID	LIB3048-019-Q1-L1-F9
Method	BLASTX
NCBI GI	g2213629
BLAST score	545
E value	6.0e-56
Match length	124
% identity	78
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	201383
Seq. ID	LIB3048-019-Q1-L1-G10
Method	BLASTX
NCBI GI	g4139038
BLAST score	158
E value	1.0e-10
Match length	115
% identity	11
NCBI Description	(AF072272) resistance protein candidate RGC2K [Lactuca sativa]

Seq. No.	201384
Seq. ID	LIB3048-019-Q1-L1-G11
Method	BLASTX
NCBI GI	g1654140
BLAST score	598
E value	3.0e-62
Match length	128
% identity	88
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	201385
Seq. ID	LIB3048-019-Q1-L1-G3
Method	BLASTX
NCBI GI	g3834308
BLAST score	218
E value	1.0e-17
Match length	80
% identity	50
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. EST gb_AA720110 comes from this gene. [Arabidopsis thaliana]

Seq. No.	201386
Seq. ID	LIB3048-019-Q1-L1-G4
Method	BLASTX
NCBI GI	g1486472
BLAST score	567
E value	1.0e-58
Match length	126
% identity	87
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	201387

Seq. ID	LIB3048-019-Q1-L1-G5
Method	BLASTX
NCBI GI	g1107526
BLAST score	391
E value	5.0e-38
Match length	98
% identity	74
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	201388
Seq. ID	LIB3048-019-Q1-L1-G6
Method	BLASTX
NCBI GI	g3746059
BLAST score	610
E value	1.0e-63
Match length	148
% identity	71
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201389
Seq. ID	LIB3048-019-Q1-L1-G7
Method	BLASTX
NCBI GI	g2342724
BLAST score	309
E value	3.0e-28
Match length	146
% identity	57
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	201390
Seq. ID	LIB3048-019-Q1-L1-G9
Method	BLASTX
NCBI GI	g2078350
BLAST score	255
E value	6.0e-22
Match length	118
% identity	49
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	201391
Seq. ID	LIB3048-019-Q1-L1-H1
Method	BLASTX
NCBI GI	g2632059
BLAST score	189
E value	1.0e-14
Match length	73
% identity	53
NCBI Description	(AJ002596) patatin-like protein [Arabidopsis thaliana]

Seq. No.	201392
Seq. ID	LIB3048-019-Q1-L1-H11
Method	BLASTX
NCBI GI	g1361973
BLAST score	493
E value	7.0e-50

Match length	144
% identity	71
NCBI Description	secA protein precursor - spinach

Seq. No.	201393
Seq. ID	LIB3048-019-Q1-L1-H12
Method	BLASTX
NCBI GI	g2129921
BLAST score	194
E value	8.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	201394
Seq. ID	LIB3048-019-Q1-L1-H2
Method	BLASTX
NCBI GI	g3204134
BLAST score	324
E value	1.0e-31
Match length	106
% identity	64
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	201395
Seq. ID	LIB3048-019-Q1-L1-H5
Method	BLASTX
NCBI GI	g2062173
BLAST score	354
E value	1.0e-33
Match length	126
% identity	59
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	201396
Seq. ID	LIB3048-019-Q1-L1-H6
Method	BLASTX
NCBI GI	g3204134
BLAST score	621
E value	6.0e-65
Match length	138
% identity	78
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	201397
Seq. ID	LIB3048-019-Q1-L1-H7
Method	BLASTX
NCBI GI	g3786025
BLAST score	249
E value	3.0e-21
Match length	54
% identity	87
NCBI Description	(AC005499) putative DNA-binding protein, 5' partial [Arabidopsis thaliana]

Seq. No.	201398
Seq. ID	LIB3048-020-Q1-L1-A2
Method	BLASTX
NCBI GI	g1706918
BLAST score	231
E value	3.0e-19
Match length	105
% identity	43
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	201399
Seq. ID	LIB3048-020-Q1-L1-A3
Method	BLASTX
NCBI GI	g3924597
BLAST score	181
E value	2.0e-13
Match length	107
% identity	33
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	201400
Seq. ID	LIB3048-020-Q1-L1-A5
Method	BLASTX
NCBI GI	g3395432
BLAST score	199
E value	1.0e-15
Match length	73
% identity	55
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	201401
Seq. ID	LIB3048-020-Q1-L1-A6
Method	BLASTX
NCBI GI	g3603401
BLAST score	301
E value	2.0e-27
Match length	75
% identity	69
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	201402
Seq. ID	LIB3048-020-Q1-L1-A7
Method	BLASTX
NCBI GI	g4433048
BLAST score	324
E value	5.0e-30
Match length	123
% identity	54
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	201403
Seq. ID	LIB3048-020-Q1-L1-A9
Method	BLASTX
NCBI GI	g2864624
BLAST score	376
E value	4.0e-36

Match length	146
% identity	26
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	201404
Seq. ID	LIB3048-020-Q1-L1-B10
Method	BLASTX
NCBI GI	g2632105
BLAST score	285
E value	2.0e-25
Match length	83
% identity	69
NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201405
Seq. ID	LIB3048-020-Q1-L1-B12
Method	BLASTX
NCBI GI	g131276
BLAST score	748
E value	9.0e-80
Match length	144
% identity	99
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	201406
Seq. ID	LIB3048-020-Q1-L1-B2
Method	BLASTX
NCBI GI	g4115371
BLAST score	254
E value	4.0e-22
Match length	77
% identity	62
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	201407
Seq. ID	LIB3048-020-Q1-L1-B3
Method	BLASTX
NCBI GI	g2507281
BLAST score	661
E value	1.0e-69
Match length	118
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	201408
Seq. ID	LIB3048-020-Q1-L1-B5
Method	BLASTX
NCBI GI	g2570164
BLAST score	445

E value	3.0e-44
Match length	123
% identity	64
NCBI Description	(D45183) chitinase [Chenopodium amaranticolor]

Seq. No.	201409
Seq. ID	LIB3048-020-Q1-L1-B8
Method	BLASTX
NCBI GI	g1346387
BLAST score	590
E value	3.0e-61
Match length	131
% identity	89
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	201410
Seq. ID	LIB3048-020-Q1-L1-C1
Method	BLASTX
NCBI GI	g2062167
BLAST score	192
E value	3.0e-16
Match length	119
% identity	46
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	201411
Seq. ID	LIB3048-020-Q1-L1-C10
Method	BLASTX
NCBI GI	g3776559
BLAST score	323
E value	6.0e-30
Match length	72
% identity	81
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	201412
Seq. ID	LIB3048-020-Q1-L1-C11
Method	BLASTX
NCBI GI	g2443329
BLAST score	326
E value	2.0e-30
Match length	132
% identity	53
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	201413
Seq. ID	LIB3048-020-Q1-L1-C12
Method	BLASTX
NCBI GI	g4262142
BLAST score	174

E value	9.0e-13
Match length	68
% identity	49
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	201414
Seq. ID	LIB3048-020-Q1-L1-C3
Method	BLASTX
NCBI GI	g82131
BLAST score	398
E value	8.0e-39
Match length	115
% identity	69
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	201415
Seq. ID	LIB3048-020-Q1-L1-C4
Method	BLASTX
NCBI GI	g4098244
BLAST score	622
E value	5.0e-65
Match length	141
% identity	84
NCBI Description	(U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No.	201416
Seq. ID	LIB3048-020-Q1-L1-C5
Method	BLASTX
NCBI GI	g2231034
BLAST score	669
E value	2.0e-70
Match length	141
% identity	88
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]

Seq. No.	201417
Seq. ID	LIB3048-020-Q1-L1-C6
Method	BLASTX
NCBI GI	g3643611
BLAST score	464
E value	1.0e-46
Match length	121
% identity	74
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	201418
Seq. ID	LIB3048-020-Q1-L1-C7
Method	BLASTX
NCBI GI	g4539383
BLAST score	560
E value	1.0e-57
Match length	147
% identity	70
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No.	201419
Seq. ID	LIB3048-020-Q1-L1-C8
Method	BLASTX
NCBI GI	g2827548
BLAST score	329
E value	1.0e-30
Match length	131
% identity	47
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201420
Seq. ID	LIB3048-020-Q1-L1-C9
Method	BLASTX
NCBI GI	g2935298
BLAST score	551
E value	1.0e-56
Match length	144
% identity	78
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	201421
Seq. ID	LIB3048-020-Q1-L1-D11
Method	BLASTX
NCBI GI	g119640
BLAST score	353
E value	2.0e-33
Match length	125
% identity	54
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir__S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	201422
Seq. ID	LIB3048-020-Q1-L1-D2
Method	BLASTX
NCBI GI	g131276
BLAST score	504
E value	1.0e-64
Match length	137
% identity	94
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	201423
Seq. ID	LIB3048-020-Q1-L1-D5
Method	BLASTX
NCBI GI	g1620009
BLAST score	170

E value	5.0e-12
Match length	146
% identity	29
NCBI Description	(D85184) flavonoid 3',5'-hydroxylase [Gentiana triflora]

Seq. No.	201424
Seq. ID	LIB3048-020-Q1-L1-D6
Method	BLASTX
NCBI GI	g2062173
BLAST score	267
E value	1.0e-23
Match length	65
% identity	77
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	201425
Seq. ID	LIB3048-020-Q1-L1-D8
Method	BLASTX
NCBI GI	g729618
BLAST score	506
E value	1.0e-51
Match length	116
% identity	86
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP 2) >gi_82172_pir__PQ0262 luminal binding protein BLP-2 - common tobacco (fragment) >gi_100338_pir__S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment) >gi_19807_emb_CAA42661_ (X60059) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	201426
Seq. ID	LIB3048-020-Q1-L1-D9
Method	BLASTX
NCBI GI	g633110
BLAST score	275
E value	1.0e-24
Match length	102
% identity	56
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	201427
Seq. ID	LIB3048-020-Q1-L1-E1
Method	BLASTX
NCBI GI	g4512018
BLAST score	159
E value	7.0e-11
Match length	46
% identity	72
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	201428
Seq. ID	LIB3048-020-Q1-L1-E10
Method	BLASTX
NCBI GI	g1778370

BLAST score	600
E value	2.0e-62
Match length	142
% identity	79
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	201429
Seq. ID	LIB3048-020-Q1-L1-E2
Method	BLASTX
NCBI GI	g1708236
BLAST score	281
E value	3.0e-25
Match length	62
% identity	85
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	201430
Seq. ID	LIB3048-020-Q1-L1-E4
Method	BLASTX
NCBI GI	g2245020
BLAST score	214
E value	3.0e-17
Match length	98
% identity	44
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	201431
Seq. ID	LIB3048-020-Q1-L1-E6
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	93
% identity	84
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201432
Seq. ID	LIB3048-020-Q1-L1-E8
Method	BLASTX
NCBI GI	g4539330
BLAST score	329
E value	9.0e-31
Match length	118
% identity	57
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No. 201433
Seq. ID LIB3048-020-Q1-L1-E9
Method BLASTX
NCBI GI g3123745
BLAST score 249
E value 3.0e-21
Match length 68
% identity 71
NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 201434
Seq. ID LIB3048-020-Q1-L1-F11
Method BLASTX
NCBI GI g4455340
BLAST score 393
E value 4.0e-38
Match length 110
% identity 65
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 201435
Seq. ID LIB3048-020-Q1-L1-F12
Method BLASTX
NCBI GI g3044212
BLAST score 674
E value 4.0e-71
Match length 145
% identity 90
NCBI Description (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 201436
Seq. ID LIB3048-020-Q1-L1-F5
Method BLASTX
NCBI GI g4455210
BLAST score 184
E value 6.0e-14
Match length 91
% identity 45
NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No. 201437
Seq. ID LIB3048-020-Q1-L1-F6
Method BLASTX
NCBI GI g2369714
BLAST score 628
E value 9.0e-66
Match length 130
% identity 92
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 201438
Seq. ID LIB3048-020-Q1-L1-F7
Method BLASTX
NCBI GI g1332579
BLAST score 679
E value 1.0e-71

Match length	141
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	201439
Seq. ID	LIB3048-020-Q1-L1-F9
Method	BLASTX
NCBI GI	g3023751
BLAST score	354
E value	1.0e-33
Match length	111
% identity	27
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	201440
Seq. ID	LIB3048-020-Q1-L1-G10
Method	BLASTX
NCBI GI	g2980770
BLAST score	322
E value	6.0e-30
Match length	91
% identity	66
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	201441
Seq. ID	LIB3048-020-Q1-L1-G2
Method	BLASTX
NCBI GI	g3738334
BLAST score	176
E value	1.0e-12
Match length	113
% identity	44
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	201442
Seq. ID	LIB3048-020-Q1-L1-G3
Method	BLASTX
NCBI GI	g2827548
BLAST score	317
E value	3.0e-29
Match length	130
% identity	45
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201443
Seq. ID	LIB3048-020-Q1-L1-G4
Method	BLASTX
NCBI GI	g1856971
BLAST score	398
E value	5.0e-39
Match length	101
% identity	78

NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	201444
Seq. ID	LIB3048-020-Q1-L1-G5
Method	BLASTX
NCBI GI	g3894387
BLAST score	227
E value	1.0e-18
Match length	136
% identity	4
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	201445
Seq. ID	LIB3048-020-Q1-L1-G6
Method	BLASTX
NCBI GI	g1142619
BLAST score	375
E value	5.0e-36
Match length	136
% identity	59
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	201446
Seq. ID	LIB3048-020-Q1-L1-G7
Method	BLASTX
NCBI GI	g2739376
BLAST score	315
E value	2.0e-31
Match length	94
% identity	78
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	201447
Seq. ID	LIB3048-020-Q1-L1-G9
Method	BLASTX
NCBI GI	g2980770
BLAST score	520
E value	5.0e-53
Match length	116
% identity	84
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	201448
Seq. ID	LIB3048-020-Q1-L1-H11
Method	BLASTX
NCBI GI	g116359
BLAST score	517
E value	1.0e-52
Match length	135
% identity	73
NCBI Description	HEVAMINE A (CHITINASE / LYSOZYME >gi_82026_pir__S17205 chitinase (EC 3.2.1.14) hevamine - Para rubber tree >gi_234388_bbs_52808 hevamine [Hevea brasiliensis, Peptide Partial, 273 aa] >gi_1311006_pdb_1HVQ_ Glycosidase, Chitin

	Degradation, Multifunctional Enzyme Mol_id: 1; Molecule: Hevamine A; Chain: Null; Ec: 3.2.1.14, 3.2.1.17; Heterogen: N-,N'-,N''-Triacetyl-Chitotriose; Other_details: Plant EndochitinaseLYSOZYME >gi_1421554_pdb_1LLO_ Hevamine A (A Plant EndochitinaseLYSOZYME) COMPLEXED WITH Allosamidin >gi_1942537_pdb_2HVM_ Hevamine A At 1.8 Angstrom Resolution
Seq. No.	201449
Seq. ID	LIB3048-020-Q1-L1-H12
Method	BLASTX
NCBI GI	g3176690
BLAST score	530
E value	2.0e-54
Match length	113
% identity	85
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]
Seq. No.	201450
Seq. ID	LIB3048-020-Q1-L1-H3
Method	BLASTX
NCBI GI	g480725
BLAST score	639
E value	5.0e-67
Match length	138
% identity	79
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]
Seq. No.	201451
Seq. ID	LIB3048-020-Q1-L1-H4
Method	BLASTX
NCBI GI	g2894599
BLAST score	416
E value	5.0e-41
Match length	83
% identity	84
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	201452
Seq. ID	LIB3048-020-Q1-L1-H5
Method	BLASTX
NCBI GI	g2244760
BLAST score	199
E value	1.0e-15
Match length	70
% identity	28
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	201453
Seq. ID	LIB3048-021-Q1-L1-A10
Method	BLASTN

NCBI GI	g556421
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No.	201454
Seq. ID	LIB3048-021-Q1-L1-A11
Method	BLASTN
NCBI GI	g4220643
BLAST score	39
E value	2.0e-12
Match length	89
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	201455
Seq. ID	LIB3048-021-Q1-L1-A12
Method	BLASTX
NCBI GI	g3738298
BLAST score	269
E value	1.0e-23
Match length	140
% identity	46
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	201456
Seq. ID	LIB3048-021-Q1-L1-A2
Method	BLASTX
NCBI GI	g1706323
BLAST score	372
E value	1.0e-35
Match length	136
% identity	55
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	201457
Seq. ID	LIB3048-021-Q1-L1-A6
Method	BLASTX
NCBI GI	g3335351
BLAST score	450
E value	7.0e-45
Match length	135
% identity	9
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	201458

Seq. ID	LIB3048-021-Q1-L1-A8
Method	BLASTX
NCBI GI	g3164222
BLAST score	267
E value	2.0e-23
Match length	82
% identity	59
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	201459
Seq. ID	LIB3048-021-Q1-L1-A9
Method	BLASTX
NCBI GI	g4098128
BLAST score	657
E value	4.0e-69
Match length	143
% identity	89
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	201460
Seq. ID	LIB3048-021-Q1-L1-B10
Method	BLASTX
NCBI GI	g3115374
BLAST score	345
E value	2.0e-32
Match length	115
% identity	63
NCBI Description	(AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

Seq. No.	201461
Seq. ID	LIB3048-021-Q1-L1-B12
Method	BLASTX
NCBI GI	g130582
BLAST score	473
E value	1.0e-47
Match length	140
% identity	64
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	201462
Seq. ID	LIB3048-021-Q1-L1-B7
Method	BLASTX
NCBI GI	g4455340
BLAST score	398
E value	1.0e-38
Match length	110
% identity	65
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	201463
Seq. ID	LIB3048-021-Q1-L1-B8

Method	BLASTX
NCBI GI	g1002800
BLAST score	230
E value	3.0e-19
Match length	109
% identity	47
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	201464
Seq. ID	LIB3048-021-Q1-L1-B9
Method	BLASTX
NCBI GI	g3158376
BLAST score	485
E value	6.0e-49
Match length	129
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201465
Seq. ID	LIB3048-021-Q1-L1-C1
Method	BLASTX
NCBI GI	g2970691
BLAST score	162
E value	4.0e-11
Match length	85
% identity	46
NCBI Description	(AF052660) thioredoxin-related protein [Mus musculus]

Seq. No.	201466
Seq. ID	LIB3048-021-Q1-L1-C11
Method	BLASTX
NCBI GI	g2369766
BLAST score	448
E value	1.0e-44
Match length	123
% identity	67
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	201467
Seq. ID	LIB3048-021-Q1-L1-C12
Method	BLASTX
NCBI GI	g3420050
BLAST score	318
E value	2.0e-29
Match length	138
% identity	44
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201468
Seq. ID	LIB3048-021-Q1-L1-C4
Method	BLASTX
NCBI GI	g3746059
BLAST score	490
E value	1.0e-49
Match length	138
% identity	63
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201469
Seq. ID	LIB3048-021-Q1-L1-C5
Method	BLASTX
NCBI GI	g3132675
BLAST score	171
E value	3.0e-12
Match length	118
% identity	37
NCBI Description	(AF061740) asparagine synthetase [Elaeagnus umbellata]

Seq. No.	201470
Seq. ID	LIB3048-021-Q1-L1-C9
Method	BLASTX
NCBI GI	g3738257
BLAST score	670
E value	1.0e-70
Match length	144
% identity	90
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	201471
Seq. ID	LIB3048-021-Q1-L1-D10
Method	BLASTX
NCBI GI	g4539423
BLAST score	606
E value	4.0e-63
Match length	136
% identity	86
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	201472
Seq. ID	LIB3048-021-Q1-L1-D12
Method	BLASTX
NCBI GI	g3377848
BLAST score	404
E value	2.0e-39
Match length	142
% identity	56
NCBI Description	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No.	201473
Seq. ID	LIB3048-021-Q1-L1-D5
Method	BLASTX
NCBI GI	g464847
BLAST score	389
E value	8.0e-38
Match length	121
% identity	60
NCBI Description	TUBULIN ALPHA CHAIN >gi_397913_emb_CAA80497_ (Z22877) tubulin [Euglena gracilis]

Seq. No.	201474
Seq. ID	LIB3048-021-Q1-L1-D6
Method	BLASTX
NCBI GI	g135440
BLAST score	176
E value	8.0e-13
Match length	113
% identity	39
NCBI Description	TUBULIN ALPHA CHAIN >gi_71581_pir__UBUTA tubulin alpha chain - Trypanosoma brucei rhodesiense >gi_162320 (K02836) alpha tubulin [Trypanosoma brucei]

Seq. No.	201475
Seq. ID	LIB3048-021-Q1-L1-D9
Method	BLASTX
NCBI GI	g2462745
BLAST score	259
E value	2.0e-22
Match length	121
% identity	39
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	201476
Seq. ID	LIB3048-021-Q1-L1-E10
Method	BLASTX
NCBI GI	g2146797
BLAST score	597
E value	4.0e-62
Match length	143
% identity	77
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	201477
Seq. ID	LIB3048-021-Q1-L1-E11
Method	BLASTX
NCBI GI	g1332579
BLAST score	616
E value	3.0e-64
Match length	126
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	201478
Seq. ID	LIB3048-021-Q1-L1-E12
Method	BLASTX
NCBI GI	g542058
BLAST score	522
E value	3.0e-53
Match length	139
% identity	68
NCBI Description	HSR203J protein - common tobacco >gi_444002_emb_CAA54393_ (X77136) HSR203J [Nicotiana tabacum]

Seq. No.	201479

Seq. ID	LIB3048-021-Q1-L1-E2
Method	BLASTX
NCBI GI	g3158376
BLAST score	247
E value	4.0e-21
Match length	127
% identity	44
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201480
Seq. ID	LIB3048-021-Q1-L1-E4
Method	BLASTX
NCBI GI	g2827551
BLAST score	277
E value	1.0e-24
Match length	111
% identity	57
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	201481
Seq. ID	LIB3048-021-Q1-L1-E9
Method	BLASTX
NCBI GI	g2146797
BLAST score	571
E value	4.0e-59
Match length	132
% identity	80
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	201482
Seq. ID	LIB3048-021-Q1-L1-F11
Method	BLASTX
NCBI GI	g1361311
BLAST score	171
E value	4.0e-12
Match length	73
% identity	47
NCBI Description	CMP-2-keto-3-deoxyoctulosonic acid synthetase homolog - Chlamydia trachomatis >gi_557478 (U15192) CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia trachomatis]

Seq. No.	201483
Seq. ID	LIB3048-021-Q1-L1-F12
Method	BLASTX
NCBI GI	g4467145
BLAST score	228
E value	1.0e-23
Match length	73
% identity	81
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No. 201484

Seq. ID	LIB3048-021-Q1-L1-F2
Method	BLASTX
NCBI GI	g4455300
BLAST score	316
E value	5.0e-29
Match length	117
% identity	50
NCBI Description	(AL035528) putative pectate lyase A11 (fragment) [Arabidopsis thaliana]

Seq. No.	201485
Seq. ID	LIB3048-021-Q1-L1-F9
Method	BLASTX
NCBI GI	g544250
BLAST score	531
E value	2.0e-54
Match length	130
% identity	77
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	201486
Seq. ID	LIB3048-021-Q1-L1-G1
Method	BLASTX
NCBI GI	g3980380
BLAST score	386
E value	2.0e-37
Match length	86
% identity	91
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	201487
Seq. ID	LIB3048-021-Q1-L1-G4
Method	BLASTX
NCBI GI	g2827548
BLAST score	176
E value	8.0e-13
Match length	113
% identity	38
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201488
Seq. ID	LIB3048-021-Q1-L1-G7
Method	BLASTX
NCBI GI	g3746059
BLAST score	230
E value	4.0e-19
Match length	124
% identity	44
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201489
Seq. ID	LIB3048-021-Q1-L1-H11

Method	BLASTX
NCBI GI	g3461820
BLAST score	209
E value	1.0e-16
Match length	48
% identity	71
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	201490
Seq. ID	LIB3048-021-Q1-L1-H2
Method	BLASTX
NCBI GI	g732004
BLAST score	208
E value	1.0e-16
Match length	86
% identity	53
NCBI Description	HYPOTHETICAL 56.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION (O514) >gi_1361186_pir__S56384 hypothetical protein o514 - Escherichia coli >gi_537000 (U14003) ORF_o514 [Escherichia coli] >gi_1790600 (AE000488) putative transport [Escherichia coli]

Seq. No.	201491
Seq. ID	LIB3048-021-Q1-L1-H3
Method	BLASTX
NCBI GI	g732004
BLAST score	119
E value	4.0e-14
Match length	94
% identity	56
NCBI Description	HYPOTHETICAL 56.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION (O514) >gi_1361186_pir__S56384 hypothetical protein o514 - Escherichia coli >gi_537000 (U14003) ORF_o514 [Escherichia coli] >gi_1790600 (AE000488) putative transport [Escherichia coli]

Seq. No.	201492
Seq. ID	LIB3048-021-Q1-L1-H6
Method	BLASTX
NCBI GI	g3212865
BLAST score	401
E value	4.0e-39
Match length	126
% identity	67
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	201493
Seq. ID	LIB3048-021-Q1-L1-H8
Method	BLASTX
NCBI GI	g2642158
BLAST score	174
E value	7.0e-13
Match length	73
% identity	51
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201494

Seq. ID LIB3048-021-Q1-L1-H9
Method BLASTX
NCBI GI g1176658
BLAST score 184
E value 1.0e-13
Match length 72
% identity 51
NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No. 201495
Seq. ID LIB3048-022-Q1-L1-A10
Method BLASTX
NCBI GI g3738298
BLAST score 161
E value 5.0e-11
Match length 109
% identity 42
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 201496
Seq. ID LIB3048-022-Q1-L1-A3
Method BLASTX
NCBI GI g3738329
BLAST score 228
E value 2.0e-21
Match length 87
% identity 61
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 201497
Seq. ID LIB3048-022-Q1-L1-A4
Method BLASTX
NCBI GI g2062173
BLAST score 401
E value 4.0e-39
Match length 138
% identity 59
NCBI Description (AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No. 201498
Seq. ID LIB3048-022-Q1-L1-A5
Method BLASTX
NCBI GI g1001309
BLAST score 222
E value 4.0e-18
Match length 126
% identity 37
NCBI Description (D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No. 201499
Seq. ID LIB3048-022-Q1-L1-A6
Method BLASTX

NCBI GI	g2062173
BLAST score	377
E value	2.0e-36
Match length	114
% identity	68
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	201500
Seq. ID	LIB3048-022-Q1-L1-A7
Method	BLASTX
NCBI GI	g2623299
BLAST score	278
E value	1.0e-24
Match length	105
% identity	51
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201501
Seq. ID	LIB3048-022-Q1-L1-B1
Method	BLASTX
NCBI GI	g4239845
BLAST score	238
E value	5.0e-20
Match length	59
% identity	78
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	201502
Seq. ID	LIB3048-022-Q1-L1-B10
Method	BLASTX
NCBI GI	g99730
BLAST score	156
E value	2.0e-10
Match length	78
% identity	36
NCBI Description	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) >gi_1345512_emb_CAA37920_ (X53975) orf 3 [Arabidopsis thaliana]

Seq. No.	201503
Seq. ID	LIB3048-022-Q1-L1-B11
Method	BLASTX
NCBI GI	g3738257
BLAST score	158
E value	4.0e-14
Match length	88
% identity	56
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	201504
Seq. ID	LIB3048-022-Q1-L1-B12
Method	BLASTX
NCBI GI	g130582
BLAST score	422

E value	1.0e-41
Match length	127
% identity	62
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	201505
Seq. ID	LIB3048-022-Q1-L1-B3
Method	BLASTX
NCBI GI	g2465923
BLAST score	184
E value	3.0e-14
Match length	127
% identity	17
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	201506
Seq. ID	LIB3048-022-Q1-L1-B5
Method	BLASTX
NCBI GI	g584825
BLAST score	249
E value	2.0e-41
Match length	138
% identity	67
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	201507
Seq. ID	LIB3048-022-Q1-L1-B7
Method	BLASTX
NCBI GI	g2529703
BLAST score	608
E value	2.0e-63
Match length	142
% identity	83
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	201508
Seq. ID	LIB3048-022-Q1-L1-C2
Method	BLASTX
NCBI GI	g399064
BLAST score	537
E value	2.0e-62
Match length	131
% identity	82
NCBI Description	ASPARAGINE SYNTHASE (GLUTAMINE-HYDROLYZING) (AS) >gi_100980_pir__S25165 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - garden asparagus >gi_16076_emb_CAA48141_ (X67958) asparagine synthase (glutamine-hydrolysing) [Asparagus officinalis]

Seq. No.	201509
Seq. ID	LIB3048-022-Q1-L1-C3
Method	BLASTX
NCBI GI	g119006
BLAST score	411
E value	3.0e-40
Match length	117
% identity	70
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC ISOFORM ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_1197520_emb_CAA37289_ (X53129) 1,3,-beta-D-glucanase [Phaseolus vulgaris]

Seq. No.	201510
Seq. ID	LIB3048-022-Q1-L1-C4
Method	BLASTX
NCBI GI	g1709498
BLAST score	561
E value	7.0e-58
Match length	125
% identity	80
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201511
Seq. ID	LIB3048-022-Q1-L1-C5
Method	BLASTX
NCBI GI	g3461815
BLAST score	182
E value	2.0e-24
Match length	80
% identity	75
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201512
Seq. ID	LIB3048-022-Q1-L1-C8
Method	BLASTX
NCBI GI	g399064
BLAST score	683
E value	3.0e-72
Match length	134
% identity	95
NCBI Description	ASPARAGINE SYNTHASE (GLUTAMINE-HYDROLYZING) (AS) >gi_100980_pir__S25165 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - garden asparagus >gi_16076_emb_CAA48141_ (X67958) asparagine synthase (glutamine-hydrolysing) [Asparagus officinalis]

Seq. No.	201513
Seq. ID	LIB3048-022-Q1-L1-D1
Method	BLASTX
NCBI GI	g2443329
BLAST score	532
E value	2.0e-54
Match length	124

% identity	77
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	201514
Seq. ID	LIB3048-022-Q1-L1-D11
Method	BLASTX
NCBI GI	g2146797
BLAST score	350
E value	3.0e-33
Match length	125
% identity	54
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	201515
Seq. ID	LIB3048-022-Q1-L1-D2
Method	BLASTX
NCBI GI	g3218396
BLAST score	156
E value	2.0e-10
Match length	64
% identity	48
NCBI Description	(AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	201516
Seq. ID	LIB3048-022-Q1-L1-D7
Method	BLASTX
NCBI GI	g399064
BLAST score	449
E value	5.0e-45
Match length	92
% identity	91
NCBI Description	ASPARAGINE SYNTHASE (GLUTAMINE-HYDROLYZING) (AS) >gi_100980_pir__S25165 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - garden asparagus >gi_16076_emb_CAA48141_ (X67958) asparagine synthase (glutamine-hydrolysing) [Asparagus officinalis]

Seq. No.	201517
Seq. ID	LIB3048-022-Q1-L1-D8
Method	BLASTX
NCBI GI	g1174592
BLAST score	738
E value	1.0e-78
Match length	141
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	201518
Seq. ID	LIB3048-022-Q1-L1-E10
Method	BLASTX
NCBI GI	g542058
BLAST score	454

E value	2.0e-45
Match length	133
% identity	62
NCBI Description	HSR203J protein - common tobacco >gi_444002_emb_CAA54393_ (X77136) HSR203J [Nicotiana tabacum]

Seq. No.	201519
Seq. ID	LIB3048-022-Q1-L1-E11
Method	BLASTX
NCBI GI	g3126967
BLAST score	292
E value	2.0e-26
Match length	106
% identity	11
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No.	201520
Seq. ID	LIB3048-022-Q1-L1-E12
Method	BLASTX
NCBI GI	g4190952
BLAST score	490
E value	2.0e-49
Match length	138
% identity	67
NCBI Description	(AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No.	201521
Seq. ID	LIB3048-022-Q1-L1-E2
Method	BLASTX
NCBI GI	g3687237
BLAST score	483
E value	7.0e-49
Match length	96
% identity	82
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	201522
Seq. ID	LIB3048-022-Q1-L1-E3
Method	BLASTX
NCBI GI	g3075392
BLAST score	549
E value	2.0e-56
Match length	143
% identity	67
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	201523
Seq. ID	LIB3048-022-Q1-L1-E4
Method	BLASTX
NCBI GI	g3402693
BLAST score	155
E value	3.0e-10
Match length	88
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	201524
Seq. ID	LIB3048-022-Q1-L1-E5
Method	BLASTX
NCBI GI	g4558664
BLAST score	290
E value	4.0e-26
Match length	141
% identity	11
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201525
Seq. ID	LIB3048-022-Q1-L1-E7
Method	BLASTX
NCBI GI	g3892055
BLAST score	595
E value	7.0e-62
Match length	140
% identity	79
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	201526
Seq. ID	LIB3048-022-Q1-L1-E9
Method	BLASTX
NCBI GI	g2146797
BLAST score	463
E value	2.0e-46
Match length	125
% identity	68
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	201527
Seq. ID	LIB3048-022-Q1-L1-F2
Method	BLASTX
NCBI GI	g2597826
BLAST score	317
E value	3.0e-29
Match length	136
% identity	50
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	201528
Seq. ID	LIB3048-022-Q1-L1-F3
Method	BLASTX
NCBI GI	g481815
BLAST score	165
E value	2.0e-11
Match length	89
% identity	36
NCBI Description	vegetative storage protein - western balsam poplar x cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides]

Seq. No.	201529
Seq. ID	LIB3048-022-Q1-L1-F7
Method	BLASTX
NCBI GI	g1477428
BLAST score	751
E value	4.0e-80
Match length	141
% identity	98
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	201530
Seq. ID	LIB3048-022-Q1-L1-F8
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	107
% identity	82
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201531
Seq. ID	LIB3048-022-Q1-L1-G1
Method	BLASTX
NCBI GI	g1931650
BLAST score	150
E value	1.0e-09
Match length	143
% identity	34
NCBI Description	(U95973) disease resistance protein RPM1 isolog [Arabidopsis thaliana]

Seq. No.	201532
Seq. ID	LIB3048-022-Q1-L1-G2
Method	BLASTX
NCBI GI	g3925703
BLAST score	289
E value	8.0e-54
Match length	130
% identity	85
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	201533
Seq. ID	LIB3048-022-Q1-L1-G3
Method	BLASTX
NCBI GI	g3126967
BLAST score	176
E value	4.0e-13
Match length	80
% identity	9
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No.	201534
Seq. ID	LIB3048-022-Q1-L1-G4
Method	BLASTX

NCBI GI	g2499946
BLAST score	637
E value	9.0e-67
Match length	134
% identity	90
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	201535
Seq. ID	LIB3048-022-Q1-L1-G5
Method	BLASTX
NCBI GI	g3461820
BLAST score	216
E value	2.0e-17
Match length	61
% identity	61
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	201536
Seq. ID	LIB3048-022-Q1-L1-G6
Method	BLASTX
NCBI GI	g2499946
BLAST score	428
E value	2.0e-42
Match length	110
% identity	75
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	201537
Seq. ID	LIB3048-022-Q1-L1-H1
Method	BLASTX
NCBI GI	g4530126
BLAST score	171
E value	3.0e-12
Match length	111
% identity	41
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	201538
Seq. ID	LIB3048-022-Q1-L1-H2
Method	BLASTX
NCBI GI	g2597826
BLAST score	176
E value	7.0e-13
Match length	57
% identity	56
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	201539
Seq. ID	LIB3048-022-Q1-L1-H5
Method	BLASTX

NCBI GI	g543867
BLAST score	222
E value	3.0e-18
Match length	77
% identity	71
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	201540
Seq. ID	LIB3048-023-Q1-L1-A1
Method	BLASTX
NCBI GI	g4185515
BLAST score	185
E value	3.0e-14
Match length	72
% identity	57
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	201541
Seq. ID	LIB3048-023-Q1-L1-A3
Method	BLASTX
NCBI GI	g464846
BLAST score	522
E value	3.0e-53
Match length	103
% identity	93
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	201542
Seq. ID	LIB3048-023-Q1-L1-A6
Method	BLASTX
NCBI GI	g4262174
BLAST score	571
E value	5.0e-59
Match length	139
% identity	71
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	201543
Seq. ID	LIB3048-023-Q1-L1-A7
Method	BLASTX
NCBI GI	g1143322
BLAST score	634
E value	2.0e-66
Match length	140
% identity	82
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	201544
Seq. ID	LIB3048-023-Q1-L1-B1
Method	BLASTX

NCBI GI	g2281115
BLAST score	526
E value	9.0e-54
Match length	131
% identity	79
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201545
Seq. ID	LIB3048-023-Q1-L1-B2
Method	BLASTX
NCBI GI	g1706323
BLAST score	245
E value	2.0e-21
Match length	75
% identity	60
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	201546
Seq. ID	LIB3048-023-Q1-L1-B3
Method	BLASTX
NCBI GI	g1709498
BLAST score	478
E value	4.0e-48
Match length	120
% identity	74
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201547
Seq. ID	LIB3048-023-Q1-L1-B5
Method	BLASTX
NCBI GI	g1709498
BLAST score	567
E value	1.0e-58
Match length	135
% identity	76
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201548
Seq. ID	LIB3048-023-Q1-L1-B7
Method	BLASTX
NCBI GI	g4454051
BLAST score	322
E value	8.0e-30
Match length	125
% identity	53
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	201549
Seq. ID	LIB3048-023-Q1-L1-B8
Method	BLASTX
NCBI GI	g3080400
BLAST score	521
E value	3.0e-53
Match length	125
% identity	78
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	201550
Seq. ID	LIB3048-023-Q1-L1-C5
Method	BLASTX
NCBI GI	g4102703
BLAST score	299
E value	4.0e-27
Match length	102
% identity	65
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	201551
Seq. ID	LIB3048-023-Q1-L1-C7
Method	BLASTX
NCBI GI	g285741
BLAST score	391
E value	4.0e-38
Match length	98
% identity	73
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	201552
Seq. ID	LIB3048-023-Q1-L1-C8
Method	BLASTX
NCBI GI	g927428
BLAST score	414
E value	1.0e-40
Match length	121
% identity	69
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	201553
Seq. ID	LIB3048-023-Q1-L1-D1
Method	BLASTX
NCBI GI	g484656
BLAST score	142
E value	3.0e-09
Match length	73
% identity	48
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	201554

Seq. ID	LIB3048-023-Q1-L1-D3
Method	BLASTX
NCBI GI	g3540200
BLAST score	216
E value	2.0e-17
Match length	84
% identity	51
NCBI Description	(AC004260) Similar to TINY [Arabidopsis thaliana]

Seq. No.	201555
Seq. ID	LIB3048-023-Q1-L1-D4
Method	BLASTX
NCBI GI	g3821280
BLAST score	476
E value	5.0e-48
Match length	117
% identity	78
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	201556
Seq. ID	LIB3048-023-Q1-L1-D5
Method	BLASTX
NCBI GI	g2829923
BLAST score	167
E value	6.0e-12
Match length	99
% identity	40
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	201557
Seq. ID	LIB3048-023-Q1-L1-D6
Method	BLASTX
NCBI GI	g4539383
BLAST score	173
E value	2.0e-12
Match length	130
% identity	38
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	201558
Seq. ID	LIB3048-023-Q1-L1-D7
Method	BLASTX
NCBI GI	g1709804
BLAST score	471
E value	2.0e-47
Match length	128
% identity	71
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No. 201559

Seq. ID	LIB3048-023-Q1-L1-D8
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	101
% identity	83
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201560
Seq. ID	LIB3048-023-Q1-L1-E1
Method	BLASTX
NCBI GI	g4158232
BLAST score	701
E value	3.0e-74
Match length	140
% identity	89
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	201561
Seq. ID	LIB3048-023-Q1-L1-E2
Method	BLASTX
NCBI GI	g3451147
BLAST score	533
E value	1.0e-54
Match length	139
% identity	73
NCBI Description	(AJ010397) chitinase [Hevea brasiliensis]

Seq. No.	201562
Seq. ID	LIB3048-023-Q1-L1-E3
Method	BLASTX
NCBI GI	g4512685
BLAST score	256
E value	4.0e-22
Match length	130
% identity	43
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201563
Seq. ID	LIB3048-023-Q1-L1-E4
Method	BLASTX
NCBI GI	g2462826
BLAST score	418
E value	4.0e-41
Match length	145
% identity	54
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	201564
Seq. ID	LIB3048-023-Q1-L1-E5

Method	BLASTX
NCBI GI	g1644427
BLAST score	473
E value	1.0e-47
Match length	114
% identity	81
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	201565
Seq. ID	LIB3048-023-Q1-L1-E6
Method	BLASTX
NCBI GI	g4455199
BLAST score	370
E value	2.0e-35
Match length	92
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	201566
Seq. ID	LIB3048-023-Q1-L1-E7
Method	BLASTX
NCBI GI	g2894599
BLAST score	517
E value	1.0e-52
Match length	108
% identity	84
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	201567
Seq. ID	LIB3048-023-Q1-L1-E8
Method	BLASTX
NCBI GI	g2129597
BLAST score	583
E value	2.0e-60
Match length	119
% identity	93
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201568
Seq. ID	LIB3048-023-Q1-L1-F2
Method	BLASTX
NCBI GI	g3738316
BLAST score	335
E value	2.0e-31
Match length	92
% identity	68
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	201569
Seq. ID	LIB3048-023-Q1-L1-F5
Method	BLASTX
NCBI GI	g3894391
BLAST score	207
E value	2.0e-16

Match length	130
% identity	4
NCBI Description	(AF053997) Hcr2-5B [Lycopersicon esculentum]

Seq. No.	201570
Seq. ID	LIB3048-023-Q1-L1-F6
Method	BLASTX
NCBI GI	g2911059
BLAST score	631
E value	5.0e-66
Match length	146
% identity	87
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201571
Seq. ID	LIB3048-023-Q1-L1-F7
Method	BLASTN
NCBI GI	g4165340
BLAST score	38
E value	6.0e-12
Match length	185
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	201572
Seq. ID	LIB3048-023-Q1-L1-G3
Method	BLASTX
NCBI GI	g2739376
BLAST score	230
E value	4.0e-21
Match length	79
% identity	70
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	201573
Seq. ID	LIB3048-023-Q1-L1-G4
Method	BLASTX
NCBI GI	g3096919
BLAST score	333
E value	1.0e-47
Match length	110
% identity	86
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	201574
Seq. ID	LIB3048-023-Q1-L1-G5
Method	BLASTX
NCBI GI	g3420906
BLAST score	237
E value	1.0e-21
Match length	72
% identity	58
NCBI Description	(AF080595) zinc finger protein; WRKY1 [Pimpinella brachycarpa]

Seq. No.	201575
Seq. ID	LIB3048-023-Q1-L1-G6
Method	BLASTX
NCBI GI	g1407705
BLAST score	613
E value	6.0e-64
Match length	137
% identity	83
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	201576
Seq. ID	LIB3048-023-Q1-L1-G7
Method	BLASTX
NCBI GI	g2317906
BLAST score	373
E value	8.0e-36
Match length	76
% identity	96
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	201577
Seq. ID	LIB3048-023-Q1-L1-G8
Method	BLASTX
NCBI GI	g4415908
BLAST score	163
E value	3.0e-11
Match length	48
% identity	54
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	201578
Seq. ID	LIB3048-023-Q1-L1-H4
Method	BLASTX
NCBI GI	g1703200
BLAST score	394
E value	2.0e-38
Match length	111
% identity	72
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	201579
Seq. ID	LIB3048-023-Q1-L1-H7
Method	BLASTX
NCBI GI	g1777312
BLAST score	403
E value	2.0e-39
Match length	112
% identity	70
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	201580
Seq. ID	LIB3048-024-Q1-L1-A2

Method	BLASTX
NCBI GI	g1777386
BLAST score	368
E value	3.0e-35
Match length	141
% identity	48
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	201581
Seq. ID	LIB3048-024-Q1-L1-A3
Method	BLASTX
NCBI GI	g3493367
BLAST score	323
E value	3.0e-30
Match length	88
% identity	74
NCBI Description	(AB017159) citrate synthase [Daucus carota]

Seq. No.	201582
Seq. ID	LIB3048-024-Q1-L1-A8
Method	BLASTX
NCBI GI	g1486472
BLAST score	570
E value	7.0e-59
Match length	126
% identity	88
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	201583
Seq. ID	LIB3048-024-Q1-L1-B1
Method	BLASTX
NCBI GI	g1076746
BLAST score	350
E value	1.0e-33
Match length	80
% identity	90
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	201584
Seq. ID	LIB3048-024-Q1-L1-B2
Method	BLASTX
NCBI GI	g3193316
BLAST score	662
E value	1.0e-69
Match length	147
% identity	84
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	201585
Seq. ID	LIB3048-024-Q1-L1-B3
Method	BLASTX
NCBI GI	g2507422
BLAST score	314

E value	7.0e-29
Match length	135
% identity	69
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201586
Seq. ID	LIB3048-024-Q1-L1-B4
Method	BLASTX
NCBI GI	g4510340
BLAST score	283
E value	3.0e-25
Match length	129
% identity	41
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201587
Seq. ID	LIB3048-024-Q1-L1-B5
Method	BLASTX
NCBI GI	g3493172
BLAST score	548
E value	2.0e-56
Match length	108
% identity	98
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	201588
Seq. ID	LIB3048-024-Q1-L1-B7
Method	BLASTX
NCBI GI	g2739381
BLAST score	411
E value	2.0e-40
Match length	114
% identity	68
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	201589
Seq. ID	LIB3048-024-Q1-L1-B8
Method	BLASTX
NCBI GI	g4538913
BLAST score	199
E value	2.0e-15
Match length	42
% identity	86
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	201590
Seq. ID	LIB3048-024-Q1-L1-C2
Method	BLASTX
NCBI GI	g542058
BLAST score	531
E value	3.0e-54
Match length	144
% identity	67
NCBI Description	HSR203J protein - common tobacco >gi_444002_emb_CAA54393_

(X77136) HSR203J [Nicotiana tabacum]

Seq. No.	201591
Seq. ID	LIB3048-024-Q1-L1-C5
Method	BLASTX
NCBI GI	g1407705
BLAST score	146
E value	5.0e-20
Match length	90
% identity	68
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	201592
Seq. ID	LIB3048-024-Q1-L1-C6
Method	BLASTX
NCBI GI	g4454012
BLAST score	328
E value	1.0e-30
Match length	113
% identity	61
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	201593
Seq. ID	LIB3048-024-Q1-L1-C7
Method	BLASTX
NCBI GI	g2960364
BLAST score	636
E value	1.0e-66
Match length	132
% identity	89
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	201594
Seq. ID	LIB3048-024-Q1-L1-C8
Method	BLASTX
NCBI GI	g1220196
BLAST score	350
E value	3.0e-33
Match length	86
% identity	83
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	201595
Seq. ID	LIB3048-024-Q1-L1-D3
Method	BLASTX
NCBI GI	g3660469
BLAST score	158
E value	1.0e-10
Match length	39
% identity	74
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	201596

Seq. ID	LIB3048-024-Q1-L1-D4
Method	BLASTX
NCBI GI	g2407617
BLAST score	226
E value	1.0e-18
Match length	91
% identity	53
NCBI Description	(AF017984) glutathione synthetase [Lycopersicon esculentum]

Seq. No.	201597
Seq. ID	LIB3048-024-Q1-L1-D6
Method	BLASTX
NCBI GI	g4140598
BLAST score	553
E value	5.0e-57
Match length	128
% identity	84
NCBI Description	(AF090148) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	201598
Seq. ID	LIB3048-024-Q1-L1-D7
Method	BLASTX
NCBI GI	g3551991
BLAST score	211
E value	7.0e-17
Match length	89
% identity	53
NCBI Description	(AF085077) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551993 (AF085078) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140618 (AF090158) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	201599
Seq. ID	LIB3048-024-Q1-L1-D8
Method	BLASTX
NCBI GI	g2459419
BLAST score	152
E value	7.0e-10
Match length	124
% identity	35
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201600
Seq. ID	LIB3048-024-Q1-L1-E3
Method	BLASTX
NCBI GI	g477819
BLAST score	397
E value	7.0e-39
Match length	104
% identity	73
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	201601

Seq. ID	LIB3048-024-Q1-L1-E6
Method	BLASTX
NCBI GI	g633110
BLAST score	671
E value	9.0e-71
Match length	137
% identity	95
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	201602
Seq. ID	LIB3048-024-Q1-L1-E7
Method	BLASTX
NCBI GI	g1946359
BLAST score	357
E value	6.0e-34
Match length	131
% identity	54
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	201603
Seq. ID	LIB3048-024-Q1-L1-E8
Method	BLASTX
NCBI GI	g4204265
BLAST score	430
E value	2.0e-42
Match length	146
% identity	60
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	201604
Seq. ID	LIB3048-024-Q1-L1-F6
Method	BLASTX
NCBI GI	g543905
BLAST score	594
E value	9.0e-62
Match length	132
% identity	84
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	201605
Seq. ID	LIB3048-024-Q1-L1-F8
Method	BLASTX
NCBI GI	g421924
BLAST score	386
E value	2.0e-37
Match length	129
% identity	59
NCBI Description	peroxidase (EC 1.11.1.7) - tomato >gi_296910_emb_CAA50597_ (X71593) peroxidase [Lycopersicon esculentum]

Seq. No.	201606
Seq. ID	LIB3048-024-Q1-L1-G2
Method	BLASTX
NCBI GI	g300265
BLAST score	554
E value	4.0e-57

Match length	126
% identity	88
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	201607
Seq. ID	LIB3048-024-Q1-L1-G3
Method	BLASTX
NCBI GI	g3044212
BLAST score	494
E value	5.0e-50
Match length	138
% identity	73
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	201608
Seq. ID	LIB3048-024-Q1-L1-G4
Method	BLASTX
NCBI GI	g1706082
BLAST score	223
E value	3.0e-18
Match length	131
% identity	44
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	201609
Seq. ID	LIB3048-024-Q1-L1-G5
Method	BLASTX
NCBI GI	g4530126
BLAST score	146
E value	3.0e-09
Match length	135
% identity	29
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	201610
Seq. ID	LIB3048-024-Q1-L1-G7
Method	BLASTX
NCBI GI	g2739376
BLAST score	234
E value	1.0e-21
Match length	100
% identity	59
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	201611
Seq. ID	LIB3048-024-Q1-L1-H1
Method	BLASTX
NCBI GI	g4337195
BLAST score	646

E value	8.0e-68
Match length	147
% identity	86
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	201612
Seq. ID	LIB3048-024-Q1-L1-H4
Method	BLASTX
NCBI GI	g2129495
BLAST score	151
E value	4.0e-10
Match length	70
% identity	50
NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]

Seq. No.	201613
Seq. ID	LIB3048-024-Q1-L1-H5
Method	BLASTX
NCBI GI	g2506139
BLAST score	321
E value	1.0e-29
Match length	82
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	201614
Seq. ID	LIB3048-024-Q1-L1-H6
Method	BLASTX
NCBI GI	g3132696
BLAST score	659
E value	2.0e-69
Match length	147
% identity	86
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201615
Seq. ID	LIB3048-024-Q1-L1-H7
Method	BLASTX
NCBI GI	g1895084
BLAST score	302
E value	2.0e-27
Match length	61
% identity	92
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	201616
Seq. ID	LIB3048-025-Q1-L1-A1
Method	BLASTX
NCBI GI	g1071912
BLAST score	346
E value	5.0e-52
Match length	131
% identity	83

NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	201617
Seq. ID	LIB3048-025-Q1-L1-A12
Method	BLASTX
NCBI GI	g2618699
BLAST score	176
E value	1.0e-12
Match length	59
% identity	54
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	201618
Seq. ID	LIB3048-025-Q1-L1-A2
Method	BLASTX
NCBI GI	g4567095
BLAST score	470
E value	3.0e-47
Match length	129
% identity	64
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	201619
Seq. ID	LIB3048-025-Q1-L1-A4
Method	BLASTX
NCBI GI	g3123745
BLAST score	249
E value	3.0e-21
Match length	68
% identity	71
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	201620
Seq. ID	LIB3048-025-Q1-L1-A5
Method	BLASTX
NCBI GI	g4567260
BLAST score	531
E value	2.0e-54
Match length	135
% identity	73
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	201621
Seq. ID	LIB3048-025-Q1-L1-A7
Method	BLASTX
NCBI GI	g1871192
BLAST score	377
E value	3.0e-36
Match length	144
% identity	63
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

09604.0004.PCUS00

Seq. No.	201622
Seq. ID	LIB3048-025-Q1-L1-A8
Method	BLASTX
NCBI GI	g477819
BLAST score	495
E value	4.0e-50
Match length	122
% identity	76
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	201623
Seq. ID	LIB3048-025-Q1-L1-B1
Method	BLASTX
NCBI GI	g3892055
BLAST score	356
E value	8.0e-34
Match length	104
% identity	68
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	201624
Seq. ID	LIB3048-025-Q1-L1-B12
Method	BLASTX
NCBI GI	g2230757
BLAST score	308
E value	3.0e-28
Match length	119
% identity	55
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	201625
Seq. ID	LIB3048-025-Q1-L1-B3
Method	BLASTX
NCBI GI	g2558512
BLAST score	149
E value	1.0e-09
Match length	92
% identity	45
NCBI Description	(AJ002020) proton pump interactor [Arabidopsis thaliana]

Seq. No.	201626
Seq. ID	LIB3048-025-Q1-L1-B4
Method	BLASTX
NCBI GI	g4218535
BLAST score	499
E value	1.0e-50
Match length	133
% identity	66
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	201627
Seq. ID	LIB3048-025-Q1-L1-B5

Method	BLASTX
NCBI GI	g1709498
BLAST score	561
E value	7.0e-58
Match length	125
% identity	80
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201628
Seq. ID	LIB3048-025-Q1-L1-B7
Method	BLASTX
NCBI GI	g132944
BLAST score	567
E value	1.0e-58
Match length	144
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	201629
Seq. ID	LIB3048-025-Q1-L1-B8
Method	BLASTX
NCBI GI	g3329294
BLAST score	149
E value	2.0e-09
Match length	129
% identity	29
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	201630
Seq. ID	LIB3048-025-Q1-L1-B9
Method	BLASTX
NCBI GI	g3763933
BLAST score	145
E value	3.0e-09
Match length	48
% identity	62
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	201631
Seq. ID	LIB3048-025-Q1-L1-C1
Method	BLASTX
NCBI GI	g2495209
BLAST score	159
E value	1.0e-10
Match length	57
% identity	53
NCBI Description	HYPOTHETICAL 12.9 KD PROTEIN SLR1417 >gi_1651819_dbj_BAA16746_ (D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	201632

Seq. ID LIB3048-025-Q1-L1-C11
Method BLASTX
NCBI GI g1001309
BLAST score 220
E value 7.0e-18
Match length 126
% identity 37
NCBI Description (D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No. 201633
Seq. ID LIB3048-025-Q1-L1-C12
Method BLASTX
NCBI GI g3329294
BLAST score 147
E value 3.0e-09
Match length 129
% identity 29
NCBI Description (AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No. 201634
Seq. ID LIB3048-025-Q1-L1-C2
Method BLASTX
NCBI GI g1332579
BLAST score 667
E value 3.0e-70
Match length 136
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 201635
Seq. ID LIB3048-025-Q1-L1-C4
Method BLASTX
NCBI GI g3738319
BLAST score 590
E value 3.0e-61
Match length 131
% identity 81
NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201636
Seq. ID LIB3048-025-Q1-L1-C5
Method BLASTX
NCBI GI g2911059
BLAST score 419
E value 3.0e-41
Match length 116
% identity 72
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 201637
Seq. ID LIB3048-025-Q1-L1-C6
Method BLASTX
NCBI GI g4138647
BLAST score 623
E value 4.0e-65
Match length 147

% identity	79
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	201638
Seq. ID	LIB3048-025-Q1-L1-D1
Method	BLASTX
NCBI GI	g2281115
BLAST score	562
E value	5.0e-58
Match length	134
% identity	82
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201639
Seq. ID	LIB3048-025-Q1-L1-D10
Method	BLASTX
NCBI GI	g3080424
BLAST score	679
E value	1.0e-71
Match length	142
% identity	89
NCBI Description	(AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	201640
Seq. ID	LIB3048-025-Q1-L1-D12
Method	BLASTX
NCBI GI	g1841464
BLAST score	317
E value	3.0e-29
Match length	61
% identity	47
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	201641
Seq. ID	LIB3048-025-Q1-L1-D2
Method	BLASTX
NCBI GI	g3122914
BLAST score	530
E value	3.0e-54
Match length	149
% identity	66
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	201642
Seq. ID	LIB3048-025-Q1-L1-D3
Method	BLASTX
NCBI GI	g2864609
BLAST score	235
E value	1.0e-22
Match length	98
% identity	60
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No.	201643
Seq. ID	LIB3048-025-Q1-L1-D4
Method	BLASTX
NCBI GI	g3763933
BLAST score	390
E value	7.0e-38
Match length	138
% identity	72
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	201644
Seq. ID	LIB3048-025-Q1-L1-D5
Method	BLASTX
NCBI GI	g1169534
BLAST score	538
E value	4.0e-55
Match length	121
% identity	87
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus communis]

Seq. No.	201645
Seq. ID	LIB3048-025-Q1-L1-D6
Method	BLASTX
NCBI GI	g3540180
BLAST score	300
E value	3.0e-27
Match length	141
% identity	53
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	201646
Seq. ID	LIB3048-025-Q1-L1-D7
Method	BLASTX
NCBI GI	g3924597
BLAST score	209
E value	1.0e-16
Match length	112
% identity	35
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	201647
Seq. ID	LIB3048-025-Q1-L1-D8
Method	BLASTX
NCBI GI	g1698548
BLAST score	636
E value	1.0e-66
Match length	146
% identity	81
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 201648

Seq. ID	LIB3048-025-Q1-L1-E10
Method	BLASTX
NCBI GI	g4115371
BLAST score	177
E value	8.0e-13
Match length	111
% identity	39
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	201649
Seq. ID	LIB3048-025-Q1-L1-E11
Method	BLASTX
NCBI GI	g3043415
BLAST score	689
E value	7.0e-73
Match length	141
% identity	97
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	201650
Seq. ID	LIB3048-025-Q1-L1-E2
Method	BLASTX
NCBI GI	g3687223
BLAST score	322
E value	8.0e-30
Match length	147
% identity	54
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201651
Seq. ID	LIB3048-025-Q1-L1-E5
Method	BLASTX
NCBI GI	g2739044
BLAST score	610
E value	1.0e-63
Match length	145
% identity	75
NCBI Description	(AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]

Seq. No.	201652
Seq. ID	LIB3048-025-Q1-L1-E8
Method	BLASTX
NCBI GI	g4204265
BLAST score	234
E value	2.0e-19
Match length	121
% identity	45
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	201653
Seq. ID	LIB3048-025-Q1-L1-E9
Method	BLASTX
NCBI GI	g2827711
BLAST score	466
E value	6.0e-47
Match length	108

% identity	80
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	201654
Seq. ID	LIB3048-025-Q1-L1-F1
Method	BLASTX
NCBI GI	g3451072
BLAST score	276
E value	2.0e-24
Match length	80
% identity	59
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	201655
Seq. ID	LIB3048-025-Q1-L1-F10
Method	BLASTX
NCBI GI	g1345979
BLAST score	322
E value	8.0e-30
Match length	128
% identity	52
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No.	201656
Seq. ID	LIB3048-025-Q1-L1-F11
Method	BLASTX
NCBI GI	g3687237
BLAST score	508
E value	1.0e-51
Match length	96
% identity	85
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	201657
Seq. ID	LIB3048-025-Q1-L1-F12
Method	BLASTX
NCBI GI	g4325338
BLAST score	663
E value	8.0e-70
Match length	141
% identity	84
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	201658
Seq. ID	LIB3048-025-Q1-L1-F2
Method	BLASTX
NCBI GI	g3451072
BLAST score	338
E value	1.0e-31
Match length	101
% identity	60
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	201659
Seq. ID	LIB3048-025-Q1-L1-F3
Method	BLASTX
NCBI GI	g3252806
BLAST score	234
E value	2.0e-19
Match length	117
% identity	37
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201660
Seq. ID	LIB3048-025-Q1-L1-F4
Method	BLASTN
NCBI GI	g3702724
BLAST score	39
E value	2.0e-12
Match length	83
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	201661
Seq. ID	LIB3048-025-Q1-L1-F5
Method	BLASTX
NCBI GI	g2827548
BLAST score	339
E value	8.0e-32
Match length	146
% identity	46
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201662
Seq. ID	LIB3048-025-Q1-L1-F6
Method	BLASTX
NCBI GI	g4567095
BLAST score	506
E value	2.0e-51
Match length	134
% identity	66
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	201663
Seq. ID	LIB3048-025-Q1-L1-F7
Method	BLASTX
NCBI GI	g3894387
BLAST score	236
E value	1.0e-19
Match length	139
% identity	3
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	201664
Seq. ID	LIB3048-025-Q1-L1-F8
Method	BLASTX
NCBI GI	g2498706

BLAST score 150
E value 4.0e-13
Match length 63
% identity 60
NCBI Description ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No. 201665
Seq. ID LIB3048-025-Q1-L1-G1
Method BLASTX
NCBI GI g3953467
BLAST score 655
E value 7.0e-69
Match length 145
% identity 43
NCBI Description (AC002328) F20N2.12 [Arabidopsis thaliana]

Seq. No. 201666
Seq. ID LIB3048-025-Q1-L1-G10
Method BLASTX
NCBI GI g2462745
BLAST score 217
E value 7.0e-19
Match length 121
% identity 38
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 201667
Seq. ID LIB3048-025-Q1-L1-G11
Method BLASTX
NCBI GI g2245060
BLAST score 265
E value 4.0e-23
Match length 73
% identity 66
NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 201668
Seq. ID LIB3048-025-Q1-L1-G3
Method BLASTX
NCBI GI g2129597
BLAST score 578
E value 7.0e-60
Match length 118
% identity 93
NCBI Description glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No. 201669
Seq. ID LIB3048-025-Q1-L1-G6
Method BLASTX
NCBI GI g2864609
BLAST score 250

E value	2.0e-21
Match length	100
% identity	51
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	201670
Seq. ID	LIB3048-025-Q1-L1-G7
Method	BLASTX
NCBI GI	g475048
BLAST score	607
E value	3.0e-63
Match length	130
% identity	63
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No.	201671
Seq. ID	LIB3048-025-Q1-L1-G8
Method	BLASTX
NCBI GI	g3763933
BLAST score	201
E value	1.0e-15
Match length	68
% identity	60
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	201672
Seq. ID	LIB3048-025-Q1-L1-H1
Method	BLASTX
NCBI GI	g2827548
BLAST score	303
E value	2.0e-28
Match length	145
% identity	48
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201673
Seq. ID	LIB3048-025-Q1-L1-H10
Method	BLASTX
NCBI GI	g3421090
BLAST score	568
E value	1.0e-58
Match length	121
% identity	93
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	201674
Seq. ID	LIB3048-025-Q1-L1-H3
Method	BLASTX
NCBI GI	g4490330
BLAST score	692
E value	3.0e-73
Match length	146

% identity	92
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	201675
Seq. ID	LIB3048-025-Q1-L1-H6
Method	BLASTX
NCBI GI	g1709804
BLAST score	485
E value	5.0e-49
Match length	129
% identity	72
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	201676
Seq. ID	LIB3048-025-Q1-L1-H9
Method	BLASTX
NCBI GI	g1518540
BLAST score	315
E value	4.0e-29
Match length	107
% identity	62
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	201677
Seq. ID	LIB3048-026-Q1-L1-A1
Method	BLASTX
NCBI GI	g2980641
BLAST score	250
E value	2.0e-21
Match length	108
% identity	44
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	201678
Seq. ID	LIB3048-026-Q1-L1-A10
Method	BLASTX
NCBI GI	g4092526
BLAST score	495
E value	4.0e-50
Match length	140
% identity	69
NCBI Description	(AF092088) putative ethylene receptor [Citrus sinensis]

Seq. No.	201679
Seq. ID	LIB3048-026-Q1-L1-A11
Method	BLASTX
NCBI GI	g2506139
BLAST score	169
E value	5.0e-12
Match length	57
% identity	65
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
archain/delta-COP [Oryza sativa]

Seq. No.	201680
Seq. ID	LIB3048-026-Q1-L1-A12
Method	BLASTX
NCBI GI	g3116212
BLAST score	294
E value	1.0e-26
Match length	138
% identity	49
NCBI Description	(AB004797) homeobox gene [Nicotiana tabacum]

Seq. No.	201681
Seq. ID	LIB3048-026-Q1-L1-A2
Method	BLASTX
NCBI GI	g2231034
BLAST score	319
E value	2.0e-54
Match length	133
% identity	77
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]

Seq. No.	201682
Seq. ID	LIB3048-026-Q1-L1-A4
Method	BLASTX
NCBI GI	g1667373
BLAST score	292
E value	2.0e-28
Match length	108
% identity	65
NCBI Description	(X82270) protein kinase [Medicago sativa]

Seq. No.	201683
Seq. ID	LIB3048-026-Q1-L1-A5
Method	BLASTX
NCBI GI	g3540200
BLAST score	213
E value	5.0e-17
Match length	84
% identity	51
NCBI Description	(AC004260) Similar to TINY [Arabidopsis thaliana]

Seq. No.	201684
Seq. ID	LIB3048-026-Q1-L1-A9
Method	BLASTX
NCBI GI	g1708236
BLAST score	198
E value	1.0e-17
Match length	75
% identity	59
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

>gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	201685
Seq. ID	LIB3048-026-Q1-L1-B1
Method	BLASTX
NCBI GI	g2739376
BLAST score	237
E value	5.0e-23
Match length	77
% identity	77
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	201686
Seq. ID	LIB3048-026-Q1-L1-B10
Method	BLASTX
NCBI GI	g3236478
BLAST score	408
E value	4.0e-40
Match length	88
% identity	94
NCBI Description	(AF071196) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	201687
Seq. ID	LIB3048-026-Q1-L1-B11
Method	BLASTX
NCBI GI	g2252830
BLAST score	232
E value	2.0e-19
Match length	80
% identity	60
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	201688
Seq. ID	LIB3048-026-Q1-L1-B12
Method	BLASTX
NCBI GI	g2440035
BLAST score	499
E value	8.0e-51
Match length	104
% identity	85
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	201689
Seq. ID	LIB3048-026-Q1-L1-B3
Method	BLASTX
NCBI GI	g3377797
BLAST score	564
E value	3.0e-58
Match length	141
% identity	79
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No.	201690
Seq. ID	LIB3048-026-Q1-L1-B4
Method	BLASTX
NCBI GI	g4104242
BLAST score	620
E value	9.0e-65
Match length	145
% identity	83
NCBI Description	(AF034266) palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]

Seq. No.	201691
Seq. ID	LIB3048-026-Q1-L1-B5
Method	BLASTX
NCBI GI	g4115377
BLAST score	424
E value	5.0e-42
Match length	108
% identity	74
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	201692
Seq. ID	LIB3048-026-Q1-L1-B7
Method	BLASTX
NCBI GI	g477819
BLAST score	568
E value	1.0e-58
Match length	143
% identity	75
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	201693
Seq. ID	LIB3048-026-Q1-L1-C1
Method	BLASTX
NCBI GI	g4098521
BLAST score	501
E value	8.0e-51
Match length	108
% identity	89
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi_4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana]

Seq. No.	201694
Seq. ID	LIB3048-026-Q1-L1-C10
Method	BLASTX
NCBI GI	g3894159
BLAST score	161
E value	5.0e-11
Match length	80
% identity	40

NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]
Seq. No.	201695
Seq. ID	LIB3048-026-Q1-L1-C11
Method	BLASTX
NCBI GI	g2506139
BLAST score	277
E value	1.0e-24
Match length	76
% identity	75
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]
Seq. No.	201696
Seq. ID	LIB3048-026-Q1-L1-C2
Method	BLASTX
NCBI GI	g627468
BLAST score	312
E value	1.0e-28
Match length	124
% identity	53
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]
Seq. No.	201697
Seq. ID	LIB3048-026-Q1-L1-C4
Method	BLASTX
NCBI GI	g2129499
BLAST score	255
E value	3.0e-22
Match length	74
% identity	72
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	201698
Seq. ID	LIB3048-026-Q1-L1-C6
Method	BLASTX
NCBI GI	g3763933
BLAST score	400
E value	5.0e-39
Match length	137
% identity	74
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.	201699
Seq. ID	LIB3048-026-Q1-L1-C7
Method	BLASTX
NCBI GI	g2827548
BLAST score	309
E value	2.0e-28
Match length	131
% identity	44
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	201700
Seq. ID	LIB3048-026-Q1-L1-D10
Method	BLASTN
NCBI GI	g2656024
BLAST score	52
E value	3.0e-20
Match length	128
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	201701
Seq. ID	LIB3048-026-Q1-L1-D11
Method	BLASTX
NCBI GI	g1617272
BLAST score	569
E value	8.0e-59
Match length	131
% identity	79
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	201702
Seq. ID	LIB3048-026-Q1-L1-D12
Method	BLASTX
NCBI GI	g1076668
BLAST score	533
E value	1.0e-54
Match length	127
% identity	79
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	201703
Seq. ID	LIB3048-026-Q1-L1-D2
Method	BLASTX
NCBI GI	g1361983
BLAST score	459
E value	6.0e-46
Match length	129
% identity	72
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	201704
Seq. ID	LIB3048-026-Q1-L1-D4
Method	BLASTX
NCBI GI	g4309698
BLAST score	571
E value	5.0e-59
Match length	147
% identity	80
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	201705
Seq. ID	LIB3048-026-Q1-L1-D5

Method	BLASTX
NCBI GI	g3047114
BLAST score	439
E value	1.0e-43
Match length	119
% identity	70
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	201706
Seq. ID	LIB3048-026-Q1-L1-D6
Method	BLASTX
NCBI GI	g3790102
BLAST score	683
E value	4.0e-72
Match length	141
% identity	88
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	201707
Seq. ID	LIB3048-026-Q1-L1-D8
Method	BLASTX
NCBI GI	g3451072
BLAST score	365
E value	7.0e-35
Match length	101
% identity	64
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	201708
Seq. ID	LIB3048-026-Q1-L1-D9
Method	BLASTX
NCBI GI	g2498706
BLAST score	143
E value	5.0e-09
Match length	42
% identity	64
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	201709
Seq. ID	LIB3048-026-Q1-L1-E1
Method	BLASTX
NCBI GI	g2231034
BLAST score	486
E value	4.0e-49
Match length	116
% identity	80
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]

Seq. No.	201710
Seq. ID	LIB3048-026-Q1-L1-E10
Method	BLASTX
NCBI GI	g483057
BLAST score	249

E value	3.0e-21
Match length	135
% identity	45
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	201711
Seq. ID	LIB3048-026-Q1-L1-E11
Method	BLASTX
NCBI GI	g4325324
BLAST score	525
E value	1.0e-53
Match length	140
% identity	68
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	201712
Seq. ID	LIB3048-026-Q1-L1-E12
Method	BLASTN
NCBI GI	g2656025
BLAST score	41
E value	9.0e-14
Match length	57
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	201713
Seq. ID	LIB3048-026-Q1-L1-E2
Method	BLASTX
NCBI GI	g1370190
BLAST score	704
E value	1.0e-74
Match length	149
% identity	92
NCBI Description	(Z73944) RAB8A [Lotus japonicus]

Seq. No.	201714
Seq. ID	LIB3048-026-Q1-L1-E3
Method	BLASTX
NCBI GI	g132944
BLAST score	618
E value	1.0e-64
Match length	122
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	201715
Seq. ID	LIB3048-026-Q1-L1-E4
Method	BLASTX
NCBI GI	g4240207
BLAST score	180
E value	3.0e-13

Match length	125
% identity	37
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]

Seq. No.	201716
Seq. ID	LIB3048-026-Q1-L1-E5
Method	BLASTX
NCBI GI	g3176708
BLAST score	270
E value	1.0e-23
Match length	126
% identity	47
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	201717
Seq. ID	LIB3048-026-Q1-L1-E6
Method	BLASTX
NCBI GI	g113116
BLAST score	485
E value	6.0e-49
Match length	149
% identity	59
NCBI Description	ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase [Rattus norvegicus]

Seq. No.	201718
Seq. ID	LIB3048-026-Q1-L1-E7
Method	BLASTX
NCBI GI	g627468
BLAST score	297
E value	7.0e-27
Match length	124
% identity	52
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	201719
Seq. ID	LIB3048-026-Q1-L1-E8
Method	BLASTN
NCBI GI	g2656024
BLAST score	38
E value	7.0e-12
Match length	96
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	201720
Seq. ID	LIB3048-026-Q1-L1-E9
Method	BLASTX
NCBI GI	g2827711
BLAST score	627
E value	1.0e-65
Match length	135

% identity	84
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	201721
Seq. ID	LIB3048-026-Q1-L1-F11
Method	BLASTX
NCBI GI	g2398521
BLAST score	334
E value	3.0e-31
Match length	110
% identity	61
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	201722
Seq. ID	LIB3048-026-Q1-L1-F2
Method	BLASTX
NCBI GI	g2979555
BLAST score	299
E value	4.0e-27
Match length	112
% identity	53
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	201723
Seq. ID	LIB3048-026-Q1-L1-F3
Method	BLASTX
NCBI GI	g3033377
BLAST score	227
E value	1.0e-18
Match length	130
% identity	38
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	201724
Seq. ID	LIB3048-026-Q1-L1-F5
Method	BLASTX
NCBI GI	g116923
BLAST score	255
E value	7.0e-25
Match length	122
% identity	59
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	201725
Seq. ID	LIB3048-026-Q1-L1-F6
Method	BLASTX
NCBI GI	g1856971
BLAST score	507
E value	2.0e-51
Match length	110
% identity	88
NCBI Description	(D26058) This gene is specifically expressed at the S phase

during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	201726
Seq. ID	LIB3048-026-Q1-L1-F7
Method	BLASTX
NCBI GI	g4558664
BLAST score	314
E value	7.0e-29
Match length	145
% identity	10
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201727
Seq. ID	LIB3048-026-Q1-L1-F8
Method	BLASTX
NCBI GI	g3402693
BLAST score	158
E value	1.0e-10
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	201728
Seq. ID	LIB3048-026-Q1-L1-G1
Method	BLASTX
NCBI GI	g1723239
BLAST score	414
E value	1.0e-40
Match length	131
% identity	60
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	201729
Seq. ID	LIB3048-026-Q1-L1-G10
Method	BLASTX
NCBI GI	g399064
BLAST score	679
E value	1.0e-71
Match length	134
% identity	94
NCBI Description	ASPARAGINE SYNTHASE (GLUTAMINE-HYDROLYZING) (AS) >gi_100980_pir__S25165 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - garden asparagus >gi_16076_emb_CAA48141_ (X67958) asparagine synthase (glutamine-hydrolysing) [Asparagus officinalis]

Seq. No.	201730
Seq. ID	LIB3048-026-Q1-L1-G3
Method	BLASTX
NCBI GI	g4455222
BLAST score	142
E value	1.0e-08
Match length	82
% identity	40

NCBI Description	(AL035440) hypothetical protein [Arabidopsis thaliana]
Seq. No.	201731
Seq. ID	LIB3048-026-Q1-L1-G4
Method	BLASTX
NCBI GI	g1361983
BLAST score	468
E value	5.0e-47
Match length	131
% identity	73
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]
Seq. No.	201732
Seq. ID	LIB3048-026-Q1-L1-G5
Method	BLASTX
NCBI GI	g3687230
BLAST score	471
E value	3.0e-47
Match length	132
% identity	70
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.	201733
Seq. ID	LIB3048-026-Q1-L1-G6
Method	BLASTX
NCBI GI	g1361983
BLAST score	563
E value	4.0e-58
Match length	147
% identity	76
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]
Seq. No.	201734
Seq. ID	LIB3048-026-Q1-L1-H1
Method	BLASTX
NCBI GI	g3176708
BLAST score	269
E value	1.0e-23
Match length	104
% identity	53
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]
Seq. No.	201735
Seq. ID	LIB3048-026-Q1-L1-H10
Method	BLASTX
NCBI GI	g3789942
BLAST score	482
E value	6.0e-49
Match length	97
% identity	20
NCBI Description	(AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]
Seq. No.	201736

Seq. ID	LIB3048-026-Q1-L1-H5
Method	BLASTX
NCBI GI	g3123515
BLAST score	665
E value	5.0e-70
Match length	141
% identity	90
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	201737
Seq. ID	LIB3048-026-Q1-L1-H7
Method	BLASTX
NCBI GI	g3560143
BLAST score	273
E value	5.0e-24
Match length	138
% identity	43
NCBI Description	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]

Seq. No.	201738
Seq. ID	LIB3048-026-Q1-L1-H8
Method	BLASTX
NCBI GI	g1170507
BLAST score	469
E value	5.0e-47
Match length	113
% identity	80
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	201739
Seq. ID	LIB3048-027-Q1-L1-A10
Method	BLASTX
NCBI GI	g1854581
BLAST score	199
E value	1.0e-16
Match length	67
% identity	70
NCBI Description	(L24120) peroxidase precursor [Linum usitatissimum]

Seq. No.	201740
Seq. ID	LIB3048-027-Q1-L1-A11
Method	BLASTX
NCBI GI	g3152576
BLAST score	226
E value	1.0e-18
Match length	119
% identity	40
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	201741
Seq. ID	LIB3048-027-Q1-L1-A3

Method	BLASTX
NCBI GI	g4185599
BLAST score	164
E value	2.0e-11
Match length	103
% identity	43
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	201742
Seq. ID	LIB3048-027-Q1-L1-A5
Method	BLASTX
NCBI GI	g3643611
BLAST score	437
E value	2.0e-43
Match length	124
% identity	71
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	201743
Seq. ID	LIB3048-027-Q1-L1-A7
Method	BLASTX
NCBI GI	g3790587
BLAST score	533
E value	1.0e-54
Match length	131
% identity	75
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	201744
Seq. ID	LIB3048-027-Q1-L1-A8
Method	BLASTX
NCBI GI	g2243118
BLAST score	282
E value	4.0e-25
Match length	74
% identity	69
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	201745
Seq. ID	LIB3048-027-Q1-L1-B1
Method	BLASTX
NCBI GI	g4454052
BLAST score	144
E value	6.0e-09
Match length	89
% identity	42
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201746
Seq. ID	LIB3048-027-Q1-L1-B12
Method	BLASTX
NCBI GI	g2911052
BLAST score	487
E value	3.0e-49
Match length	126

% identity	75
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201747
Seq. ID	LIB3048-027-Q1-L1-B2
Method	BLASTX
NCBI GI	g4455225
BLAST score	619
E value	1.0e-64
Match length	141
% identity	75
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	201748
Seq. ID	LIB3048-027-Q1-L1-B3
Method	BLASTX
NCBI GI	g3600060
BLAST score	317
E value	3.0e-29
Match length	93
% identity	67
NCBI Description	(AF080120) contains similarity to protein kinases (Pfam: pkinase.hmm, score: 24.94) [Arabidopsis thaliana]

Seq. No.	201749
Seq. ID	LIB3048-027-Q1-L1-B5
Method	BLASTX
NCBI GI	g2827641
BLAST score	348
E value	7.0e-33
Match length	144
% identity	50
NCBI Description	(AL021636) Cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	201750
Seq. ID	LIB3048-027-Q1-L1-B7
Method	BLASTX
NCBI GI	g1173253
BLAST score	539
E value	3.0e-55
Match length	124
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_543317_pir__S41170 ribosomal protein S3 - mouse >gi_57728_emb_CAA35916_ (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi_439522_emb_CAA54167_ (X76772) ribosomal protein S3 [Mus musculus]

Seq. No.	201751
Seq. ID	LIB3048-027-Q1-L1-B8
Method	BLASTX
NCBI GI	g3426037
BLAST score	333
E value	4.0e-31
Match length	122
% identity	30

NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No.	201752
Seq. ID	LIB3048-027-Q1-L1-C1
Method	BLASTX
NCBI GI	g130828
BLAST score	394
E value	3.0e-38
Match length	122
% identity	65
NCBI Description	PATHOGENESIS-RELATED PROTEIN 1C PRECURSOR (PR-1C) >gi_2119762_pir__C24620 pathogenesis-related protein 1c precursor - common tobacco >gi_19958_emb_CAA35666_ (X17681) pathogenesis-related protein 1b (AA 1-168) [Nicotiana tabacum]

Seq. No.	201753
Seq. ID	LIB3048-027-Q1-L1-C10
Method	BLASTX
NCBI GI	g1304227
BLAST score	404
E value	1.0e-39
Match length	107
% identity	66
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	201754
Seq. ID	LIB3048-027-Q1-L1-C11
Method	BLASTX
NCBI GI	g3158376
BLAST score	355
E value	7.0e-34
Match length	99
% identity	71
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201755
Seq. ID	LIB3048-027-Q1-L1-C12
Method	BLASTX
NCBI GI	g1399275
BLAST score	426
E value	3.0e-42
Match length	107
% identity	78
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	201756
Seq. ID	LIB3048-027-Q1-L1-C2
Method	BLASTX
NCBI GI	g126894
BLAST score	352

E value	2.0e-33
Match length	90
% identity	80
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi_167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]

Seq. No.	201757
Seq. ID	LIB3048-027-Q1-L1-C3
Method	BLASTX
NCBI GI	g1255951
BLAST score	480
E value	2.0e-48
Match length	113
% identity	79
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	201758
Seq. ID	LIB3048-027-Q1-L1-C4
Method	BLASTX
NCBI GI	g4204265
BLAST score	229
E value	6.0e-19
Match length	121
% identity	45
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	201759
Seq. ID	LIB3048-027-Q1-L1-C5
Method	BLASTX
NCBI GI	g4490732
BLAST score	233
E value	2.0e-19
Match length	101
% identity	51
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	201760
Seq. ID	LIB3048-027-Q1-L1-C6
Method	BLASTX
NCBI GI	g4432844
BLAST score	191
E value	1.0e-14
Match length	104
% identity	39
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	201761
Seq. ID	LIB3048-027-Q1-L1-C7
Method	BLASTX
NCBI GI	g3947733
BLAST score	425
E value	7.0e-42
Match length	144

% identity	58
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	201762
Seq. ID	LIB3048-027-Q1-L1-C9
Method	BLASTX
NCBI GI	g2961372
BLAST score	535
E value	6.0e-55
Match length	109
% identity	92
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	201763
Seq. ID	LIB3048-027-Q1-L1-D1
Method	BLASTX
NCBI GI	g2995953
BLAST score	225
E value	2.0e-18
Match length	61
% identity	74
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	201764
Seq. ID	LIB3048-027-Q1-L1-D10
Method	BLASTX
NCBI GI	g4490732
BLAST score	154
E value	2.0e-10
Match length	55
% identity	62
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	201765
Seq. ID	LIB3048-027-Q1-L1-D11
Method	BLASTX
NCBI GI	g765203
BLAST score	244
E value	8.0e-21
Match length	64
% identity	72
NCBI Description	(S73865) linoleate:oxygen oxidoreductase, lipoxygenase, LOX {EC 1.13.11.12} [Solanum tuberosum, cv. Desiree, roots, Peptide, 857 aa] [Solanum tuberosum]

Seq. No.	201766
Seq. ID	LIB3048-027-Q1-L1-D12
Method	BLASTX
NCBI GI	g3492803
BLAST score	260
E value	1.0e-22
Match length	110
% identity	51
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	201767
Seq. ID	LIB3048-027-Q1-L1-D3
Method	BLASTX
NCBI GI	g1709498
BLAST score	528
E value	5.0e-54
Match length	120
% identity	79
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201768
Seq. ID	LIB3048-027-Q1-L1-D5
Method	BLASTX
NCBI GI	g729668
BLAST score	339
E value	8.0e-32
Match length	78
% identity	86
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	201769
Seq. ID	LIB3048-027-Q1-L1-D8
Method	BLASTX
NCBI GI	g2506139
BLAST score	296
E value	8.0e-27
Match length	77
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	201770
Seq. ID	LIB3048-027-Q1-L1-D9
Method	BLASTX
NCBI GI	g2244759
BLAST score	481
E value	1.0e-48
Match length	117
% identity	71
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	201771
Seq. ID	LIB3048-027-Q1-L1-E1
Method	BLASTX
NCBI GI	g2996096
BLAST score	653
E value	1.0e-68
Match length	125
% identity	99
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No.	201772
Seq. ID	LIB3048-027-Q1-L1-E6
Method	BLASTX
NCBI GI	g82131
BLAST score	363
E value	7.0e-35
Match length	94
% identity	73
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	201773
Seq. ID	LIB3048-027-Q1-L1-E7
Method	BLASTX
NCBI GI	g2462746
BLAST score	526
E value	9.0e-54
Match length	121
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	201774
Seq. ID	LIB3048-027-Q1-L1-E8
Method	BLASTX
NCBI GI	g3123745
BLAST score	240
E value	2.0e-20
Match length	68
% identity	69
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	201775
Seq. ID	LIB3048-027-Q1-L1-F1
Method	BLASTX
NCBI GI	g1402912
BLAST score	475
E value	8.0e-48
Match length	113
% identity	79
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	201776
Seq. ID	LIB3048-027-Q1-L1-F10
Method	BLASTX
NCBI GI	g3334147
BLAST score	303
E value	1.0e-27
Match length	86
% identity	65
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No. 201777

Seq. ID LIB3048-027-Q1-L1-F11
Method BLASTX
NCBI GI g2129798
BLAST score 317
E value 2.0e-29
Match length 93
% identity 67
NCBI Description pathogenesis-related protein 1a homolog precursor - rape >gi_722274 (U21849) PR-1a [Brassica napus] >gi_1575758 (U70666) pathogenesis-related protein PR1 [Brassica napus]

Seq. No. 201778
Seq. ID LIB3048-027-Q1-L1-F3
Method BLASTX
NCBI GI g2388585
BLAST score 597
E value 4.0e-62
Match length 142
% identity 86
NCBI Description (AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No. 201779
Seq. ID LIB3048-027-Q1-L1-F5
Method BLASTX
NCBI GI g3924597
BLAST score 237
E value 7.0e-20
Match length 141
% identity 34
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 201780
Seq. ID LIB3048-027-Q1-L1-F6
Method BLASTX
NCBI GI g4206122
BLAST score 463
E value 2.0e-46
Match length 141
% identity 62
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No. 201781
Seq. ID LIB3048-027-Q1-L1-F7
Method BLASTX
NCBI GI g3451072
BLAST score 271
E value 6.0e-24
Match length 78
% identity 59
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 201782
Seq. ID LIB3048-027-Q1-L1-F8
Method BLASTX
NCBI GI g4539400

BLAST score	422
E value	9.0e-42
Match length	104
% identity	77
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	201783
Seq. ID	LIB3048-027-Q1-L1-G1
Method	BLASTX
NCBI GI	g3492803
BLAST score	319
E value	2.0e-29
Match length	106
% identity	58
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	201784
Seq. ID	LIB3048-027-Q1-L1-G10
Method	BLASTX
NCBI GI	g2342724
BLAST score	337
E value	1.0e-31
Match length	126
% identity	67
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	201785
Seq. ID	LIB3048-027-Q1-L1-G11
Method	BLASTX
NCBI GI	g2286153
BLAST score	539
E value	2.0e-55
Match length	112
% identity	96
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	201786
Seq. ID	LIB3048-027-Q1-L1-G12
Method	BLASTX
NCBI GI	g3687223
BLAST score	376
E value	3.0e-36
Match length	124
% identity	66
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201787
Seq. ID	LIB3048-027-Q1-L1-G4
Method	BLASTX
NCBI GI	g1345930
BLAST score	364
E value	3.0e-35
Match length	81
% identity	86
NCBI Description	CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_602331_emb_CAA56594_ (X80377) O-acetylserine (thiol)

lyase [Arabidopsis thaliana]

Seq. No.	201788
Seq. ID	LIB3048-027-Q1-L1-G5
Method	BLASTN
NCBI GI	g3241927
BLAST score	44
E value	2.0e-15
Match length	212
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	201789
Seq. ID	LIB3048-027-Q1-L1-G8
Method	BLASTX
NCBI GI	g399333
BLAST score	271
E value	4.0e-24
Match length	75
% identity	73
NCBI Description	CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No.	201790
Seq. ID	LIB3048-027-Q1-L1-G9
Method	BLASTX
NCBI GI	g1174592
BLAST score	614
E value	3.0e-64
Match length	117
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	201791
Seq. ID	LIB3048-027-Q1-L1-H1
Method	BLASTX
NCBI GI	g4337189
BLAST score	185
E value	3.0e-29
Match length	105
% identity	63
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	201792
Seq. ID	LIB3048-027-Q1-L1-H10
Method	BLASTX
NCBI GI	g4263709
BLAST score	165
E value	2.0e-11
Match length	37

% identity	76
NCBI Description	(AC006223) unknown protein [Arabidopsis thaliana]

Seq. No.	201793
Seq. ID	LIB3048-027-Q1-L1-H11
Method	BLASTX
NCBI GI	g1766046
BLAST score	529
E value	3.0e-54
Match length	114
% identity	86
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	201794
Seq. ID	LIB3048-027-Q1-L1-H12
Method	BLASTX
NCBI GI	g2316016
BLAST score	310
E value	2.0e-28
Match length	118
% identity	54
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	201795
Seq. ID	LIB3048-027-Q1-L1-H3
Method	BLASTX
NCBI GI	g2462756
BLAST score	431
E value	1.0e-42
Match length	136
% identity	66
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	201796
Seq. ID	LIB3048-027-Q1-L1-H6
Method	BLASTX
NCBI GI	g464849
BLAST score	499
E value	8.0e-51
Match length	103
% identity	94
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	201797
Seq. ID	LIB3048-027-Q1-L1-H7
Method	BLASTX
NCBI GI	g3044212
BLAST score	669
E value	2.0e-70
Match length	143
% identity	91
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	201798

Seq. ID LIB3048-027-Q1-L1-H9
Method BLASTX
NCBI GI g2213619
BLAST score 252
E value 1.0e-21
Match length 132
% identity 45
NCBI Description (AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No. 201799
Seq. ID LIB3048-028-Q1-L1-A10
Method BLASTX
NCBI GI g2827546
BLAST score 320
E value 1.0e-29
Match length 126
% identity 48
NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No. 201800
Seq. ID LIB3048-028-Q1-L1-A11
Method BLASTX
NCBI GI g3152576
BLAST score 366
E value 4.0e-35
Match length 124
% identity 57
NCBI Description (AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No. 201801
Seq. ID LIB3048-028-Q1-L1-A12
Method BLASTX
NCBI GI g1174592
BLAST score 631
E value 3.0e-66
Match length 118
% identity 100
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No. 201802
Seq. ID LIB3048-028-Q1-L1-A2
Method BLASTX
NCBI GI g3264767
BLAST score 242
E value 2.0e-20
Match length 123
% identity 42
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 201803
Seq. ID LIB3048-028-Q1-L1-A8
Method BLASTX
NCBI GI g4138265

BLAST score	416
E value	3.0e-41
Match length	91
% identity	88
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	201804
Seq. ID	LIB3048-028-Q1-L1-B1
Method	BLASTX
NCBI GI	g3935168
BLAST score	310
E value	2.0e-28
Match length	116
% identity	59
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	201805
Seq. ID	LIB3048-028-Q1-L1-B10
Method	BLASTX
NCBI GI	g1076668
BLAST score	501
E value	7.0e-51
Match length	122
% identity	77
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	201806
Seq. ID	LIB3048-028-Q1-L1-B12
Method	BLASTX
NCBI GI	g4580575
BLAST score	490
E value	1.0e-49
Match length	127
% identity	70
NCBI Description	(AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No.	201807
Seq. ID	LIB3048-028-Q1-L1-B2
Method	BLASTX
NCBI GI	g483057
BLAST score	166
E value	8.0e-12
Match length	68
% identity	47
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	201808
Seq. ID	LIB3048-028-Q1-L1-B3
Method	BLASTX
NCBI GI	g2194118
BLAST score	202
E value	7.0e-16

Match length	97
% identity	40
NCBI Description	(AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No.	201809
Seq. ID	LIB3048-028-Q1-L1-B4
Method	BLASTX
NCBI GI	g4522005
BLAST score	150
E value	6.0e-10
Match length	97
% identity	31
NCBI Description	(AC007069) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	201810
Seq. ID	LIB3048-028-Q1-L1-B5
Method	BLASTX
NCBI GI	g1619300
BLAST score	180
E value	3.0e-13
Match length	46
% identity	76
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	201811
Seq. ID	LIB3048-028-Q1-L1-B7
Method	BLASTX
NCBI GI	g2230757
BLAST score	283
E value	2.0e-25
Match length	97
% identity	60
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	201812
Seq. ID	LIB3048-028-Q1-L1-C1
Method	BLASTX
NCBI GI	g2281115
BLAST score	446
E value	1.0e-44
Match length	102
% identity	84
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201813
Seq. ID	LIB3048-028-Q1-L1-C11
Method	BLASTX
NCBI GI	g2435511
BLAST score	181
E value	2.0e-13
Match length	57
% identity	60
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	201814
Seq. ID	LIB3048-028-Q1-L1-C12
Method	BLASTX
NCBI GI	g4512018
BLAST score	216
E value	2.0e-17
Match length	58
% identity	72
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	201815
Seq. ID	LIB3048-028-Q1-L1-C3
Method	BLASTX
NCBI GI	g3128209
BLAST score	319
E value	7.0e-30
Match length	85
% identity	72
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	201816
Seq. ID	LIB3048-028-Q1-L1-C5
Method	BLASTX
NCBI GI	g1709498
BLAST score	443
E value	4.0e-44
Match length	97
% identity	81
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201817
Seq. ID	LIB3048-028-Q1-L1-C6
Method	BLASTX
NCBI GI	g2462762
BLAST score	151
E value	4.0e-13
Match length	77
% identity	53
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	201818
Seq. ID	LIB3048-028-Q1-L1-C9
Method	BLASTX
NCBI GI	g4138265
BLAST score	282
E value	3.0e-25
Match length	66
% identity	68
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	201819

Seq. ID	LIB3048-028-Q1-L1-D10
Method	BLASTX
NCBI GI	g4337189
BLAST score	563
E value	3.0e-58
Match length	121
% identity	86
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	201820
Seq. ID	LIB3048-028-Q1-L1-D11
Method	BLASTX
NCBI GI	g1279654
BLAST score	407
E value	7.0e-40
Match length	124
% identity	67
NCBI Description	(X97351) peroxidase [Populus balsamifera subsp. trichocarpa]

Seq. No.	201821
Seq. ID	LIB3048-028-Q1-L1-D12
Method	BLASTX
NCBI GI	g2739381
BLAST score	270
E value	7.0e-24
Match length	94
% identity	59
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	201822
Seq. ID	LIB3048-028-Q1-L1-D3
Method	BLASTX
NCBI GI	g2244792
BLAST score	322
E value	5.0e-30
Match length	81
% identity	77
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	201823
Seq. ID	LIB3048-028-Q1-L1-D6
Method	BLASTX
NCBI GI	g3641837
BLAST score	443
E value	4.0e-44
Match length	134
% identity	70
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	201824
Seq. ID	LIB3048-028-Q1-L1-D7
Method	BLASTX
NCBI GI	g1707857
BLAST score	524

E value	1.0e-53
Match length	109
% identity	89
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	201825
Seq. ID	LIB3048-028-Q1-L1-D9
Method	BLASTX
NCBI GI	g3128168
BLAST score	284
E value	2.0e-25
Match length	112
% identity	47
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	201826
Seq. ID	LIB3048-028-Q1-L1-E1
Method	BLASTX
NCBI GI	g2435395
BLAST score	174
E value	5.0e-23
Match length	67
% identity	87
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	201827
Seq. ID	LIB3048-028-Q1-L1-E10
Method	BLASTX
NCBI GI	g2462756
BLAST score	403
E value	2.0e-39
Match length	122
% identity	68
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	201828
Seq. ID	LIB3048-028-Q1-L1-E11
Method	BLASTX
NCBI GI	g4098128
BLAST score	629
E value	7.0e-66
Match length	136
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	201829
Seq. ID	LIB3048-028-Q1-L1-E2
Method	BLASTX
NCBI GI	g1706918
BLAST score	290
E value	4.0e-26
Match length	115
% identity	45
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	201830
Seq. ID	LIB3048-028-Q1-L1-E9
Method	BLASTX
NCBI GI	g2642158
BLAST score	284
E value	1.0e-25
Match length	94
% identity	60
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201831
Seq. ID	LIB3048-028-Q1-L1-F1
Method	BLASTX
NCBI GI	g1129145
BLAST score	490
E value	1.0e-49
Match length	110
% identity	85
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	201832
Seq. ID	LIB3048-028-Q1-L1-F12
Method	BLASTX
NCBI GI	g3834309
BLAST score	351
E value	3.0e-33
Match length	110
% identity	55
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	201833
Seq. ID	LIB3048-028-Q1-L1-F2
Method	BLASTX
NCBI GI	g2622920
BLAST score	238
E value	4.0e-20
Match length	108
% identity	43
NCBI Description	(AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium thermoautotrophicum]

Seq. No.	201834
Seq. ID	LIB3048-028-Q1-L1-F8
Method	BLASTX
NCBI GI	g4566614
BLAST score	518
E value	7.0e-53
Match length	130
% identity	76
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	201835

Seq. ID	LIB3048-028-Q1-L1-G1
Method	BLASTX
NCBI GI	g82131
BLAST score	354
E value	1.0e-33
Match length	91
% identity	74
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	201836
Seq. ID	LIB3048-028-Q1-L1-G10
Method	BLASTX
NCBI GI	g1361983
BLAST score	417
E value	4.0e-41
Match length	115
% identity	72
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	201837
Seq. ID	LIB3048-028-Q1-L1-G11
Method	BLASTX
NCBI GI	g4102703
BLAST score	164
E value	2.0e-11
Match length	71
% identity	56
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	201838
Seq. ID	LIB3048-028-Q1-L1-G2
Method	BLASTX
NCBI GI	g3158376
BLAST score	390
E value	7.0e-38
Match length	110
% identity	73
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201839
Seq. ID	LIB3048-028-Q1-L1-G3
Method	BLASTX
NCBI GI	g2290683
BLAST score	351
E value	2.0e-33
Match length	76
% identity	83
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	201840
Seq. ID	LIB3048-028-Q1-L1-G4
Method	BLASTX
NCBI GI	g1362003

BLAST score	272
E value	3.0e-24
Match length	96
% identity	60
NCBI Description	protein phosphatase 2A B regulatory chain 55K - Arabidopsis thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana]

Seq. No.	201841
Seq. ID	LIB3048-028-Q1-L1-G6
Method	BLASTX
NCBI GI	g603074
BLAST score	437
E value	2.0e-43
Match length	134
% identity	58
NCBI Description	(U18197) ATP:citrate lyase [Homo sapiens]

Seq. No.	201842
Seq. ID	LIB3048-028-Q1-L1-G7
Method	BLASTX
NCBI GI	g1703200
BLAST score	606
E value	3.0e-63
Match length	124
% identity	93
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	201843
Seq. ID	LIB3048-028-Q1-L1-G8
Method	BLASTX
NCBI GI	g4567095
BLAST score	385
E value	2.0e-37
Match length	103
% identity	65
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	201844
Seq. ID	LIB3048-028-Q1-L1-G9
Method	BLASTX
NCBI GI	g1666096
BLAST score	271
E value	6.0e-24
Match length	103
% identity	53
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	201845
Seq. ID	LIB3048-028-Q1-L1-H1
Method	BLASTX
NCBI GI	g2583128

BLAST score	437
E value	2.0e-43
Match length	111
% identity	74
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201846
Seq. ID	LIB3048-028-Q1-L1-H10
Method	BLASTX
NCBI GI	g1483230
BLAST score	376
E value	3.0e-36
Match length	100
% identity	81
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	201847
Seq. ID	LIB3048-028-Q1-L1-H2
Method	BLASTX
NCBI GI	g133867
BLAST score	460
E value	4.0e-46
Match length	108
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	201848
Seq. ID	LIB3048-028-Q1-L1-H4
Method	BLASTX
NCBI GI	g1495251
BLAST score	282
E value	3.0e-25
Match length	113
% identity	52
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	201849
Seq. ID	LIB3048-028-Q1-L1-H6
Method	BLASTX
NCBI GI	g4185142
BLAST score	289
E value	3.0e-26
Match length	70
% identity	77
NCBI Description	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]

Seq. No.	201850
Seq. ID	LIB3048-028-Q1-L1-H9
Method	BLASTX
NCBI GI	g3152605
BLAST score	197
E value	3.0e-15
Match length	98
% identity	45

NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201851
Seq. ID	LIB3048-029-Q1-L1-A10
Method	BLASTX
NCBI GI	g2129550
BLAST score	566
E value	2.0e-58
Match length	126
% identity	84
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	201852
Seq. ID	LIB3048-029-Q1-L1-A11
Method	BLASTX
NCBI GI	g1352683
BLAST score	456
E value	1.0e-45
Match length	128
% identity	64
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	201853
Seq. ID	LIB3048-029-Q1-L1-A12
Method	BLASTX
NCBI GI	g3242720
BLAST score	365
E value	6.0e-35
Match length	117
% identity	55
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	201854
Seq. ID	LIB3048-029-Q1-L1-A3
Method	BLASTX
NCBI GI	g2281115
BLAST score	652
E value	1.0e-68
Match length	135
% identity	90
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	201855
Seq. ID	LIB3048-029-Q1-L1-A5
Method	BLASTX
NCBI GI	g548488
BLAST score	501

E value	8.0e-51
Match length	139
% identity	63
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	201856
Seq. ID	LIB3048-029-Q1-L1-A6
Method	BLASTX
NCBI GI	g3450842
BLAST score	190
E value	2.0e-14
Match length	63
% identity	62
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	201857
Seq. ID	LIB3048-029-Q1-L1-A7
Method	BLASTX
NCBI GI	g170753
BLAST score	509
E value	9.0e-52
Match length	109
% identity	80
NCBI Description	(M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	201858
Seq. ID	LIB3048-029-Q1-L1-A8
Method	BLASTX
NCBI GI	g2911059
BLAST score	415
E value	1.0e-40
Match length	115
% identity	71
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201859
Seq. ID	LIB3048-029-Q1-L1-A9
Method	BLASTX
NCBI GI	g2507422
BLAST score	313
E value	6.0e-29
Match length	103
% identity	72
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	201860
Seq. ID	LIB3048-029-Q1-L1-B1
Method	BLASTX
NCBI GI	g3935168
BLAST score	322
E value	7.0e-30

Match length	118
% identity	59
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	201861
Seq. ID	LIB3048-029-Q1-L1-B11
Method	BLASTX
NCBI GI	g2772934
BLAST score	473
E value	1.0e-47
Match length	116
% identity	74
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	201862
Seq. ID	LIB3048-029-Q1-L1-B12
Method	BLASTX
NCBI GI	g2244905
BLAST score	429
E value	2.0e-42
Match length	126
% identity	61
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	201863
Seq. ID	LIB3048-029-Q1-L1-B2
Method	BLASTX
NCBI GI	g485742
BLAST score	516
E value	1.0e-52
Match length	104
% identity	99
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	201864
Seq. ID	LIB3048-029-Q1-L1-B3
Method	BLASTX
NCBI GI	g1709498
BLAST score	518
E value	7.0e-53
Match length	129
% identity	75
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201865
Seq. ID	LIB3048-029-Q1-L1-B4
Method	BLASTX
NCBI GI	g1184075
BLAST score	218
E value	1.0e-17
Match length	133
% identity	3

NCBI Description	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No.	201866
Seq. ID	LIB3048-029-Q1-L1-B5
Method	BLASTX
NCBI GI	g3986701
BLAST score	238
E value	5.0e-20
Match length	69
% identity	70
NCBI Description	(AF101426) ferrochelatase [Cichorium intybus]

Seq. No.	201867
Seq. ID	LIB3048-029-Q1-L1-B6
Method	BLASTX
NCBI GI	g3482933
BLAST score	544
E value	7.0e-56
Match length	144
% identity	70
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	201868
Seq. ID	LIB3048-029-Q1-L1-B7
Method	BLASTX
NCBI GI	g1155261
BLAST score	395
E value	2.0e-38
Match length	106
% identity	75
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	201869
Seq. ID	LIB3048-029-Q1-L1-B8
Method	BLASTX
NCBI GI	g3935168
BLAST score	368
E value	3.0e-35
Match length	125
% identity	62
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	201870
Seq. ID	LIB3048-029-Q1-L1-B9
Method	BLASTX
NCBI GI	g1723239
BLAST score	368
E value	2.0e-35
Match length	119
% identity	60
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	201871
Seq. ID	LIB3048-029-Q1-L1-C1
Method	BLASTX
NCBI GI	g1169014
BLAST score	181
E value	3.0e-13
Match length	117
% identity	38
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_472343 (L31852) bcop [Drosophila melanogaster]

Seq. No.	201872
Seq. ID	LIB3048-029-Q1-L1-C3
Method	BLASTX
NCBI GI	g4539315
BLAST score	266
E value	3.0e-23
Match length	132
% identity	47
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	201873
Seq. ID	LIB3048-029-Q1-L1-C5
Method	BLASTX
NCBI GI	g2894612
BLAST score	666
E value	4.0e-70
Match length	143
% identity	85
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	201874
Seq. ID	LIB3048-029-Q1-L1-C6
Method	BLASTX
NCBI GI	g2316016
BLAST score	349
E value	5.0e-33
Match length	125
% identity	31
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	201875
Seq. ID	LIB3048-029-Q1-L1-C7
Method	BLASTX
NCBI GI	g1346387
BLAST score	670
E value	1.0e-70
Match length	143
% identity	90
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	201876

Seq. ID LIB3048-029-Q1-L1-C8
Method BLASTX
NCBI GI g4309698
BLAST score 547
E value 3.0e-56
Match length 125
% identity 89
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 201877
Seq. ID LIB3048-029-Q1-L1-C9
Method BLASTX
NCBI GI g3599974
BLAST score 353
E value 2.0e-33
Match length 132
% identity 50
NCBI Description (AF038651) GTP pyrophosphokinase [Corynebacterium glutamicum]

Seq. No. 201878
Seq. ID LIB3048-029-Q1-L1-D10
Method BLASTX
NCBI GI g2262173
BLAST score 349
E value 5.0e-33
Match length 110
% identity 63
NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 201879
Seq. ID LIB3048-029-Q1-L1-D2
Method BLASTX
NCBI GI g3582328
BLAST score 293
E value 2.0e-26
Match length 122
% identity 48
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201880
Seq. ID LIB3048-029-Q1-L1-D4
Method BLASTX
NCBI GI g3551954
BLAST score 340
E value 6.0e-32
Match length 144
% identity 44
NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 201881
Seq. ID LIB3048-029-Q1-L1-D5
Method BLASTX
NCBI GI g4539423

BLAST score	587
E value	6.0e-61
Match length	135
% identity	83
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	201882
Seq. ID	LIB3048-029-Q1-L1-D6
Method	BLASTX
NCBI GI	g4539423
BLAST score	229
E value	5.0e-19
Match length	110
% identity	47
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	201883
Seq. ID	LIB3048-029-Q1-L1-D7
Method	BLASTX
NCBI GI	g266944
BLAST score	351
E value	1.0e-33
Match length	86
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]

Seq. No.	201884
Seq. ID	LIB3048-029-Q1-L1-D8
Method	BLASTX
NCBI GI	g2642158
BLAST score	626
E value	2.0e-65
Match length	143
% identity	78
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201885
Seq. ID	LIB3048-029-Q1-L1-D9
Method	BLASTX
NCBI GI	g2500378
BLAST score	408
E value	6.0e-40
Match length	82
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	201886
Seq. ID	LIB3048-029-Q1-L1-E11
Method	BLASTN
NCBI GI	g3241927
BLAST score	44
E value	2.0e-15

Match length	215
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	201887
Seq. ID	LIB3048-029-Q1-L1-E4
Method	BLASTX
NCBI GI	g1709358
BLAST score	333
E value	4.0e-31
Match length	136
% identity	49
NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859 nucleoside triphosphatase - garden pea >gi_2129890_pir__S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	201888
Seq. ID	LIB3048-029-Q1-L1-E5
Method	BLASTX
NCBI GI	g2467088
BLAST score	278
E value	1.0e-24
Match length	129
% identity	49
NCBI Description	(AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No.	201889
Seq. ID	LIB3048-029-Q1-L1-E6
Method	BLASTX
NCBI GI	g4510346
BLAST score	236
E value	4.0e-27
Match length	92
% identity	66
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201890
Seq. ID	LIB3048-029-Q1-L1-E9
Method	BLASTX
NCBI GI	g3132696
BLAST score	571
E value	4.0e-59
Match length	125
% identity	87
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	201891
Seq. ID	LIB3048-029-Q1-L1-F1
Method	BLASTX
NCBI GI	g232024
BLAST score	291

E value	2.0e-26
Match length	102
% identity	60
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	201892
Seq. ID	LIB3048-029-Q1-L1-F11
Method	BLASTX
NCBI GI	g3033377
BLAST score	201
E value	1.0e-15
Match length	98
% identity	44
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	201893
Seq. ID	LIB3048-029-Q1-L1-F2
Method	BLASTX
NCBI GI	g3152609
BLAST score	352
E value	2.0e-33
Match length	119
% identity	55
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	201894
Seq. ID	LIB3048-029-Q1-L1-F3
Method	BLASTX
NCBI GI	g3451147
BLAST score	527
E value	7.0e-54
Match length	144
% identity	70
NCBI Description	(AJ010397) chitinase [Hevea brasiliensis]

Seq. No.	201895
Seq. ID	LIB3048-029-Q1-L1-F6
Method	BLASTX
NCBI GI	g1491615
BLAST score	235
E value	8.0e-20
Match length	83
% identity	58
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	201896
Seq. ID	LIB3048-029-Q1-L1-F7
Method	BLASTX
NCBI GI	g1407705
BLAST score	610

E value	1.0e-63
Match length	140
% identity	81
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	201897
Seq. ID	LIB3048-029-Q1-L1-G1
Method	BLASTX
NCBI GI	g1549335
BLAST score	248
E value	1.0e-24
Match length	130
% identity	49
NCBI Description	(U52848) class IV chitinase EP3B/E6 [Daucus carota]

Seq. No.	201898
Seq. ID	LIB3048-029-Q1-L1-G11
Method	BLASTX
NCBI GI	g3337352
BLAST score	328
E value	1.0e-30
Match length	107
% identity	65
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	201899
Seq. ID	LIB3048-029-Q1-L1-G2
Method	BLASTX
NCBI GI	g3236238
BLAST score	194
E value	7.0e-15
Match length	126
% identity	42
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	201900
Seq. ID	LIB3048-029-Q1-L1-G3
Method	BLASTX
NCBI GI	g4314362
BLAST score	181
E value	2.0e-13
Match length	41
% identity	78
NCBI Description	(AC006340) putative D-amino acid dehydrogenase [Arabidopsis thaliana]

Seq. No.	201901
Seq. ID	LIB3048-029-Q1-L1-G6
Method	BLASTX
NCBI GI	g2739376
BLAST score	329
E value	6.0e-32
Match length	98
% identity	76

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 201902
Seq. ID LIB3048-029-Q1-L1-G8
Method BLASTX
NCBI GI g3702335
BLAST score 181
E value 3.0e-13
Match length 41
% identity 71
NCBI Description (AC005397) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 201903
Seq. ID LIB3048-029-Q1-L1-G9
Method BLASTX
NCBI GI g4191774
BLAST score 316
E value 4.0e-29
Match length 118
% identity 52
NCBI Description (AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 201904
Seq. ID LIB3048-029-Q1-L1-H1
Method BLASTX
NCBI GI g2832623
BLAST score 555
E value 4.0e-57
Match length 140
% identity 74
NCBI Description (AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 201905
Seq. ID LIB3048-029-Q1-L1-H10
Method BLASTX
NCBI GI g1084349
BLAST score 540
E value 2.0e-57
Match length 123
% identity 93
NCBI Description aldehyde dehydrogenase homolog btg-26 - rape >gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No. 201906
Seq. ID LIB3048-029-Q1-L1-H11
Method BLASTX
NCBI GI g3426037
BLAST score 311
E value 1.0e-28
Match length 122
% identity 28
NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No.	201907
Seq. ID	LIB3048-029-Q1-L1-H6
Method	BLASTX
NCBI GI	g1107526
BLAST score	457
E value	9.0e-46
Match length	113
% identity	76
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	201908
Seq. ID	LIB3048-029-Q1-L1-H7
Method	BLASTX
NCBI GI	g1703200
BLAST score	625
E value	2.0e-65
Match length	128
% identity	92
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	201909
Seq. ID	LIB3048-029-Q1-L1-H9
Method	BLASTX
NCBI GI	g3123515
BLAST score	571
E value	5.0e-59
Match length	130
% identity	86
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	201910
Seq. ID	LIB3048-030-Q1-L1-A11
Method	BLASTX
NCBI GI	g548488
BLAST score	467
E value	7.0e-47
Match length	135
% identity	67
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	201911
Seq. ID	LIB3048-030-Q1-L1-A2
Method	BLASTX
NCBI GI	g2979555
BLAST score	324
E value	4.0e-30
Match length	115
% identity	55
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	201912
Seq. ID	LIB3048-030-Q1-L1-A3
Method	BLASTX
NCBI GI	g1103712
BLAST score	188
E value	2.0e-14
Match length	82
% identity	57
NCBI Description	(X83729) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	201913
Seq. ID	LIB3048-030-Q1-L1-A4
Method	BLASTX
NCBI GI	g2827546
BLAST score	326
E value	3.0e-30
Match length	131
% identity	46
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	201914
Seq. ID	LIB3048-030-Q1-L1-A5
Method	BLASTX
NCBI GI	g2462745
BLAST score	261
E value	9.0e-23
Match length	121
% identity	39
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	201915
Seq. ID	LIB3048-030-Q1-L1-A7
Method	BLASTX
NCBI GI	g3158376
BLAST score	456
E value	1.0e-45
Match length	122
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201916
Seq. ID	LIB3048-030-Q1-L1-A8
Method	BLASTX
NCBI GI	g3329294
BLAST score	156
E value	2.0e-10
Match length	129
% identity	29
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	201917
Seq. ID	LIB3048-030-Q1-L1-B10
Method	BLASTX
NCBI GI	g3319457
BLAST score	142

E value	9.0e-09
Match length	79
% identity	39
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	201918
Seq. ID	LIB3048-030-Q1-L1-B2
Method	BLASTX
NCBI GI	g2911044
BLAST score	440
E value	9.0e-44
Match length	124
% identity	71
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	201919
Seq. ID	LIB3048-030-Q1-L1-B3
Method	BLASTX
NCBI GI	g3123515
BLAST score	610
E value	1.0e-63
Match length	129
% identity	91
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	201920
Seq. ID	LIB3048-030-Q1-L1-B4
Method	BLASTX
NCBI GI	g3329294
BLAST score	152
E value	6.0e-10
Match length	115
% identity	30
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	201921
Seq. ID	LIB3048-030-Q1-L1-B5
Method	BLASTX
NCBI GI	g1361983
BLAST score	511
E value	5.0e-52
Match length	137
% identity	75
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	201922
Seq. ID	LIB3048-030-Q1-L1-B8
Method	BLASTX
NCBI GI	g4249382
BLAST score	489
E value	2.0e-49
Match length	119
% identity	74
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	201923
Seq. ID	LIB3048-030-Q1-L1-B9
Method	BLASTX
NCBI GI	g2224933
BLAST score	241
E value	6.0e-21
Match length	67
% identity	42
NCBI Description	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] >gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]

Seq. No.	201924
Seq. ID	LIB3048-030-Q1-L1-C11
Method	BLASTX
NCBI GI	g2078350
BLAST score	183
E value	1.0e-13
Match length	109
% identity	40
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	201925
Seq. ID	LIB3048-030-Q1-L1-C12
Method	BLASTX
NCBI GI	g2181180
BLAST score	162
E value	4.0e-11
Match length	121
% identity	32
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	201926
Seq. ID	LIB3048-030-Q1-L1-C2
Method	BLASTX
NCBI GI	g462147
BLAST score	686
E value	2.0e-72
Match length	137
% identity	94
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	201927
Seq. ID	LIB3048-030-Q1-L1-C3
Method	BLASTX
NCBI GI	g4220533
BLAST score	317
E value	2.0e-29
Match length	107

% identity	64
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	201928
Seq. ID	LIB3048-030-Q1-L1-C4
Method	BLASTX
NCBI GI	g1142619
BLAST score	392
E value	5.0e-38
Match length	140
% identity	59
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	201929
Seq. ID	LIB3048-030-Q1-L1-C5
Method	BLASTX
NCBI GI	g3044212
BLAST score	633
E value	2.0e-66
Match length	137
% identity	88
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	201930
Seq. ID	LIB3048-030-Q1-L1-C6
Method	BLASTX
NCBI GI	g4056469
BLAST score	343
E value	8.0e-51
Match length	124
% identity	86
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	201931
Seq. ID	LIB3048-030-Q1-L1-C7
Method	BLASTX
NCBI GI	g464846
BLAST score	480
E value	2.0e-48
Match length	95
% identity	93
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	201932
Seq. ID	LIB3048-030-Q1-L1-C8
Method	BLASTX
NCBI GI	g4468046
BLAST score	298
E value	4.0e-27

Match length 115
% identity 57
NCBI Description (X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No. 201933
Seq. ID LIB3048-030-Q1-L1-D1
Method BLASTX
NCBI GI g4263709
BLAST score 196
E value 4.0e-15
Match length 48
% identity 71
NCBI Description (AC006223) unknown protein [Arabidopsis thaliana]

Seq. No. 201934
Seq. ID LIB3048-030-Q1-L1-D10
Method BLASTX
NCBI GI g3641836
BLAST score 524
E value 1.0e-53
Match length 127
% identity 81
NCBI Description (AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 201935
Seq. ID LIB3048-030-Q1-L1-D11
Method BLASTX
NCBI GI g2244841
BLAST score 190
E value 2.0e-14
Match length 40
% identity 72
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201936
Seq. ID LIB3048-030-Q1-L1-D12
Method BLASTX
NCBI GI g2245070
BLAST score 357
E value 6.0e-34
Match length 120
% identity 62
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 201937
Seq. ID LIB3048-030-Q1-L1-D2
Method BLASTX
NCBI GI g1332579
BLAST score 592
E value 1.0e-65
Match length 137
% identity 9
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 201938
Seq. ID LIB3048-030-Q1-L1-D3

Method	BLASTX
NCBI GI	g1076641
BLAST score	161
E value	5.0e-11
Match length	41
% identity	71
NCBI Description	tau-protein kinase (EC 2.7.1.135) homolog - common tobacco >gi_456356_emb_CAA54803_ (X77763) shaggy like protein kinase [Nicotiana tabacum] >gi_1094395_prf__2106142A Ser/Thr protein kinase [Nicotiana tabacum]

Seq. No.	201939
Seq. ID	LIB3048-030-Q1-L1-D4
Method	BLASTX
NCBI GI	g3297827
BLAST score	448
E value	1.0e-44
Match length	105
% identity	83
NCBI Description	(AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	201940
Seq. ID	LIB3048-030-Q1-L1-D6
Method	BLASTX
NCBI GI	g2244806
BLAST score	236
E value	9.0e-20
Match length	139
% identity	43
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201941
Seq. ID	LIB3048-030-Q1-L1-D7
Method	BLASTX
NCBI GI	g3552003
BLAST score	604
E value	6.0e-63
Match length	137
% identity	85
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	201942
Seq. ID	LIB3048-030-Q1-L1-D9
Method	BLASTX
NCBI GI	g1706323
BLAST score	391
E value	5.0e-38
Match length	122

% identity	63
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	201943
Seq. ID	LIB3048-030-Q1-L1-E1
Method	BLASTX
NCBI GI	g2956783
BLAST score	316
E value	4.0e-29
Match length	137
% identity	49
NCBI Description	(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq. No.	201944
Seq. ID	LIB3048-030-Q1-L1-E11
Method	BLASTX
NCBI GI	g2944180
BLAST score	157
E value	2.0e-10
Match length	57
% identity	54
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	201945
Seq. ID	LIB3048-030-Q1-L1-E2
Method	BLASTX
NCBI GI	g1709498
BLAST score	556
E value	3.0e-57
Match length	124
% identity	80
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	201946
Seq. ID	LIB3048-030-Q1-L1-E3
Method	BLASTX
NCBI GI	g1841464
BLAST score	270
E value	9.0e-24
Match length	52
% identity	48
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	201947
Seq. ID	LIB3048-030-Q1-L1-E4
Method	BLASTX
NCBI GI	g483057
BLAST score	224
E value	2.0e-18

Match length	113
% identity	45
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	201948
Seq. ID	LIB3048-030-Q1-L1-E5
Method	BLASTX
NCBI GI	g1408460
BLAST score	413
E value	2.0e-40
Match length	137
% identity	60
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No.	201949
Seq. ID	LIB3048-030-Q1-L1-E6
Method	BLASTX
NCBI GI	g3420906
BLAST score	237
E value	4.0e-22
Match length	72
% identity	59
NCBI Description	(AF080595) zinc finger protein; WRKY1 [Pimpinella brachycarpa]

Seq. No.	201950
Seq. ID	LIB3048-030-Q1-L1-E7
Method	BLASTX
NCBI GI	g3063699
BLAST score	341
E value	4.0e-32
Match length	133
% identity	50
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	201951
Seq. ID	LIB3048-030-Q1-L1-E8
Method	BLASTX
NCBI GI	g2739279
BLAST score	372
E value	1.0e-35
Match length	126
% identity	59
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	201952
Seq. ID	LIB3048-030-Q1-L1-F1
Method	BLASTX
NCBI GI	g1142619
BLAST score	390
E value	8.0e-38
Match length	139

% identity	59
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	201953
Seq. ID	LIB3048-030-Q1-L1-F10
Method	BLASTX
NCBI GI	g231610
BLAST score	278
E value	4.0e-25
Match length	112
% identity	63
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	201954
Seq. ID	LIB3048-030-Q1-L1-F12
Method	BLASTX
NCBI GI	g2979550
BLAST score	278
E value	1.0e-24
Match length	120
% identity	48
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	201955
Seq. ID	LIB3048-030-Q1-L1-F3
Method	BLASTX
NCBI GI	g4531442
BLAST score	489
E value	2.0e-49
Match length	123
% identity	76
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	201956
Seq. ID	LIB3048-030-Q1-L1-F5
Method	BLASTX
NCBI GI	g4038056
BLAST score	166
E value	1.0e-21
Match length	122
% identity	47
NCBI Description	(AC005897) putative transposon [Arabidopsis thaliana]

Seq. No.	201957
Seq. ID	LIB3048-030-Q1-L1-F6
Method	BLASTX
NCBI GI	g232024
BLAST score	351
E value	3.0e-33
Match length	120
% identity	61

NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	201958
Seq. ID	LIB3048-030-Q1-L1-G11
Method	BLASTX
NCBI GI	g4539298
BLAST score	543
E value	3.0e-56
Match length	134
% identity	82
NCBI Description	(AL049480) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	201959
Seq. ID	LIB3048-030-Q1-L1-G12
Method	BLASTX
NCBI GI	g2129597
BLAST score	510
E value	6.0e-52
Match length	101
% identity	96
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	201960
Seq. ID	LIB3048-030-Q1-L1-G2
Method	BLASTX
NCBI GI	g3158376
BLAST score	458
E value	8.0e-46
Match length	124
% identity	74
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201961
Seq. ID	LIB3048-030-Q1-L1-G3
Method	BLASTX
NCBI GI	g4539383
BLAST score	483
E value	9.0e-49
Match length	128
% identity	69
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	201962
Seq. ID	LIB3048-030-Q1-L1-G4
Method	BLASTX
NCBI GI	g3158376
BLAST score	467
E value	7.0e-47

Match length	125
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	201963
Seq. ID	LIB3048-030-Q1-L1-G5
Method	BLASTX
NCBI GI	g1076282
BLAST score	157
E value	2.0e-10
Match length	32
% identity	91
NCBI Description	aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase [Arabidopsis thaliana]

Seq. No.	201964
Seq. ID	LIB3048-030-Q1-L1-G7
Method	BLASTN
NCBI GI	g1890351
BLAST score	36
E value	7.0e-11
Match length	64
% identity	89
NCBI Description	A.thaliana mRNA for transcription factor L2

Seq. No.	201965
Seq. ID	LIB3048-030-Q1-L1-G9
Method	BLASTX
NCBI GI	g167367
BLAST score	654
E value	8.0e-69
Match length	124
% identity	99
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	201966
Seq. ID	LIB3048-030-Q1-L1-H1
Method	BLASTX
NCBI GI	g4262236
BLAST score	467
E value	7.0e-47
Match length	123
% identity	72
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	201967
Seq. ID	LIB3048-030-Q1-L1-H10
Method	BLASTX
NCBI GI	g132944
BLAST score	545
E value	4.0e-56
Match length	106
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279

(M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	201968
Seq. ID	LIB3048-030-Q1-L1-H2
Method	BLASTX
NCBI GI	g548774
BLAST score	393
E value	3.0e-38
Match length	109
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	201969
Seq. ID	LIB3048-030-Q1-L1-H3
Method	BLASTX
NCBI GI	g4262236
BLAST score	204
E value	2.0e-16
Match length	73
% identity	58
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	201970
Seq. ID	LIB3048-030-Q1-L1-H5
Method	BLASTX
NCBI GI	g232024
BLAST score	350
E value	4.0e-33
Match length	120
% identity	61
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	201971
Seq. ID	LIB3048-030-Q1-L1-H6
Method	BLASTX
NCBI GI	g3492803
BLAST score	313
E value	9.0e-29
Match length	136
% identity	50
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	201972
Seq. ID	LIB3048-030-Q1-L1-H7
Method	BLASTX
NCBI GI	g2342724
BLAST score	391
E value	6.0e-38
Match length	137
% identity	70

NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	201973
Seq. ID	LIB3048-030-Q1-L1-H8
Method	BLASTX
NCBI GI	g4239845
BLAST score	299
E value	3.0e-27
Match length	127
% identity	53
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	201974
Seq. ID	LIB3048-030-Q1-L1-H9
Method	BLASTX
NCBI GI	g548488
BLAST score	446
E value	2.0e-44
Match length	122
% identity	63
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	201975
Seq. ID	LIB3048-031-Q1-L1-A1
Method	BLASTX
NCBI GI	g729470
BLAST score	629
E value	8.0e-66
Match length	140
% identity	86
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	201976
Seq. ID	LIB3048-031-Q1-L1-A10
Method	BLASTX
NCBI GI	g1620009
BLAST score	166
E value	1.0e-11
Match length	140
% identity	31
NCBI Description	(D85184) flavonoid 3',5'-hydroxylase [Gentiana triflora]

Seq. No.	201977
Seq. ID	LIB3048-031-Q1-L1-A11
Method	BLASTX
NCBI GI	g3492803
BLAST score	257
E value	2.0e-22
Match length	114
% identity	50
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	201978
Seq. ID	LIB3048-031-Q1-L1-A3
Method	BLASTX
NCBI GI	g167367
BLAST score	337
E value	3.0e-32
Match length	71
% identity	93
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	201979
Seq. ID	LIB3048-031-Q1-L1-A4
Method	BLASTX
NCBI GI	g3047114
BLAST score	418
E value	3.0e-41
Match length	113
% identity	72
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	201980
Seq. ID	LIB3048-031-Q1-L1-A5
Method	BLASTX
NCBI GI	g2443329
BLAST score	99
E value	2.0e-10
Match length	119
% identity	39
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	201981
Seq. ID	LIB3048-031-Q1-L1-A6
Method	BLASTX
NCBI GI	g3297816
BLAST score	216
E value	2.0e-17
Match length	90
% identity	49
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	201982
Seq. ID	LIB3048-031-Q1-L1-A9
Method	BLASTX
NCBI GI	g1706918
BLAST score	261
E value	8.0e-23
Match length	94
% identity	50
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	201983
Seq. ID	LIB3048-031-Q1-L1-B10
Method	BLASTX
NCBI GI	g4432844
BLAST score	190

E value	2.0e-14
Match length	66
% identity	55
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	201984
Seq. ID	LIB3048-031-Q1-L1-B11
Method	BLASTX
NCBI GI	g3152559
BLAST score	500
E value	8.0e-51
Match length	132
% identity	71
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	201985
Seq. ID	LIB3048-031-Q1-L1-B12
Method	BLASTX
NCBI GI	g548488
BLAST score	396
E value	1.0e-38
Match length	107
% identity	64
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	201986
Seq. ID	LIB3048-031-Q1-L1-B5
Method	BLASTX
NCBI GI	g4539383
BLAST score	485
E value	6.0e-49
Match length	132
% identity	70
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	201987
Seq. ID	LIB3048-031-Q1-L1-B6
Method	BLASTX
NCBI GI	g4106061
BLAST score	190
E value	2.0e-14
Match length	55
% identity	64
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	201988
Seq. ID	LIB3048-031-Q1-L1-B7
Method	BLASTX
NCBI GI	g1856971
BLAST score	589
E value	4.0e-61
Match length	144
% identity	80

NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	201989
Seq. ID	LIB3048-031-Q1-L1-B8
Method	BLASTX
NCBI GI	g1703028
BLAST score	149
E value	1.0e-09
Match length	82
% identity	39
NCBI Description	CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1 47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPL... >gi_2134919_pir__A57170 clathrin-associated protein AP47 homolog CLA20 - human >gi_807815_dbj_BAA07415_ (D38293) clathrin-like protein [Homo sapiens]

Seq. No.	201990
Seq. ID	LIB3048-031-Q1-L1-B9
Method	BLASTX
NCBI GI	g2959767
BLAST score	434
E value	5.0e-43
Match length	124
% identity	69
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	201991
Seq. ID	LIB3048-031-Q1-L1-C10
Method	BLASTX
NCBI GI	g1184075
BLAST score	215
E value	3.0e-17
Match length	131
% identity	3
NCBI Description	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No.	201992
Seq. ID	LIB3048-031-Q1-L1-C12
Method	BLASTX
NCBI GI	g3426043
BLAST score	351
E value	2.0e-33
Match length	115
% identity	62
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	201993
Seq. ID	LIB3048-031-Q1-L1-C3
Method	BLASTX

NCBI GI	g117988
BLAST score	570
E value	7.0e-59
Match length	111
% identity	94
NCBI Description	CYTOCHROME C >gi_65503_pir__CCCN cytochrome c - sea-island cotton

Seq. No.	201994
Seq. ID	LIB3048-031-Q1-L1-C5
Method	BLASTX
NCBI GI	g4539315
BLAST score	271
E value	8.0e-24
Match length	146
% identity	44
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	201995
Seq. ID	LIB3048-031-Q1-L1-C6
Method	BLASTX
NCBI GI	g2826786
BLAST score	340
E value	6.0e-32
Match length	104
% identity	63
NCBI Description	(Y10905) RAPB protein [Oryza sativa]

Seq. No.	201996
Seq. ID	LIB3048-031-Q1-L1-C8
Method	BLASTX
NCBI GI	g3552003
BLAST score	611
E value	1.0e-63
Match length	138
% identity	86
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	201997
Seq. ID	LIB3048-031-Q1-L1-C9
Method	BLASTX
NCBI GI	g1684855
BLAST score	474
E value	8.0e-48
Match length	100
% identity	21
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	201998
Seq. ID	LIB3048-031-Q1-L1-D1
Method	BLASTX
NCBI GI	g2791278
BLAST score	247
E value	4.0e-21
Match length	116
% identity	38
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	201999
Seq. ID	LIB3048-031-Q1-L1-D11
Method	BLASTX
NCBI GI	g3738257
BLAST score	492
E value	7.0e-50
Match length	104
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202000
Seq. ID	LIB3048-031-Q1-L1-D6
Method	BLASTX
NCBI GI	g2583123
BLAST score	262
E value	8.0e-23
Match length	60
% identity	80
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	202001
Seq. ID	LIB3048-031-Q1-L1-D7
Method	BLASTX
NCBI GI	g3687237
BLAST score	516
E value	1.0e-52
Match length	96
% identity	86
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	202002
Seq. ID	LIB3048-031-Q1-L1-D8
Method	BLASTX
NCBI GI	g2662343
BLAST score	223
E value	2.0e-18
Match length	75
% identity	68
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	202003
Seq. ID	LIB3048-031-Q1-L1-D9
Method	BLASTX
NCBI GI	g2463577

BLAST score 439
E value 9.0e-44
Match length 103
% identity 82
NCBI Description (AB007510) PRP8 protein [Homo sapiens]

Seq. No. 202004
Seq. ID LIB3048-031-Q1-L1-E1
Method BLASTX
NCBI GI g4490330
BLAST score 648
E value 4.0e-68
Match length 139
% identity 91
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 202005
Seq. ID LIB3048-031-Q1-L1-E12
Method BLASTX
NCBI GI g1332579
BLAST score 524
E value 1.0e-53
Match length 109
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 202006
Seq. ID LIB3048-031-Q1-L1-E3
Method BLASTX
NCBI GI g4558664
BLAST score 305
E value 8.0e-28
Match length 145
% identity 10
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 202007
Seq. ID LIB3048-031-Q1-L1-E6
Method BLASTX
NCBI GI g4218121
BLAST score 145
E value 5.0e-09
Match length 121
% identity 33
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 202008
Seq. ID LIB3048-031-Q1-L1-E7
Method BLASTX
NCBI GI g1778378
BLAST score 216
E value 2.0e-17
Match length 62
% identity 74
NCBI Description (U81289) NAP1Ps [Pisum sativum]

Seq. No.	202009
Seq. ID	LIB3048-031-Q1-L1-F1
Method	BLASTX
NCBI GI	g3892059
BLAST score	156
E value	2.0e-10
Match length	130
% identity	36
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	202010
Seq. ID	LIB3048-031-Q1-L1-F10
Method	BLASTX
NCBI GI	g1407705
BLAST score	416
E value	4.0e-41
Match length	100
% identity	79
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	202011
Seq. ID	LIB3048-031-Q1-L1-F2
Method	BLASTX
NCBI GI	g1906830
BLAST score	268
E value	5.0e-24
Match length	76
% identity	74
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	202012
Seq. ID	LIB3048-031-Q1-L1-F4
Method	BLASTX
NCBI GI	g2498706
BLAST score	150
E value	1.0e-09
Match length	42
% identity	67
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	202013
Seq. ID	LIB3048-031-Q1-L1-F5
Method	BLASTX
NCBI GI	g1742951
BLAST score	194
E value	8.0e-15
Match length	45
% identity	89
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	202014
Seq. ID	LIB3048-031-Q1-L1-F6
Method	BLASTX

NCBI GI	g2827561
BLAST score	223
E value	3.0e-18
Match length	117
% identity	41
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292809_emb_CAA19799_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	202015
Seq. ID	LIB3048-031-Q1-L1-F7
Method	BLASTX
NCBI GI	g4455340
BLAST score	442
E value	7.0e-44
Match length	116
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	202016
Seq. ID	LIB3048-031-Q1-L1-G1
Method	BLASTX
NCBI GI	g1129145
BLAST score	621
E value	7.0e-65
Match length	136
% identity	89
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	202017
Seq. ID	LIB3048-031-Q1-L1-G10
Method	BLASTX
NCBI GI	g2980641
BLAST score	248
E value	3.0e-21
Match length	112
% identity	43
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	202018
Seq. ID	LIB3048-031-Q1-L1-G11
Method	BLASTN
NCBI GI	g2829205
BLAST score	141
E value	2.0e-73
Match length	374
% identity	19
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	202019
Seq. ID	LIB3048-031-Q1-L1-G12
Method	BLASTX
NCBI GI	g2791278
BLAST score	170
E value	5.0e-12
Match length	105

% identity	40
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	202020
Seq. ID	LIB3048-031-Q1-L1-G7
Method	BLASTX
NCBI GI	g2507422
BLAST score	321
E value	1.0e-29
Match length	135
% identity	75
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202021
Seq. ID	LIB3048-031-Q1-L1-G8
Method	BLASTX
NCBI GI	g4539400
BLAST score	589
E value	4.0e-61
Match length	138
% identity	80
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	202022
Seq. ID	LIB3048-031-Q1-L1-G9
Method	BLASTX
NCBI GI	g2961372
BLAST score	646
E value	7.0e-68
Match length	129
% identity	91
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	202023
Seq. ID	LIB3048-031-Q1-L1-H1
Method	BLASTN
NCBI GI	g167336
BLAST score	189
E value	1.0e-102
Match length	337
% identity	89
NCBI Description	Gossypium hirsutum Lea4-A gene, complete CDS

Seq. No.	202024
Seq. ID	LIB3048-031-Q1-L1-H11
Method	BLASTX
NCBI GI	g3158376
BLAST score	336
E value	1.0e-31
Match length	122
% identity	57
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202025
Seq. ID	LIB3048-031-Q1-L1-H3
Method	BLASTX
NCBI GI	g2462756
BLAST score	388
E value	1.0e-37
Match length	122
% identity	66
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	202026
Seq. ID	LIB3048-031-Q1-L1-H5
Method	BLASTX
NCBI GI	g3928083
BLAST score	322
E value	8.0e-30
Match length	117
% identity	53
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	202027
Seq. ID	LIB3048-031-Q1-L1-H6
Method	BLASTX
NCBI GI	g2618699
BLAST score	206
E value	1.0e-31
Match length	112
% identity	63
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	202028
Seq. ID	LIB3048-031-Q1-L1-H8
Method	BLASTX
NCBI GI	g2244971
BLAST score	573
E value	3.0e-59
Match length	142
% identity	73
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202029
Seq. ID	LIB3048-031-Q1-L1-H9
Method	BLASTX
NCBI GI	g167367
BLAST score	781
E value	1.0e-83
Match length	148
% identity	99
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	202030
Seq. ID	LIB3048-032-Q1-L1-A1
Method	BLASTX
NCBI GI	g3152576
BLAST score	372
E value	9.0e-36

Match length	123
% identity	59
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	202031
Seq. ID	LIB3048-032-Q1-L1-A10
Method	BLASTX
NCBI GI	g3426043
BLAST score	340
E value	5.0e-32
Match length	113
% identity	61
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	202032
Seq. ID	LIB3048-032-Q1-L1-A11
Method	BLASTX
NCBI GI	g1943751
BLAST score	194
E value	7.0e-15
Match length	45
% identity	89
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	202033
Seq. ID	LIB3048-032-Q1-L1-A2
Method	BLASTX
NCBI GI	g232031
BLAST score	281
E value	4.0e-25
Match length	95
% identity	58
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	202034
Seq. ID	LIB3048-032-Q1-L1-A3
Method	BLASTX
NCBI GI	g1890575
BLAST score	287
E value	8.0e-26
Match length	68
% identity	78
NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	202035
Seq. ID	LIB3048-032-Q1-L1-A7
Method	BLASTX
NCBI GI	g4454484
BLAST score	262
E value	8.0e-23

Match length	103
% identity	57
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	202036
Seq. ID	LIB3048-032-Q1-L1-A8
Method	BLASTX
NCBI GI	g1703108
BLAST score	651
E value	2.0e-68
Match length	126
% identity	96
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	202037
Seq. ID	LIB3048-032-Q1-L1-A9
Method	BLASTX
NCBI GI	g4432866
BLAST score	365
E value	7.0e-35
Match length	138
% identity	49
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	202038
Seq. ID	LIB3048-032-Q1-L1-B1
Method	BLASTX
NCBI GI	g1002796
BLAST score	514
E value	2.0e-52
Match length	119
% identity	76
NCBI Description	(U33915) Cpm10 [Craterostigma plantagineum]

Seq. No.	202039
Seq. ID	LIB3048-032-Q1-L1-B11
Method	BLASTX
NCBI GI	g2330885
BLAST score	189
E value	2.0e-14
Match length	117
% identity	38
NCBI Description	(AJ000486) methionine gamma-lyase [Trichomonas vaginalis]

Seq. No.	202040
Seq. ID	LIB3048-032-Q1-L1-B12
Method	BLASTX
NCBI GI	g1255951
BLAST score	553
E value	6.0e-57
Match length	134

% identity	77
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	202041
Seq. ID	LIB3048-032-Q1-L1-B6
Method	BLASTX
NCBI GI	g1483230
BLAST score	297
E value	4.0e-27
Match length	76
% identity	80
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	202042
Seq. ID	LIB3048-032-Q1-L1-B7
Method	BLASTX
NCBI GI	g585419
BLAST score	234
E value	9.0e-26
Match length	85
% identity	68
NCBI Description	LIPOXYGENASE A >gi_482903 (U09026) lipoxygenase [Lycopersicon esculentum]

Seq. No.	202043
Seq. ID	LIB3048-032-Q1-L1-B8
Method	BLASTX
NCBI GI	g4100123
BLAST score	158
E value	7.0e-11
Match length	93
% identity	40
NCBI Description	(U94347) elongation factor EF-1alpha [Pyrobaculum aerophilum]

Seq. No.	202044
Seq. ID	LIB3048-032-Q1-L1-B9
Method	BLASTX
NCBI GI	g3395432
BLAST score	230
E value	3.0e-19
Match length	69
% identity	61
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	202045
Seq. ID	LIB3048-032-Q1-L1-C11
Method	BLASTX
NCBI GI	g2369766
BLAST score	376
E value	3.0e-36
Match length	102
% identity	69
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	202046
Seq. ID	LIB3048-032-Q1-L1-C12

Method	BLASTX
NCBI GI	g3426043
BLAST score	156
E value	2.0e-10
Match length	82
% identity	46
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	202047
Seq. ID	LIB3048-032-Q1-L1-C2
Method	BLASTX
NCBI GI	g3096919
BLAST score	163
E value	1.0e-11
Match length	40
% identity	78
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	202048
Seq. ID	LIB3048-032-Q1-L1-C4
Method	BLASTX
NCBI GI	g2130149
BLAST score	418
E value	2.0e-41
Match length	85
% identity	94
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	202049
Seq. ID	LIB3048-032-Q1-L1-C6
Method	BLASTX
NCBI GI	g3096919
BLAST score	171
E value	1.0e-12
Match length	43
% identity	70
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	202050
Seq. ID	LIB3048-032-Q1-L1-D1
Method	BLASTX
NCBI GI	g2129550
BLAST score	441
E value	5.0e-44
Match length	99
% identity	84
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	202051
Seq. ID	LIB3048-032-Q1-L1-D10
Method	BLASTN
NCBI GI	g4388705
BLAST score	39
E value	2.0e-12
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	202052
Seq. ID	LIB3048-032-Q1-L1-D12
Method	BLASTX
NCBI GI	g1174592
BLAST score	650
E value	2.0e-68
Match length	122
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	202053
Seq. ID	LIB3048-032-Q1-L1-D2
Method	BLASTX
NCBI GI	g1931640
BLAST score	277
E value	5.0e-25
Match length	74
% identity	65
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	202054
Seq. ID	LIB3048-032-Q1-L1-D3
Method	BLASTX
NCBI GI	g4539292
BLAST score	166
E value	4.0e-12
Match length	44
% identity	70
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	202055
Seq. ID	LIB3048-032-Q1-L1-D4
Method	BLASTX
NCBI GI	g3482933
BLAST score	387
E value	1.0e-37
Match length	98
% identity	72
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	202056
Seq. ID	LIB3048-032-Q1-L1-D6
Method	BLASTX
NCBI GI	g1174592
BLAST score	348
E value	3.0e-42
Match length	95
% identity	96
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	202057
Seq. ID	LIB3048-032-Q1-L1-D7
Method	BLASTX
NCBI GI	g3152576
BLAST score	208
E value	1.0e-16
Match length	96
% identity	45
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	202058
Seq. ID	LIB3048-032-Q1-L1-D9
Method	BLASTX
NCBI GI	g3738257
BLAST score	339
E value	5.0e-32
Match length	71
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202059
Seq. ID	LIB3048-032-Q1-L1-E12
Method	BLASTX
NCBI GI	g2492681
BLAST score	245
E value	7.0e-21
Match length	123
% identity	41
NCBI Description	PROBABLE COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_1432173 (U62960) CopB [Dictyostelium discoideum]

Seq. No.	202060
Seq. ID	LIB3048-032-Q1-L1-E4
Method	BLASTX
NCBI GI	g4239845
BLAST score	238
E value	3.0e-20
Match length	104
% identity	54
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202061

Seq. ID	LIB3048-032-Q1-L1-E7
Method	BLASTX
NCBI GI	g4235430
BLAST score	220
E value	3.0e-18
Match length	66
% identity	68
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	202062
Seq. ID	LIB3048-032-Q1-L1-E9
Method	BLASTX
NCBI GI	g133940
BLAST score	137
E value	1.0e-08
Match length	56
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	202063
Seq. ID	LIB3048-032-Q1-L1-F1
Method	BLASTX
NCBI GI	g1174162
BLAST score	592
E value	1.0e-61
Match length	114
% identity	91
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	202064
Seq. ID	LIB3048-032-Q1-L1-F10
Method	BLASTX
NCBI GI	g3892712
BLAST score	536
E value	5.0e-55
Match length	127
% identity	82
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	202065
Seq. ID	LIB3048-032-Q1-L1-F11
Method	BLASTX
NCBI GI	g2146797
BLAST score	532
E value	1.0e-54
Match length	121
% identity	80
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	202066
Seq. ID	LIB3048-032-Q1-L1-F12
Method	BLASTX
NCBI GI	g3297827
BLAST score	398
E value	8.0e-39
Match length	96
% identity	82
NCBI Description	(AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	202067
Seq. ID	LIB3048-032-Q1-L1-F6
Method	BLASTX
NCBI GI	g3158376
BLAST score	246
E value	4.0e-21
Match length	105
% identity	50
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202068
Seq. ID	LIB3048-032-Q1-L1-F8
Method	BLASTX
NCBI GI	g1272410
BLAST score	395
E value	1.0e-38
Match length	83
% identity	88
NCBI Description	(U52045) immunophilin precursor [Vicia faba]

Seq. No.	202069
Seq. ID	LIB3048-032-Q1-L1-G10
Method	BLASTX
NCBI GI	g1929056
BLAST score	527
E value	6.0e-54
Match length	124
% identity	81
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	202070
Seq. ID	LIB3048-032-Q1-L1-G3
Method	BLASTX
NCBI GI	g4406818
BLAST score	375
E value	4.0e-36
Match length	89
% identity	74
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	202071
Seq. ID	LIB3048-032-Q1-L1-G6
Method	BLASTX

NCBI GI	g625509
BLAST score	495
E value	2.0e-50
Match length	100
% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No.	202072
Seq. ID	LIB3048-032-Q1-L1-H10
Method	BLASTX
NCBI GI	g1168256
BLAST score	559
E value	9.0e-58
Match length	119
% identity	80
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	202073
Seq. ID	LIB3048-032-Q1-L1-H12
Method	BLASTX
NCBI GI	g119640
BLAST score	207
E value	1.0e-16
Match length	84
% identity	48
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir__S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	202074
Seq. ID	LIB3048-032-Q1-L1-H3
Method	BLASTX
NCBI GI	g2499524
BLAST score	143
E value	4.0e-09
Match length	88
% identity	44
NCBI Description	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_2137022_pir__I46528 sodium/dicarboxylate cotransporter - rabbit (fragment) >gi_758384 (U12186) sodium/dicarboxylate cotransporter [Oryctolagus cuniculus]

Seq. No.	202075
Seq. ID	LIB3048-032-Q1-L1-H7
Method	BLASTX
NCBI GI	g3393062
BLAST score	399
E value	6.0e-39
Match length	130
% identity	55
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202076
Seq. ID	LIB3048-032-Q1-L1-H8
Method	BLASTX
NCBI GI	g3142303
BLAST score	278
E value	8.0e-25
Match length	114
% identity	50
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	202077
Seq. ID	LIB3048-032-Q1-L1-H9
Method	BLASTX
NCBI GI	g2624383
BLAST score	353
E value	3.0e-58
Match length	137
% identity	77
NCBI Description	(Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]

Seq. No.	202078
Seq. ID	LIB3048-033-Q1-L1-A1
Method	BLASTX
NCBI GI	g1703200
BLAST score	625
E value	2.0e-65
Match length	128
% identity	92
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	202079
Seq. ID	LIB3048-033-Q1-L1-A10
Method	BLASTX
NCBI GI	g2351380
BLAST score	283
E value	3.0e-25
Match length	126
% identity	44
NCBI Description	(U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN

Seq. No.	202080
Seq. ID	LIB3048-033-Q1-L1-A3
Method	BLASTX
NCBI GI	g2245060
BLAST score	216
E value	2.0e-17
Match length	68
% identity	59

NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]
Seq. No.	202081
Seq. ID	LIB3048-033-Q1-L1-A4
Method	BLASTX
NCBI GI	g2827143
BLAST score	732
E value	7.0e-78
Match length	144
% identity	93
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	202082
Seq. ID	LIB3048-033-Q1-L1-A6
Method	BLASTX
NCBI GI	g282881
BLAST score	199
E value	2.0e-15
Match length	122
% identity	39
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	202083
Seq. ID	LIB3048-033-Q1-L1-A8
Method	BLASTX
NCBI GI	g543867
BLAST score	421
E value	2.0e-41
Match length	112
% identity	80
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]
Seq. No.	202084
Seq. ID	LIB3048-033-Q1-L1-A9
Method	BLASTX
NCBI GI	g4508068
BLAST score	190
E value	2.0e-14
Match length	66
% identity	62
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]
Seq. No.	202085
Seq. ID	LIB3048-033-Q1-L1-B1
Method	BLASTX
NCBI GI	g4204265
BLAST score	231
E value	3.0e-19
Match length	121
% identity	45

NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]
Seq. No.	202086
Seq. ID	LIB3048-033-Q1-L1-B10
Method	BLASTX
NCBI GI	g1708401
BLAST score	606
E value	4.0e-63
Match length	128
% identity	92
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)
Seq. No.	202087
Seq. ID	LIB3048-033-Q1-L1-B11
Method	BLASTX
NCBI GI	g4106061
BLAST score	185
E value	8.0e-14
Match length	52
% identity	65
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]
Seq. No.	202088
Seq. ID	LIB3048-033-Q1-L1-B12
Method	BLASTX
NCBI GI	g2440035
BLAST score	515
E value	1.0e-52
Match length	105
% identity	88
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]
Seq. No.	202089
Seq. ID	LIB3048-033-Q1-L1-B2
Method	BLASTX
NCBI GI	g1362109
BLAST score	366
E value	5.0e-35
Match length	105
% identity	62
NCBI Description	PAR-1a protein - common tobacco >gi_871485_emb_CAA58733_ (X83853) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]
Seq. No.	202090
Seq. ID	LIB3048-033-Q1-L1-B5
Method	BLASTX
NCBI GI	g3142303
BLAST score	273
E value	4.0e-24
Match length	136
% identity	44
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No.	202091
Seq. ID	LIB3048-033-Q1-L1-B8
Method	BLASTX
NCBI GI	g548488
BLAST score	509
E value	9.0e-52
Match length	143
% identity	62
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	202092
Seq. ID	LIB3048-033-Q1-L1-B9
Method	BLASTX
NCBI GI	g3947733
BLAST score	400
E value	5.0e-39
Match length	130
% identity	59
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	202093
Seq. ID	LIB3048-033-Q1-L1-C1
Method	BLASTX
NCBI GI	g2231034
BLAST score	550
E value	1.0e-56
Match length	130
% identity	82
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]

Seq. No.	202094
Seq. ID	LIB3048-033-Q1-L1-C10
Method	BLASTX
NCBI GI	g1272410
BLAST score	518
E value	7.0e-53
Match length	106
% identity	91
NCBI Description	(U52045) immunophilin precursor [Vicia faba]

Seq. No.	202095
Seq. ID	LIB3048-033-Q1-L1-C11
Method	BLASTX
NCBI GI	g3598857
BLAST score	195
E value	2.0e-27
Match length	117
% identity	55
NCBI Description	(AF072447) short-chain alcohol dehydrogenase [Ipomoea trifida]

Seq. No.	202096
Seq. ID	LIB3048-033-Q1-L1-C12
Method	BLASTX

NCBI GI	g2369766
BLAST score	420
E value	2.0e-41
Match length	115
% identity	68
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	202097
Seq. ID	LIB3048-033-Q1-L1-C7
Method	BLASTX
NCBI GI	g2443320
BLAST score	289
E value	6.0e-26
Match length	106
% identity	54
NCBI Description	(D85597) polyprotein [Oryza australiensis]

Seq. No.	202098
Seq. ID	LIB3048-033-Q1-L1-C9
Method	BLASTX
NCBI GI	g3063392
BLAST score	400
E value	5.0e-39
Match length	113
% identity	73
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	202099
Seq. ID	LIB3048-033-Q1-L1-D1
Method	BLASTX
NCBI GI	g3355467
BLAST score	166
E value	1.0e-11
Match length	134
% identity	31
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202100
Seq. ID	LIB3048-033-Q1-L1-D10
Method	BLASTX
NCBI GI	g1399265
BLAST score	201
E value	5.0e-16
Match length	71
% identity	58
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	202101
Seq. ID	LIB3048-033-Q1-L1-D12
Method	BLASTX
NCBI GI	g4325338
BLAST score	630
E value	5.0e-66
Match length	127
% identity	88
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	202102
Seq. ID	LIB3048-033-Q1-L1-D2
Method	BLASTX
NCBI GI	g4539423
BLAST score	343
E value	2.0e-32
Match length	92
% identity	75
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202103
Seq. ID	LIB3048-033-Q1-L1-D3
Method	BLASTX
NCBI GI	g1928981
BLAST score	221
E value	2.0e-18
Match length	64
% identity	72
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	202104
Seq. ID	LIB3048-033-Q1-L1-D5
Method	BLASTX
NCBI GI	g2494896
BLAST score	547
E value	3.0e-56
Match length	123
% identity	46
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	202105
Seq. ID	LIB3048-033-Q1-L1-D8
Method	BLASTX
NCBI GI	g1001135
BLAST score	189
E value	3.0e-14
Match length	51
% identity	75
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	202106
Seq. ID	LIB3048-033-Q1-L1-D9
Method	BLASTX
NCBI GI	g2980770
BLAST score	361
E value	2.0e-34
Match length	101
% identity	67
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	202107
Seq. ID	LIB3048-033-Q1-L1-E11
Method	BLASTN
NCBI GI	g899121
BLAST score	43
E value	6.0e-15
Match length	91
% identity	87
NCBI Description	Arabidopsis thaliana syntaxin homologue mRNA, complete cds

Seq. No.	202108
Seq. ID	LIB3048-033-Q1-L1-E12
Method	BLASTX
NCBI GI	g2129578
BLAST score	567
E value	1.0e-58
Match length	113
% identity	93
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	202109
Seq. ID	LIB3048-033-Q1-L1-E3
Method	BLASTX
NCBI GI	g1407705
BLAST score	615
E value	3.0e-64
Match length	144
% identity	81
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	202110
Seq. ID	LIB3048-033-Q1-L1-E4
Method	BLASTX
NCBI GI	g2129771
BLAST score	668
E value	2.0e-70
Match length	146
% identity	82
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	202111
Seq. ID	LIB3048-033-Q1-L1-E5
Method	BLASTX
NCBI GI	g1361983
BLAST score	502
E value	6.0e-51
Match length	143
% identity	73

NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	202112
Seq. ID	LIB3048-033-Q1-L1-E7
Method	BLASTX
NCBI GI	g3785978
BLAST score	185
E value	9.0e-14
Match length	40
% identity	75
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	202113
Seq. ID	LIB3048-033-Q1-L1-E8
Method	BLASTX
NCBI GI	g3294180
BLAST score	149
E value	1.0e-09
Match length	102
% identity	35
NCBI Description	(Z99129) dJ425C14.2 (Placental protein DIFF33 LIKE) [Homo sapiens]

Seq. No.	202114
Seq. ID	LIB3048-033-Q1-L1-E9
Method	BLASTX
NCBI GI	g1707857
BLAST score	641
E value	3.0e-67
Match length	134
% identity	90
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	202115
Seq. ID	LIB3048-033-Q1-L1-F1
Method	BLASTX
NCBI GI	g2443329
BLAST score	489
E value	2.0e-49
Match length	143
% identity	69
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	202116
Seq. ID	LIB3048-033-Q1-L1-F10
Method	BLASTX
NCBI GI	g3598857
BLAST score	318
E value	2.0e-29
Match length	113
% identity	55
NCBI Description	(AF072447) short-chain alcohol dehydrogenase [Ipomoea trifida]

Seq. No.	202117

Seq. ID LIB3048-033-Q1-L1-F12
Method BLASTX
NCBI GI g2597826
BLAST score 201
E value 1.0e-15
Match length 51
% identity 71
NCBI Description (Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No. 202118
Seq. ID LIB3048-033-Q1-L1-F3
Method BLASTX
NCBI GI g1245182
BLAST score 174
E value 1.0e-12
Match length 33
% identity 88
NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 202119
Seq. ID LIB3048-033-Q1-L1-F4
Method BLASTX
NCBI GI g3288823
BLAST score 194
E value 8.0e-15
Match length 57
% identity 70
NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]

Seq. No. 202120
Seq. ID LIB3048-033-Q1-L1-F7
Method BLASTX
NCBI GI g170354
BLAST score 700
E value 3.0e-74
Match length 141
% identity 22
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No. 202121
Seq. ID LIB3048-033-Q1-L1-F9
Method BLASTX
NCBI GI g2501850
BLAST score 625
E value 2.0e-65
Match length 127
% identity 94
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No. 202122
Seq. ID LIB3048-033-Q1-L1-G10
Method BLASTX
NCBI GI g3334147
BLAST score 518
E value 8.0e-53
Match length 124
% identity 81

NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202123
Seq. ID	LIB3048-033-Q1-L1-G11
Method	BLASTX
NCBI GI	g2997591
BLAST score	370
E value	2.0e-35
Match length	121
% identity	64
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	202124
Seq. ID	LIB3048-033-Q1-L1-G12
Method	BLASTX
NCBI GI	g3924597
BLAST score	205
E value	4.0e-16
Match length	113
% identity	37
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	202125
Seq. ID	LIB3048-033-Q1-L1-G2
Method	BLASTX
NCBI GI	g2944180
BLAST score	260
E value	2.0e-22
Match length	78
% identity	64
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	202126
Seq. ID	LIB3048-033-Q1-L1-G3
Method	BLASTX
NCBI GI	g2894598
BLAST score	157
E value	2.0e-10
Match length	82
% identity	38
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	202127
Seq. ID	LIB3048-033-Q1-L1-G8
Method	BLASTX
NCBI GI	g3319457
BLAST score	170
E value	5.0e-12
Match length	98
% identity	38
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	202128

Seq. ID	LIB3048-033-Q1-L1-H2
Method	BLASTX
NCBI GI	g3426048
BLAST score	392
E value	5.0e-38
Match length	140
% identity	77
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	202129
Seq. ID	LIB3048-033-Q1-L1-H3
Method	BLASTX
NCBI GI	g3834323
BLAST score	174
E value	2.0e-12
Match length	135
% identity	33
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	202130
Seq. ID	LIB3048-033-Q1-L1-H4
Method	BLASTX
NCBI GI	g417073
BLAST score	698
E value	7.0e-74
Match length	147
% identity	87
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	202131
Seq. ID	LIB3048-033-Q1-L1-H7
Method	BLASTX
NCBI GI	g2642158
BLAST score	620
E value	9.0e-65
Match length	142
% identity	78
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202132
Seq. ID	LIB3048-034-Q1-L1-A1
Method	BLASTX
NCBI GI	g2369714
BLAST score	700
E value	4.0e-74
Match length	140
% identity	95
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	202133
Seq. ID	LIB3048-034-Q1-L1-A10
Method	BLASTX
NCBI GI	g2642158

BLAST score	436
E value	3.0e-45
Match length	106
% identity	83
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202134
Seq. ID	LIB3048-034-Q1-L1-A11
Method	BLASTX
NCBI GI	g2739381
BLAST score	187
E value	9.0e-28
Match length	110
% identity	60
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202135
Seq. ID	LIB3048-034-Q1-L1-A2
Method	BLASTX
NCBI GI	g4262142
BLAST score	332
E value	5.0e-31
Match length	105
% identity	58
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	202136
Seq. ID	LIB3048-034-Q1-L1-A4
Method	BLASTX
NCBI GI	g4098244
BLAST score	612
E value	7.0e-64
Match length	138
% identity	84
NCBI Description	(U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No.	202137
Seq. ID	LIB3048-034-Q1-L1-A6
Method	BLASTX
NCBI GI	g3218396
BLAST score	241
E value	2.0e-20
Match length	91
% identity	51
NCBI Description	(AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	202138
Seq. ID	LIB3048-034-Q1-L1-A9
Method	BLASTX
NCBI GI	g1332579
BLAST score	567
E value	1.0e-58
Match length	116
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	202139
Seq. ID	LIB3048-034-Q1-L1-B1
Method	BLASTX
NCBI GI	g3336903
BLAST score	476
E value	7.0e-48
Match length	127
% identity	72
NCBI Description	(Y10809) bZIP DNA-binding protein [Petroselinum crispum]

Seq. No.	202140
Seq. ID	LIB3048-034-Q1-L1-B12
Method	BLASTX
NCBI GI	g4455317
BLAST score	177
E value	7.0e-13
Match length	123
% identity	12
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	202141
Seq. ID	LIB3048-034-Q1-L1-B2
Method	BLASTX
NCBI GI	g3892055
BLAST score	367
E value	4.0e-35
Match length	104
% identity	70
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	202142
Seq. ID	LIB3048-034-Q1-L1-B5
Method	BLASTX
NCBI GI	g3738257
BLAST score	456
E value	1.0e-45
Match length	105
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202143
Seq. ID	LIB3048-034-Q1-L1-B8
Method	BLASTX
NCBI GI	g4263695
BLAST score	279
E value	6.0e-25
Match length	139
% identity	22
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	202144
Seq. ID	LIB3048-034-Q1-L1-B9
Method	BLASTX

NCBI GI	g4432860
BLAST score	301
E value	1.0e-27
Match length	88
% identity	10
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	202145
Seq. ID	LIB3048-034-Q1-L1-C10
Method	BLASTX
NCBI GI	g2369766
BLAST score	435
E value	4.0e-43
Match length	115
% identity	70
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	202146
Seq. ID	LIB3048-034-Q1-L1-C12
Method	BLASTX
NCBI GI	g4336426
BLAST score	419
E value	3.0e-41
Match length	119
% identity	66
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	202147
Seq. ID	LIB3048-034-Q1-L1-C3
Method	BLASTX
NCBI GI	g2739279
BLAST score	356
E value	7.0e-34
Match length	121
% identity	60
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	202148
Seq. ID	LIB3048-034-Q1-L1-C6
Method	BLASTX
NCBI GI	g4239845
BLAST score	175
E value	1.0e-12
Match length	49
% identity	71
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202149
Seq. ID	LIB3048-034-Q1-L1-C7
Method	BLASTX
NCBI GI	g2130051
BLAST score	595
E value	6.0e-62

Match length	127
% identity	83
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	202150
Seq. ID	LIB3048-034-Q1-L1-C8
Method	BLASTX
NCBI GI	g465010
BLAST score	455
E value	1.0e-45
Match length	107
% identity	81
NCBI Description	URICASE II CLONE PCCLNUO-01 (URATE OXIDASE) >gi_1086286_pir__S38911 uricase II - Canavalia lineata >gi_432629_emb_CAA53904_ (X76286) uricase II [Canavalia lineata]

Seq. No.	202151
Seq. ID	LIB3048-034-Q1-L1-D1
Method	BLASTX
NCBI GI	g2827718
BLAST score	259
E value	2.0e-22
Match length	129
% identity	51
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	202152
Seq. ID	LIB3048-034-Q1-L1-D11
Method	BLASTX
NCBI GI	g872116
BLAST score	250
E value	7.0e-22
Match length	77
% identity	29
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	202153
Seq. ID	LIB3048-034-Q1-L1-D3
Method	BLASTX
NCBI GI	g1657621
BLAST score	551
E value	1.0e-56
Match length	128
% identity	80
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	202154
Seq. ID	LIB3048-034-Q1-L1-D4
Method	BLASTX
NCBI GI	g3152609
BLAST score	347

E value 9.0e-33
Match length 119
% identity 55
NCBI Description (AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No. 202155
Seq. ID LIB3048-034-Q1-L1-D6
Method BLASTX
NCBI GI g3687230
BLAST score 488
E value 3.0e-49
Match length 132
% identity 73
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 202156
Seq. ID LIB3048-034-Q1-L1-D7
Method BLASTX
NCBI GI g1888357
BLAST score 189
E value 3.0e-14
Match length 129
% identity 40
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No. 202157
Seq. ID LIB3048-034-Q1-L1-D8
Method BLASTX
NCBI GI g2088647
BLAST score 487
E value 2.0e-49
Match length 114
% identity 82
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No. 202158
Seq. ID LIB3048-034-Q1-L1-E1
Method BLASTX
NCBI GI g4455210
BLAST score 307
E value 4.0e-28
Match length 127
% identity 50
NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No. 202159
Seq. ID LIB3048-034-Q1-L1-E12
Method BLASTX
NCBI GI g1486472
BLAST score 311
E value 3.0e-45

Match length	114
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	202160
Seq. ID	LIB3048-034-Q1-L1-E2
Method	BLASTX
NCBI GI	g4454012
BLAST score	201
E value	3.0e-16
Match length	52
% identity	73
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	202161
Seq. ID	LIB3048-034-Q1-L1-E3
Method	BLASTX
NCBI GI	g282881
BLAST score	183
E value	9.0e-14
Match length	90
% identity	41
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	202162
Seq. ID	LIB3048-034-Q1-L1-E4
Method	BLASTX
NCBI GI	g2369714
BLAST score	361
E value	2.0e-34
Match length	124
% identity	71
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	202163
Seq. ID	LIB3048-034-Q1-L1-E5
Method	BLASTX
NCBI GI	g3297816
BLAST score	409
E value	5.0e-40
Match length	114
% identity	74
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	202164
Seq. ID	LIB3048-034-Q1-L1-E6
Method	BLASTX
NCBI GI	g2369714
BLAST score	298
E value	2.0e-46
Match length	115
% identity	80
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	202165
Seq. ID	LIB3048-034-Q1-L1-E8
Method	BLASTX
NCBI GI	g1620009
BLAST score	165
E value	2.0e-11
Match length	140
% identity	29
NCBI Description	(D85184) flavonoid 3',5'-hydroxylase [Gentiana triflora]

Seq. No.	202166
Seq. ID	LIB3048-034-Q1-L1-F1
Method	BLASTX
NCBI GI	g3552003
BLAST score	612
E value	7.0e-64
Match length	138
% identity	86
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	202167
Seq. ID	LIB3048-034-Q1-L1-F2
Method	BLASTX
NCBI GI	g3021336
BLAST score	376
E value	3.0e-36
Match length	96
% identity	74
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	202168
Seq. ID	LIB3048-034-Q1-L1-F5
Method	BLASTX
NCBI GI	g113742
BLAST score	173
E value	2.0e-12
Match length	124
% identity	34
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	202169
Seq. ID	LIB3048-034-Q1-L1-F6

Method	BLASTX
NCBI GI	g3297816
BLAST score	577
E value	1.0e-59
Match length	141
% identity	80
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	202170
Seq. ID	LIB3048-034-Q1-L1-F7
Method	BLASTX
NCBI GI	g3894165
BLAST score	146
E value	3.0e-09
Match length	53
% identity	53
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202171
Seq. ID	LIB3048-034-Q1-L1-F8
Method	BLASTX
NCBI GI	g4204297
BLAST score	712
E value	1.0e-75
Match length	142
% identity	94
NCBI Description	(AC003027) ADK1 [Arabidopsis thaliana]

Seq. No.	202172
Seq. ID	LIB3048-034-Q1-L1-G10
Method	BLASTX
NCBI GI	g4115371
BLAST score	339
E value	5.0e-32
Match length	82
% identity	74
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	202173
Seq. ID	LIB3048-034-Q1-L1-G12
Method	BLASTX
NCBI GI	g3158376
BLAST score	352
E value	2.0e-33
Match length	127
% identity	57
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202174
Seq. ID	LIB3048-034-Q1-L1-G4
Method	BLASTX
NCBI GI	g2129759
BLAST score	491
E value	1.0e-49
Match length	130
% identity	76
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana

>gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	202175
Seq. ID	LIB3048-034-Q1-L1-G7
Method	BLASTX
NCBI GI	g82131
BLAST score	425
E value	6.0e-42
Match length	126
% identity	68
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	202176
Seq. ID	LIB3048-034-Q1-L1-G9
Method	BLASTX
NCBI GI	g4454052
BLAST score	144
E value	5.0e-09
Match length	89
% identity	42
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202177
Seq. ID	LIB3048-034-Q1-L1-H1
Method	BLASTX
NCBI GI	g1841464
BLAST score	236
E value	9.0e-20
Match length	83
% identity	40
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	202178
Seq. ID	LIB3048-034-Q1-L1-H10
Method	BLASTX
NCBI GI	g3152576
BLAST score	353
E value	1.0e-33
Match length	123
% identity	57
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	202179
Seq. ID	LIB3048-034-Q1-L1-H2
Method	BLASTX
NCBI GI	g2499819
BLAST score	541
E value	2.0e-55
Match length	141
% identity	71
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease

[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	202180
Seq. ID	LIB3048-034-Q1-L1-H4
Method	BLASTX
NCBI GI	g3152609
BLAST score	153
E value	1.0e-10
Match length	55
% identity	49
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	202181
Seq. ID	LIB3048-034-Q1-L1-H5
Method	BLASTX
NCBI GI	g2624383
BLAST score	357
E value	2.0e-60
Match length	138
% identity	78
NCBI Description	(Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]

Seq. No.	202182
Seq. ID	LIB3048-034-Q1-L1-H7
Method	BLASTX
NCBI GI	g1304227
BLAST score	504
E value	3.0e-51
Match length	137
% identity	64
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	202183
Seq. ID	LIB3048-035-Q1-L1-A10
Method	BLASTX
NCBI GI	g3582328
BLAST score	210
E value	3.0e-20
Match length	105
% identity	51
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202184
Seq. ID	LIB3048-035-Q1-L1-A2
Method	BLASTX
NCBI GI	g4433048
BLAST score	393
E value	3.0e-38
Match length	123
% identity	62
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No. 202185

Seq. ID	LIB3048-035-Q1-L1-A3
Method	BLASTX
NCBI GI	g2275204
BLAST score	144
E value	5.0e-09
Match length	107
% identity	33
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	202186
Seq. ID	LIB3048-035-Q1-L1-A4
Method	BLASTX
NCBI GI	g4033424
BLAST score	463
E value	2.0e-46
Match length	104
% identity	85
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No.	202187
Seq. ID	LIB3048-035-Q1-L1-A6
Method	BLASTX
NCBI GI	g2642158
BLAST score	509
E value	9.0e-52
Match length	140
% identity	71
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202188
Seq. ID	LIB3048-035-Q1-L1-A7
Method	BLASTX
NCBI GI	g464707
BLAST score	516
E value	1.0e-52
Match length	105
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	202189

Seq. ID	LIB3048-035-Q1-L1-A8
Method	BLASTX
NCBI GI	g2497538
BLAST score	243
E value	1.0e-20
Match length	94
% identity	56
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	202190
Seq. ID	LIB3048-035-Q1-L1-A9
Method	BLASTX
NCBI GI	g1654140
BLAST score	584
E value	1.0e-60
Match length	128
% identity	86
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	202191
Seq. ID	LIB3048-035-Q1-L1-B1
Method	BLASTX
NCBI GI	g3158376
BLAST score	350
E value	3.0e-33
Match length	122
% identity	58
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202192
Seq. ID	LIB3048-035-Q1-L1-B12
Method	BLASTX
NCBI GI	g2129844
BLAST score	435
E value	4.0e-43
Match length	108
% identity	40
NCBI Description	stress-induced protein sti1 - soybean

Seq. No.	202193
Seq. ID	LIB3048-035-Q1-L1-B2
Method	BLASTX
NCBI GI	g1001135
BLAST score	169
E value	5.0e-12
Match length	51
% identity	67
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	202194
Seq. ID	LIB3048-035-Q1-L1-B3
Method	BLASTX
NCBI GI	g126770
BLAST score	713
E value	1.0e-75
Match length	135

% identity	99
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate synthase (EC 4.1.3.2) - upland cotton >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567) [Gossypium hirsutum]

Seq. No.	202195
Seq. ID	LIB3048-035-Q1-L1-B4
Method	BLASTX
NCBI GI	g2827546
BLAST score	329
E value	1.0e-30
Match length	126
% identity	48
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	202196
Seq. ID	LIB3048-035-Q1-L1-B5
Method	BLASTX
NCBI GI	g3914002
BLAST score	462
E value	3.0e-46
Match length	133
% identity	71
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	202197
Seq. ID	LIB3048-035-Q1-L1-B6
Method	BLASTX
NCBI GI	g1841464
BLAST score	270
E value	9.0e-24
Match length	52
% identity	48
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	202198
Seq. ID	LIB3048-035-Q1-L1-B7
Method	BLASTX
NCBI GI	g1407705
BLAST score	606
E value	3.0e-63
Match length	130
% identity	85
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	202199
Seq. ID	LIB3048-035-Q1-L1-B9
Method	BLASTX
NCBI GI	g4455365
BLAST score	256
E value	4.0e-22
Match length	57
% identity	77
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202200
Seq. ID	LIB3048-035-Q1-L1-C1
Method	BLASTX
NCBI GI	g2244792
BLAST score	606
E value	3.0e-63
Match length	127
% identity	83
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202201
Seq. ID	LIB3048-035-Q1-L1-C2
Method	BLASTX
NCBI GI	g3559816
BLAST score	530
E value	3.0e-54
Match length	137
% identity	74
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	202202
Seq. ID	LIB3048-035-Q1-L1-C8
Method	BLASTX
NCBI GI	g3367522
BLAST score	137
E value	6.0e-16
Match length	105
% identity	50
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	202203
Seq. ID	LIB3048-035-Q1-L1-C9
Method	BLASTX
NCBI GI	g2827546
BLAST score	329
E value	1.0e-30
Match length	131
% identity	47
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	202204
Seq. ID	LIB3048-035-Q1-L1-D10
Method	BLASTX
NCBI GI	g2443878
BLAST score	331
E value	6.0e-31
Match length	128
% identity	56
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	202205
Seq. ID	LIB3048-035-Q1-L1-D12
Method	BLASTX
NCBI GI	g2507421

BLAST score	179
E value	5.0e-14
Match length	48
% identity	90
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	202206
Seq. ID	LIB3048-035-Q1-L1-D2
Method	BLASTX
NCBI GI	g3025276
BLAST score	258
E value	2.0e-22
Match length	135
% identity	40
NCBI Description	HYPOTHETICAL 62.8 KD PROTEIN IN SSE1-CAR1 INTERGENIC REGION >gi_2132982_pir__S62012 probable membrane protein YPL109c - yeast (Saccharomyces cerevisiae) >gi_1163104 (U43503) Lph17p [Saccharomyces cerevisiae]

Seq. No.	202207
Seq. ID	LIB3048-035-Q1-L1-D3
Method	BLASTX
NCBI GI	g2618699
BLAST score	176
E value	9.0e-13
Match length	59
% identity	54
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	202208
Seq. ID	LIB3048-035-Q1-L1-D6
Method	BLASTN
NCBI GI	g3128135
BLAST score	37
E value	2.0e-11
Match length	161
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	202209
Seq. ID	LIB3048-035-Q1-L1-D7
Method	BLASTX
NCBI GI	g4454012
BLAST score	465
E value	1.0e-46
Match length	135
% identity	66
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	202210
Seq. ID	LIB3048-035-Q1-L1-D9
Method	BLASTX

NCBI GI	g2275204
BLAST score	362
E value	1.0e-34
Match length	85
% identity	78
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	202211
Seq. ID	LIB3048-035-Q1-L1-E10
Method	BLASTX
NCBI GI	g2465923
BLAST score	213
E value	4.0e-17
Match length	123
% identity	22
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	202212
Seq. ID	LIB3048-035-Q1-L1-E11
Method	BLASTN
NCBI GI	g2656025
BLAST score	41
E value	9.0e-14
Match length	57
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	202213
Seq. ID	LIB3048-035-Q1-L1-E12
Method	BLASTX
NCBI GI	g2827718
BLAST score	256
E value	4.0e-22
Match length	132
% identity	50
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	202214
Seq. ID	LIB3048-035-Q1-L1-E2
Method	BLASTX
NCBI GI	g1009232
BLAST score	204
E value	5.0e-16
Match length	73
% identity	60
NCBI Description	(L38828) EF-1-alpha-related GTP-binding protein [Nicotiana tabacum]

Seq. No.	202215
Seq. ID	LIB3048-035-Q1-L1-E3
Method	BLASTX
NCBI GI	g2245060
BLAST score	253

E value	9.0e-22
Match length	70
% identity	66
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	202216
Seq. ID	LIB3048-035-Q1-L1-E4
Method	BLASTX
NCBI GI	g4262228
BLAST score	386
E value	2.0e-37
Match length	136
% identity	32
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	202217
Seq. ID	LIB3048-035-Q1-L1-E6
Method	BLASTX
NCBI GI	g2995953
BLAST score	225
E value	2.0e-18
Match length	61
% identity	74
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	202218
Seq. ID	LIB3048-035-Q1-L1-E7
Method	BLASTX
NCBI GI	g2252830
BLAST score	186
E value	6.0e-14
Match length	80
% identity	54
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	202219
Seq. ID	LIB3048-035-Q1-L1-E9
Method	BLASTX
NCBI GI	g1174592
BLAST score	601
E value	1.0e-66
Match length	128
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	202220
Seq. ID	LIB3048-035-Q1-L1-F1
Method	BLASTX
NCBI GI	g3047082
BLAST score	321
E value	9.0e-30
Match length	92
% identity	65

NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	202221
Seq. ID	LIB3048-035-Q1-L1-F10
Method	BLASTX
NCBI GI	g1407705
BLAST score	571
E value	5.0e-59
Match length	135
% identity	81
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	202222
Seq. ID	LIB3048-035-Q1-L1-F11
Method	BLASTX
NCBI GI	g132944
BLAST score	611
E value	9.0e-64
Match length	120
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	202223
Seq. ID	LIB3048-035-Q1-L1-F2
Method	BLASTX
NCBI GI	g2642158
BLAST score	509
E value	9.0e-52
Match length	140
% identity	71
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202224
Seq. ID	LIB3048-035-Q1-L1-F3
Method	BLASTX
NCBI GI	g3738257
BLAST score	459
E value	5.0e-46
Match length	99
% identity	91
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202225
Seq. ID	LIB3048-035-Q1-L1-F4
Method	BLASTX
NCBI GI	g2827551
BLAST score	299
E value	4.0e-27
Match length	111
% identity	59
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	202226

Seq. ID	LIB3048-035-Q1-L1-F5
Method	BLASTX
NCBI GI	g4104972
BLAST score	510
E value	6.0e-52
Match length	130
% identity	76
NCBI Description	(AF043108) spermidine synthase 1 [Pisum sativum]

Seq. No.	202227
Seq. ID	LIB3048-035-Q1-L1-F6
Method	BLASTX
NCBI GI	g3297816
BLAST score	565
E value	2.0e-58
Match length	140
% identity	79
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	202228
Seq. ID	LIB3048-035-Q1-L1-G1
Method	BLASTX
NCBI GI	g3650032
BLAST score	274
E value	3.0e-24
Match length	60
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	202229
Seq. ID	LIB3048-035-Q1-L1-G4
Method	BLASTX
NCBI GI	g2118961
BLAST score	323
E value	1.0e-30
Match length	72
% identity	43
NCBI Description	ubiquitin - chicken >gi_3954791_emb_CAA26488_ (X02650) ubiquitin [Gallus gallus]

Seq. No.	202230
Seq. ID	LIB3048-035-Q1-L1-G5
Method	BLASTX
NCBI GI	g3687223
BLAST score	470
E value	3.0e-47
Match length	130
% identity	75
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202231
Seq. ID	LIB3048-035-Q1-L1-G8
Method	BLASTX
NCBI GI	g2462746
BLAST score	526
E value	9.0e-54

Match length	121
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	202232
Seq. ID	LIB3048-035-Q1-L1-H10
Method	BLASTX
NCBI GI	g4468046
BLAST score	298
E value	4.0e-27
Match length	115
% identity	57
NCBI Description	(X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No.	202233
Seq. ID	LIB3048-035-Q1-L1-H12
Method	BLASTX
NCBI GI	g4325338
BLAST score	658
E value	3.0e-69
Match length	135
% identity	87
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	202234
Seq. ID	LIB3048-035-Q1-L1-H2
Method	BLASTX
NCBI GI	g2827718
BLAST score	250
E value	2.0e-21
Match length	114
% identity	52
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	202235
Seq. ID	LIB3048-035-Q1-L1-H4
Method	BLASTX
NCBI GI	g2995953
BLAST score	196
E value	4.0e-15
Match length	52
% identity	71
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	202236
Seq. ID	LIB3048-035-Q1-L1-H9
Method	BLASTX
NCBI GI	g3212865
BLAST score	524
E value	1.0e-53
Match length	130
% identity	79
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	202237

Seq. ID	LIB3048-036-Q1-L1-A11
Method	BLASTX
NCBI GI	g2827143
BLAST score	694
E value	2.0e-73
Match length	140
% identity	87
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	202238
Seq. ID	LIB3048-036-Q1-L1-A2
Method	BLASTX
NCBI GI	g4239845
BLAST score	326
E value	2.0e-30
Match length	136
% identity	52
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202239
Seq. ID	LIB3048-036-Q1-L1-A4
Method	BLASTX
NCBI GI	g3075394
BLAST score	510
E value	6.0e-52
Match length	130
% identity	78
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	202240
Seq. ID	LIB3048-036-Q1-L1-A6
Method	BLASTX
NCBI GI	g2129825
BLAST score	479
E value	3.0e-48
Match length	108
% identity	84
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	202241
Seq. ID	LIB3048-036-Q1-L1-A7
Method	BLASTX
NCBI GI	g586339
BLAST score	158
E value	2.0e-21
Match length	95
% identity	53
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c [Saccharomyces cerevisiae]

Seq. No.	202242

Seq. ID	LIB3048-036-Q1-L1-B1
Method	BLASTX
NCBI GI	g2130149
BLAST score	681
E value	5.0e-72
Match length	131
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	202243
Seq. ID	LIB3048-036-Q1-L1-B11
Method	BLASTX
NCBI GI	g4567283
BLAST score	504
E value	4.0e-51
Match length	135
% identity	69
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	202244
Seq. ID	LIB3048-036-Q1-L1-B2
Method	BLASTX
NCBI GI	g3236476
BLAST score	357
E value	6.0e-34
Match length	81
% identity	91
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	202245
Seq. ID	LIB3048-036-Q1-L1-B5
Method	BLASTX
NCBI GI	g3158376
BLAST score	395
E value	2.0e-38
Match length	111
% identity	73
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202246
Seq. ID	LIB3048-036-Q1-L1-B8
Method	BLASTX
NCBI GI	g4006887
BLAST score	494
E value	5.0e-50
Match length	113
% identity	76
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	202247
Seq. ID	LIB3048-036-Q1-L1-C12
Method	BLASTX
NCBI GI	g730456
BLAST score	587
E value	7.0e-61

Match length	112
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	202248
Seq. ID	LIB3048-036-Q1-L1-C3
Method	BLASTX
NCBI GI	g464846
BLAST score	485
E value	6.0e-49
Match length	96
% identity	93
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	202249
Seq. ID	LIB3048-036-Q1-L1-C6
Method	BLASTX
NCBI GI	g3935168
BLAST score	350
E value	4.0e-33
Match length	113
% identity	65
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	202250
Seq. ID	LIB3048-036-Q1-L1-C7
Method	BLASTN
NCBI GI	g556421
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No.	202251
Seq. ID	LIB3048-036-Q1-L1-D10
Method	BLASTX
NCBI GI	g1351136
BLAST score	391
E value	6.0e-38
Match length	78
% identity	97
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_514946 (L22296) UDP-glucose:D-fructose 2-glucosyl-transferase [Zea mays] >gi_533252 (L33244) sucrose synthase 2 [Zea mays]

Seq. No.	202252
Seq. ID	LIB3048-036-Q1-L1-D2
Method	BLASTX
NCBI GI	g3493172
BLAST score	379
E value	1.0e-36
Match length	78

% identity	92
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	202253
Seq. ID	LIB3048-036-Q1-L1-D3
Method	BLASTX
NCBI GI	g170753
BLAST score	494
E value	5.0e-50
Match length	108
% identity	79
NCBI Description	(M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	202254
Seq. ID	LIB3048-036-Q1-L1-E10
Method	BLASTX
NCBI GI	g556409
BLAST score	257
E value	3.0e-22
Match length	107
% identity	55
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	202255
Seq. ID	LIB3048-036-Q1-L1-E11
Method	BLASTX
NCBI GI	g3068705
BLAST score	192
E value	1.0e-14
Match length	135
% identity	32
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	202256
Seq. ID	LIB3048-036-Q1-L1-E12
Method	BLASTX
NCBI GI	g417154
BLAST score	398
E value	1.0e-38
Match length	133
% identity	65
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	202257
Seq. ID	LIB3048-036-Q1-L1-E2
Method	BLASTX
NCBI GI	g416758
BLAST score	618
E value	1.0e-64
Match length	140
% identity	79
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]

>gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	202258
Seq. ID	LIB3048-036-Q1-L1-E3
Method	BLASTX
NCBI GI	g3158376
BLAST score	390
E value	7.0e-38
Match length	110
% identity	73
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202259
Seq. ID	LIB3048-036-Q1-L1-E9
Method	BLASTX
NCBI GI	g1173055
BLAST score	165
E value	2.0e-18
Match length	104
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	202260
Seq. ID	LIB3048-036-Q1-L1-F10
Method	BLASTX
NCBI GI	g3063710
BLAST score	364
E value	1.0e-34
Match length	133
% identity	53
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	202261
Seq. ID	LIB3048-036-Q1-L1-F2
Method	BLASTX
NCBI GI	g3142303
BLAST score	271
E value	7.0e-24
Match length	136
% identity	40
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	202262
Seq. ID	LIB3048-036-Q1-L1-F4
Method	BLASTX
NCBI GI	g2894599
BLAST score	524
E value	2.0e-53
Match length	108
% identity	85

NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	202263
Seq. ID	LIB3048-036-Q1-L1-F6
Method	BLASTX
NCBI GI	g2499498
BLAST score	106
E value	3.0e-09
Match length	65
% identity	54
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_1161602_emb_CAA88840_ (Z48976) phosphoglycerate kinase (PGK) [Nicotiana tabacum]

Seq. No.	202264
Seq. ID	LIB3048-036-Q1-L1-F7
Method	BLASTX
NCBI GI	g2864624
BLAST score	340
E value	6.0e-32
Match length	137
% identity	28
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	202265
Seq. ID	LIB3048-036-Q1-L1-F9
Method	BLASTX
NCBI GI	g401687
BLAST score	210
E value	1.0e-16
Match length	61
% identity	66
NCBI Description	HYPOTHETICAL PROTEIN IN RPCF 3'REGION >gi_322042_pir__C46448 hypothetical protein 65 (rpcF or cpeB 3' region) - Synechococcus sp. (fragment) >gi_552029 (M95288) phosphotyrosine protein phosphatase [Synechococcus sp.]

Seq. No.	202266
Seq. ID	LIB3048-036-Q1-L1-G11
Method	BLASTX
NCBI GI	g2661840
BLAST score	487
E value	4.0e-49
Match length	139
% identity	65
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	202267
Seq. ID	LIB3048-036-Q1-L1-G2
Method	BLASTX
NCBI GI	g3142303
BLAST score	179
E value	3.0e-13
Match length	80
% identity	42
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter

gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	202268
Seq. ID	LIB3048-036-Q1-L1-G3
Method	BLASTX
NCBI GI	g170753
BLAST score	501
E value	8.0e-51
Match length	106
% identity	80
NCBI Description	(M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	202269
Seq. ID	LIB3048-036-Q1-L1-G4
Method	BLASTX
NCBI GI	g481812
BLAST score	167
E value	3.0e-12
Match length	48
% identity	58
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	202270
Seq. ID	LIB3048-036-Q1-L1-G5
Method	BLASTX
NCBI GI	g2978452
BLAST score	412
E value	2.0e-40
Match length	113
% identity	71
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	202271
Seq. ID	LIB3048-036-Q1-L1-G6
Method	BLASTX
NCBI GI	g2827555
BLAST score	398
E value	9.0e-39
Match length	137
% identity	62
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	202272
Seq. ID	LIB3048-036-Q1-L1-G7
Method	BLASTX
NCBI GI	g2290683
BLAST score	510
E value	7.0e-52
Match length	111
% identity	83
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	202273
Seq. ID	LIB3048-036-Q1-L1-G8
Method	BLASTX
NCBI GI	g3540180
BLAST score	338
E value	1.0e-31
Match length	136
% identity	55
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	202274
Seq. ID	LIB3048-036-Q1-L1-H1
Method	BLASTX
NCBI GI	g4530126
BLAST score	260
E value	9.0e-23
Match length	80
% identity	62
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	202275
Seq. ID	LIB3048-036-Q1-L1-H10
Method	BLASTX
NCBI GI	g1399275
BLAST score	390
E value	3.0e-38
Match length	85
% identity	86
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	202276
Seq. ID	LIB3048-036-Q1-L1-H11
Method	BLASTX
NCBI GI	g3024122
BLAST score	675
E value	3.0e-71
Match length	140
% identity	91
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	202277
Seq. ID	LIB3048-036-Q1-L1-H12
Method	BLASTX
NCBI GI	g1709449
BLAST score	500
E value	7.0e-51
Match length	108
% identity	87
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate

dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No.	202278
Seq. ID	LIB3048-036-Q1-L1-H3
Method	BLASTX
NCBI GI	g1658197
BLAST score	508
E value	1.0e-51
Match length	105
% identity	88
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	202279
Seq. ID	LIB3048-036-Q1-L1-H4
Method	BLASTX
NCBI GI	g2369714
BLAST score	233
E value	7.0e-40
Match length	124
% identity	73
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	202280
Seq. ID	LIB3048-036-Q1-L1-H7
Method	BLASTX
NCBI GI	g2864624
BLAST score	346
E value	1.0e-32
Match length	137
% identity	28
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	202281
Seq. ID	LIB3048-036-Q1-L1-H8
Method	BLASTX
NCBI GI	g3128174
BLAST score	275
E value	2.0e-24
Match length	79
% identity	73
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202282
Seq. ID	LIB3048-036-Q1-L1-H9
Method	BLASTX
NCBI GI	g3355487
BLAST score	193
E value	1.0e-14
Match length	115
% identity	39
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	202283
Seq. ID	LIB3048-037-Q1-L1-A1
Method	BLASTX
NCBI GI	g1743354

BLAST score	404
E value	8.0e-40
Match length	90
% identity	74
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	202284
Seq. ID	LIB3048-037-Q1-L1-A10
Method	BLASTX
NCBI GI	g1762148
BLAST score	251
E value	1.0e-21
Match length	95
% identity	54
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]

Seq. No.	202285
Seq. ID	LIB3048-037-Q1-L1-A11
Method	BLASTX
NCBI GI	g3687223
BLAST score	261
E value	1.0e-22
Match length	135
% identity	50
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202286
Seq. ID	LIB3048-037-Q1-L1-A2
Method	BLASTX
NCBI GI	g135409
BLAST score	158
E value	5.0e-11
Match length	71
% identity	48
NCBI Description	TUBULIN ALPHA-2 CHAIN >gi_539004_pir__B53298 tubulin alpha-2 chain - Chlamydomonas reinhardtii >gi_167450 (M11448) alpha-2 tubulin [Chlamydomonas reinhardtii]

Seq. No.	202287
Seq. ID	LIB3048-037-Q1-L1-A7
Method	BLASTX
NCBI GI	g2739381
BLAST score	503
E value	5.0e-51
Match length	144
% identity	63
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202288
Seq. ID	LIB3048-037-Q1-L1-A8
Method	BLASTX
NCBI GI	g2739381
BLAST score	196
E value	3.0e-15
Match length	109
% identity	39
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202289
Seq. ID	LIB3048-037-Q1-L1-B1
Method	BLASTX
NCBI GI	g1399275
BLAST score	401
E value	2.0e-39
Match length	87
% identity	85
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	202290
Seq. ID	LIB3048-037-Q1-L1-B10
Method	BLASTX
NCBI GI	g2632105
BLAST score	245
E value	8.0e-21
Match length	74
% identity	68
NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	202291
Seq. ID	LIB3048-037-Q1-L1-B3
Method	BLASTX
NCBI GI	g3337352
BLAST score	382
E value	7.0e-37
Match length	134
% identity	61
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	202292
Seq. ID	LIB3048-037-Q1-L1-B5
Method	BLASTX
NCBI GI	g1346387
BLAST score	189
E value	4.0e-25
Match length	89
% identity	76
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	202293
Seq. ID	LIB3048-037-Q1-L1-B6
Method	BLASTX
NCBI GI	g4239845
BLAST score	207
E value	1.0e-16
Match length	93

% identity	52
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202294
Seq. ID	LIB3048-037-Q1-L1-B7
Method	BLASTX
NCBI GI	g1346387
BLAST score	415
E value	9.0e-41
Match length	134
% identity	71
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	202295
Seq. ID	LIB3048-037-Q1-L1-B8
Method	BLASTX
NCBI GI	g633110
BLAST score	600
E value	2.0e-62
Match length	133
% identity	89
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	202296
Seq. ID	LIB3048-037-Q1-L1-B9
Method	BLASTX
NCBI GI	g3080428
BLAST score	268
E value	5.0e-24
Match length	61
% identity	75
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	202297
Seq. ID	LIB3048-037-Q1-L1-C1
Method	BLASTX
NCBI GI	g1709804
BLAST score	379
E value	1.0e-36
Match length	108
% identity	69
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	202298
Seq. ID	LIB3048-037-Q1-L1-C11
Method	BLASTX
NCBI GI	g4432844
BLAST score	244
E value	1.0e-20
Match length	119

% identity	45
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	202299
Seq. ID	LIB3048-037-Q1-L1-C12
Method	BLASTN
NCBI GI	g304040
BLAST score	100
E value	6.0e-49
Match length	372
% identity	82
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	202300
Seq. ID	LIB3048-037-Q1-L1-C2
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	106
% identity	83
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202301
Seq. ID	LIB3048-037-Q1-L1-C3
Method	BLASTX
NCBI GI	g3335341
BLAST score	161
E value	6.0e-11
Match length	39
% identity	85
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	202302
Seq. ID	LIB3048-037-Q1-L1-C4
Method	BLASTX
NCBI GI	g4530126
BLAST score	445
E value	3.0e-44
Match length	143
% identity	63
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	202303
Seq. ID	LIB3048-037-Q1-L1-C6
Method	BLASTX
NCBI GI	g4530126
BLAST score	416
E value	7.0e-41
Match length	112
% identity	71
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	202304
Seq. ID	LIB3048-037-Q1-L1-C7
Method	BLASTX
NCBI GI	g3335341
BLAST score	171
E value	4.0e-12
Match length	41
% identity	85
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	202305
Seq. ID	LIB3048-037-Q1-L1-C8
Method	BLASTX
NCBI GI	g4239845
BLAST score	237
E value	7.0e-20
Match length	60
% identity	75
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202306
Seq. ID	LIB3048-037-Q1-L1-D1
Method	BLASTX
NCBI GI	g3873807
BLAST score	163
E value	3.0e-11
Match length	66
% identity	45
NCBI Description	(Z49907) B0491.1 [Caenorhabditis elegans]

Seq. No.	202307
Seq. ID	LIB3048-037-Q1-L1-D10
Method	BLASTX
NCBI GI	g4510346
BLAST score	353
E value	2.0e-33
Match length	97
% identity	72
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202308
Seq. ID	LIB3048-037-Q1-L1-D11
Method	BLASTX
NCBI GI	g1483230
BLAST score	426
E value	5.0e-42
Match length	116
% identity	78
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	202309
Seq. ID	LIB3048-037-Q1-L1-D12
Method	BLASTX
NCBI GI	g4220533
BLAST score	325
E value	3.0e-30

Match length	119
% identity	60
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	202310
Seq. ID	LIB3048-037-Q1-L1-D3
Method	BLASTX
NCBI GI	g3413425
BLAST score	252
E value	1.0e-21
Match length	123
% identity	44
NCBI Description	(AJ006309) protein tyrosine phosphatase [Arabidopsis thaliana]

Seq. No.	202311
Seq. ID	LIB3048-037-Q1-L1-D5
Method	BLASTN
NCBI GI	g556421
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No.	202312
Seq. ID	LIB3048-037-Q1-L1-D6
Method	BLASTX
NCBI GI	g4539315
BLAST score	258
E value	2.0e-22
Match length	132
% identity	46
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	202313
Seq. ID	LIB3048-037-Q1-L1-D9
Method	BLASTX
NCBI GI	g2494113
BLAST score	385
E value	1.0e-37
Match length	81
% identity	86
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	202314
Seq. ID	LIB3048-037-Q1-L1-E10
Method	BLASTX
NCBI GI	g2739381
BLAST score	329
E value	1.0e-30
Match length	112

% identity	58
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202315
Seq. ID	LIB3048-037-Q1-L1-E3
Method	BLASTX
NCBI GI	g2507422
BLAST score	311
E value	1.0e-28
Match length	125
% identity	68
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202316
Seq. ID	LIB3048-037-Q1-L1-E4
Method	BLASTX
NCBI GI	g2102691
BLAST score	347
E value	9.0e-33
Match length	107
% identity	66
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	202317
Seq. ID	LIB3048-037-Q1-L1-E5
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	106
% identity	83
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202318
Seq. ID	LIB3048-037-Q1-L1-E7
Method	BLASTX
NCBI GI	g119354
BLAST score	483
E value	7.0e-57
Match length	127
% identity	84
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	202319
Seq. ID	LIB3048-037-Q1-L1-E8
Method	BLASTX
NCBI GI	g3980264

BLAST score	743
E value	3.0e-79
Match length	145
% identity	95
NCBI Description	(AJ011383) 20S proteasome beta subunit [Cicer arietinum]

Seq. No.	202320
Seq. ID	LIB3048-037-Q1-L1-F11
Method	BLASTX
NCBI GI	g2996096
BLAST score	618
E value	1.0e-64
Match length	123
% identity	97
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	202321
Seq. ID	LIB3048-037-Q1-L1-F12
Method	BLASTX
NCBI GI	g4006829
BLAST score	205
E value	2.0e-16
Match length	92
% identity	48
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	202322
Seq. ID	LIB3048-037-Q1-L1-F6
Method	BLASTX
NCBI GI	g2642158
BLAST score	523
E value	2.0e-53
Match length	144
% identity	70
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202323
Seq. ID	LIB3048-037-Q1-L1-F7
Method	BLASTX
NCBI GI	g4262142
BLAST score	237
E value	5.0e-20
Match length	88
% identity	49
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	202324
Seq. ID	LIB3048-037-Q1-L1-F8
Method	BLASTX
NCBI GI	g1304227
BLAST score	381
E value	6.0e-37
Match length	103
% identity	64
NCBI Description	(D63781) Epoxide hydrolase [Glycine max]

>gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	202325
Seq. ID	LIB3048-037-Q1-L1-G1
Method	BLASTX
NCBI GI	g232024
BLAST score	279
E value	6.0e-25
Match length	103
% identity	56
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	202326
Seq. ID	LIB3048-037-Q1-L1-G11
Method	BLASTX
NCBI GI	g82083
BLAST score	568
E value	1.0e-58
Match length	118
% identity	93
NCBI Description	phosphopyruvate hydratase (EC 4.2.1.11) - tomato (fragment) >gi_1161573_emb_CAA41116_ (X58109) enolase [Lycopersicon esculentum]

Seq. No.	202327
Seq. ID	LIB3048-037-Q1-L1-G12
Method	BLASTX
NCBI GI	g2317906
BLAST score	430
E value	1.0e-42
Match length	87
% identity	94
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	202328
Seq. ID	LIB3048-037-Q1-L1-G2
Method	BLASTX
NCBI GI	g82426
BLAST score	380
E value	5.0e-37
Match length	85
% identity	42
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	202329
Seq. ID	LIB3048-037-Q1-L1-G3
Method	BLASTX
NCBI GI	g120673
BLAST score	546
E value	4.0e-56

Match length	131
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No.	202330
Seq. ID	LIB3048-037-Q1-L1-G4
Method	BLASTX
NCBI GI	g4539543
BLAST score	159
E value	5.0e-11
Match length	85
% identity	40
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	202331
Seq. ID	LIB3048-037-Q1-L1-G5
Method	BLASTX
NCBI GI	g629602
BLAST score	182
E value	6.0e-14
Match length	76
% identity	53
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	202332
Seq. ID	LIB3048-037-Q1-L1-G6
Method	BLASTX
NCBI GI	g4103243
BLAST score	303
E value	8.0e-28
Match length	103
% identity	63
NCBI Description	(AF022368) BIPOSTO [Arabidopsis thaliana]

Seq. No.	202333
Seq. ID	LIB3048-037-Q1-L1-G8
Method	BLASTX
NCBI GI	g3128209
BLAST score	420
E value	2.0e-41
Match length	116
% identity	72
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	202334
Seq. ID	LIB3048-037-Q1-L1-G9
Method	BLASTX
NCBI GI	g2642158
BLAST score	444
E value	2.0e-44

Match length	103
% identity	79
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202335
Seq. ID	LIB3048-037-Q1-L1-H1
Method	BLASTX
NCBI GI	g4309698
BLAST score	538
E value	4.0e-55
Match length	143
% identity	80
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	202336
Seq. ID	LIB3048-037-Q1-L1-H5
Method	BLASTX
NCBI GI	g2781345
BLAST score	486
E value	5.0e-49
Match length	138
% identity	61
NCBI Description	(AC003113) F24O1.2 [Arabidopsis thaliana]

Seq. No.	202337
Seq. ID	LIB3048-037-Q1-L1-H6
Method	BLASTN
NCBI GI	g167366
BLAST score	37
E value	5.0e-12
Match length	77
% identity	87
NCBI Description	Gossypium hirsutum peroxidase mRNA, complete cds

Seq. No.	202338
Seq. ID	LIB3048-037-Q1-L1-H7
Method	BLASTX
NCBI GI	g2462745
BLAST score	259
E value	2.0e-22
Match length	121
% identity	38
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	202339
Seq. ID	LIB3048-037-Q1-L1-H8
Method	BLASTX
NCBI GI	g464849
BLAST score	347
E value	2.0e-33
Match length	70
% identity	93
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202340
Seq. ID	LIB3048-038-Q1-L1-A11
Method	BLASTX
NCBI GI	g1724100
BLAST score	501
E value	7.0e-51
Match length	112
% identity	85
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	202341
Seq. ID	LIB3048-038-Q1-L1-A2
Method	BLASTX
NCBI GI	g4098128
BLAST score	419
E value	1.0e-55
Match length	134
% identity	82
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	202342
Seq. ID	LIB3048-038-Q1-L1-A3
Method	BLASTX
NCBI GI	g872116
BLAST score	434
E value	6.0e-43
Match length	138
% identity	33
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	202343
Seq. ID	LIB3048-038-Q1-L1-A4
Method	BLASTX
NCBI GI	g1706918
BLAST score	264
E value	5.0e-23
Match length	120
% identity	42
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202344
Seq. ID	LIB3048-038-Q1-L1-A5
Method	BLASTX
NCBI GI	g4455365
BLAST score	272
E value	5.0e-24
Match length	57
% identity	81
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202345
Seq. ID	LIB3048-038-Q1-L1-A6
Method	BLASTX
NCBI GI	g2465923
BLAST score	154
E value	4.0e-10

Match length	64
% identity	52
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	202346
Seq. ID	LIB3048-038-Q1-L1-A9
Method	BLASTX
NCBI GI	g2980641
BLAST score	250
E value	2.0e-21
Match length	108
% identity	45
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	202347
Seq. ID	LIB3048-038-Q1-L1-B1
Method	BLASTX
NCBI GI	g3297816
BLAST score	141
E value	8.0e-09
Match length	93
% identity	38
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	202348
Seq. ID	LIB3048-038-Q1-L1-B12
Method	BLASTX
NCBI GI	g3493172
BLAST score	561
E value	6.0e-58
Match length	118
% identity	93
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	202349
Seq. ID	LIB3048-038-Q1-L1-B2
Method	BLASTX
NCBI GI	g3044212
BLAST score	345
E value	1.0e-41
Match length	131
% identity	70
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	202350
Seq. ID	LIB3048-038-Q1-L1-B3
Method	BLASTX
NCBI GI	g3152576
BLAST score	233
E value	2.0e-30
Match length	111
% identity	64
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	202351

Seq. ID	LIB3048-038-Q1-L1-B4
Method	BLASTX
NCBI GI	g4544390
BLAST score	174
E value	1.0e-12
Match length	80
% identity	45
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202352
Seq. ID	LIB3048-038-Q1-L1-C1
Method	BLASTX
NCBI GI	g2739381
BLAST score	471
E value	3.0e-47
Match length	138
% identity	67
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202353
Seq. ID	LIB3048-038-Q1-L1-C10
Method	BLASTX
NCBI GI	g2597826
BLAST score	321
E value	9.0e-30
Match length	120
% identity	55
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	202354
Seq. ID	LIB3048-038-Q1-L1-C11
Method	BLASTX
NCBI GI	g3335375
BLAST score	285
E value	8.0e-45
Match length	122
% identity	72
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	202355
Seq. ID	LIB3048-038-Q1-L1-C12
Method	BLASTX
NCBI GI	g3492803
BLAST score	277
E value	1.0e-24
Match length	127
% identity	47
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	202356
Seq. ID	LIB3048-038-Q1-L1-C5
Method	BLASTX
NCBI GI	g2827755
BLAST score	386
E value	2.0e-37
Match length	93
% identity	87

NCBI Description	INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467) pyrophosphatase [Vigna radiata]

Seq. No.	202357
Seq. ID	LIB3048-038-Q1-L1-C7
Method	BLASTX
NCBI GI	g3738257
BLAST score	265
E value	2.0e-26
Match length	88
% identity	81
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202358
Seq. ID	LIB3048-038-Q1-L1-D1
Method	BLASTX
NCBI GI	g2435395
BLAST score	602
E value	1.0e-62
Match length	137
% identity	82
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	202359
Seq. ID	LIB3048-038-Q1-L1-D10
Method	BLASTX
NCBI GI	g4455365
BLAST score	254
E value	2.0e-22
Match length	56
% identity	79
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202360
Seq. ID	LIB3048-038-Q1-L1-D11
Method	BLASTX
NCBI GI	g3132698
BLAST score	127
E value	7.0e-16
Match length	104
% identity	57
NCBI Description	(AF061963) SAR DNA-binding protein-2 [Pisum sativum]

Seq. No.	202361
Seq. ID	LIB3048-038-Q1-L1-D4
Method	BLASTX
NCBI GI	g2739376
BLAST score	176
E value	2.0e-15
Match length	65
% identity	71
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	202362
Seq. ID	LIB3048-038-Q1-L1-D5

Method	BLASTX
NCBI GI	g3395432
BLAST score	120
E value	2.0e-12
Match length	96
% identity	45
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	202363
Seq. ID	LIB3048-038-Q1-L1-E1
Method	BLASTX
NCBI GI	g4220537
BLAST score	400
E value	5.0e-39
Match length	109
% identity	74
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	202364
Seq. ID	LIB3048-038-Q1-L1-E4
Method	BLASTX
NCBI GI	g4098128
BLAST score	324
E value	3.0e-48
Match length	128
% identity	83
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	202365
Seq. ID	LIB3048-038-Q1-L1-E5
Method	BLASTX
NCBI GI	g1129145
BLAST score	226
E value	9.0e-21
Match length	86
% identity	57
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	202366
Seq. ID	LIB3048-038-Q1-L1-E6
Method	BLASTX
NCBI GI	g1575556
BLAST score	531
E value	2.0e-54
Match length	132
% identity	80
NCBI Description	(U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']

Seq. No.	202367
Seq. ID	LIB3048-038-Q1-L1-E8
Method	BLASTX
NCBI GI	g3176690
BLAST score	570
E value	6.0e-59
Match length	136
% identity	82

NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	202368
Seq. ID	LIB3048-038-Q1-L1-E9
Method	BLASTX
NCBI GI	g541847
BLAST score	442
E value	5.0e-44
Match length	104
% identity	80
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	202369
Seq. ID	LIB3048-038-Q1-L1-F1
Method	BLASTX
NCBI GI	g3249105
BLAST score	191
E value	5.0e-16
Match length	123
% identity	42
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	202370
Seq. ID	LIB3048-038-Q1-L1-F12
Method	BLASTX
NCBI GI	g1706323
BLAST score	364
E value	7.0e-35
Match length	114
% identity	63
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	202371
Seq. ID	LIB3048-038-Q1-L1-F4
Method	BLASTX
NCBI GI	g1107526
BLAST score	244
E value	6.0e-21
Match length	72
% identity	68
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	202372
Seq. ID	LIB3048-038-Q1-L1-F5
Method	BLASTX
NCBI GI	g4508068
BLAST score	171
E value	2.0e-12
Match length	66
% identity	58
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	202373
Seq. ID	LIB3048-038-Q1-L1-F7
Method	BLASTX
NCBI GI	g3687223
BLAST score	401
E value	4.0e-39
Match length	127
% identity	69
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202374
Seq. ID	LIB3048-038-Q1-L1-G1
Method	BLASTX
NCBI GI	g2244792
BLAST score	211
E value	3.0e-17
Match length	77
% identity	53
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202375
Seq. ID	LIB3048-038-Q1-L1-G10
Method	BLASTX
NCBI GI	g3335355
BLAST score	271
E value	5.0e-24
Match length	76
% identity	19
NCBI Description	(AC004512) Match to polyubiquitin DNA gb_L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this region. [Arabi

Seq. No.	202376
Seq. ID	LIB3048-038-Q1-L1-G11
Method	BLASTX
NCBI GI	g2281085
BLAST score	273
E value	4.0e-24
Match length	128
% identity	50
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	202377
Seq. ID	LIB3048-038-Q1-L1-G12
Method	BLASTX
NCBI GI	g2231034
BLAST score	479
E value	2.0e-48
Match length	117
% identity	79
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]

Seq. No.	202378

Seq. ID	LIB3048-038-Q1-L1-G8
Method	BLASTX
NCBI GI	g584863
BLAST score	142
E value	2.0e-12
Match length	85
% identity	43
NCBI Description	CYTOCHROME P450 71A4 (CYPLXXIA4) (P-450EG2) >gi_480395_pir__S36805 cytochrome P450 71A4 - eggplant >gi_402224_emb_CAA50312_ (X70981) P450 hydroxylase [Solanum melongena]

Seq. No.	202379
Seq. ID	LIB3048-038-Q1-L1-G9
Method	BLASTX
NCBI GI	g4567260
BLAST score	599
E value	2.0e-62
Match length	132
% identity	83
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	202380
Seq. ID	LIB3048-038-Q1-L1-H1
Method	BLASTX
NCBI GI	g3132698
BLAST score	321
E value	4.0e-30
Match length	77
% identity	83
NCBI Description	(AF061963) SAR DNA-binding protein-2 [Pisum sativum]

Seq. No.	202381
Seq. ID	LIB3048-038-Q1-L1-H10
Method	BLASTX
NCBI GI	g4098244
BLAST score	453
E value	2.0e-45
Match length	106
% identity	83
NCBI Description	(U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No.	202382
Seq. ID	LIB3048-038-Q1-L1-H11
Method	BLASTX
NCBI GI	g4185142
BLAST score	216
E value	2.0e-26
Match length	107
% identity	68
NCBI Description	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]

Seq. No.	202383
Seq. ID	LIB3048-038-Q1-L1-H12
Method	BLASTX

NCBI GI	g543867
BLAST score	216
E value	1.0e-17
Match length	68
% identity	75
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	202384
Seq. ID	LIB3048-038-Q1-L1-H2
Method	BLASTX
NCBI GI	g1706918
BLAST score	223
E value	3.0e-18
Match length	120
% identity	38
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202385
Seq. ID	LIB3048-038-Q1-L1-H3
Method	BLASTX
NCBI GI	g2500399
BLAST score	429
E value	2.0e-42
Match length	108
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098) ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls, embryos, Peptide, 253 aa] [Ambystoma mexicanum]

Seq. No.	202386
Seq. ID	LIB3048-038-Q1-L1-H4
Method	BLASTX
NCBI GI	g1399307
BLAST score	323
E value	3.0e-30
Match length	93
% identity	75
NCBI Description	(U41475) phosphoinositide-specific phospholipase C P25 [Glycine max]

Seq. No.	202387
Seq. ID	LIB3048-038-Q1-L1-H7
Method	BLASTX
NCBI GI	g1856971
BLAST score	317
E value	3.0e-36
Match length	105
% identity	74
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	202388
Seq. ID	LIB3048-038-Q1-L1-H8
Method	BLASTX
NCBI GI	g1107526
BLAST score	281
E value	9.0e-39
Match length	106
% identity	75
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	202389
Seq. ID	LIB3048-038-Q1-L1-H9
Method	BLASTX
NCBI GI	g3492803
BLAST score	255
E value	4.0e-22
Match length	114
% identity	49
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	202390
Seq. ID	LIB3048-039-Q1-L1-A11
Method	BLASTX
NCBI GI	g3158376
BLAST score	345
E value	1.0e-32
Match length	97
% identity	70
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202391
Seq. ID	LIB3048-039-Q1-L1-A12
Method	BLASTX
NCBI GI	g4309889
BLAST score	151
E value	7.0e-10
Match length	78
% identity	37
NCBI Description	(AC004983) similar to PID:g3877944 [Homo sapiens]

Seq. No.	202392
Seq. ID	LIB3048-039-Q1-L1-A2
Method	BLASTX
NCBI GI	g3461820
BLAST score	301
E value	2.0e-27
Match length	62
% identity	81
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	202393
Seq. ID	LIB3048-039-Q1-L1-A3
Method	BLASTX
NCBI GI	g4490732
BLAST score	180
E value	3.0e-13
Match length	71

% identity	56
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	202394
Seq. ID	LIB3048-039-Q1-L1-A4
Method	BLASTX
NCBI GI	g4210451
BLAST score	150
E value	1.0e-09
Match length	57
% identity	60
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No.	202395
Seq. ID	LIB3048-039-Q1-L1-A5
Method	BLASTX
NCBI GI	g417073
BLAST score	597
E value	4.0e-62
Match length	146
% identity	77
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	202396
Seq. ID	LIB3048-039-Q1-L1-A6
Method	BLASTX
NCBI GI	g120669
BLAST score	451
E value	5.0e-45
Match length	91
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	202397
Seq. ID	LIB3048-039-Q1-L1-A8
Method	BLASTN
NCBI GI	g3582780
BLAST score	47
E value	2.0e-17
Match length	67
% identity	93
NCBI Description	Nicotiana tabacum clone 354 peroxisomal targeting sequence 1 receptor (PEX5) mRNA, partial cds

Seq. No.	202398
Seq. ID	LIB3048-039-Q1-L1-A9
Method	BLASTX
NCBI GI	g1335862
BLAST score	400

E value	3.0e-39
Match length	96
% identity	82
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	202399
Seq. ID	LIB3048-039-Q1-L1-B10
Method	BLASTX
NCBI GI	g2499710
BLAST score	572
E value	3.0e-59
Match length	116
% identity	91
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	202400
Seq. ID	LIB3048-039-Q1-L1-B4
Method	BLASTX
NCBI GI	g606942
BLAST score	165
E value	2.0e-11
Match length	77
% identity	52
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	202401
Seq. ID	LIB3048-039-Q1-L1-B5
Method	BLASTX
NCBI GI	g2052383
BLAST score	213
E value	3.0e-17
Match length	43
% identity	88
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]

Seq. No.	202402
Seq. ID	LIB3048-039-Q1-L1-B6
Method	BLASTX
NCBI GI	g1762148
BLAST score	559
E value	1.0e-57
Match length	112
% identity	94
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]

Seq. No.	202403
Seq. ID	LIB3048-039-Q1-L1-B7
Method	BLASTX
NCBI GI	g1174592
BLAST score	745
E value	2.0e-79
Match length	141
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No.	202404
Seq. ID	LIB3048-039-Q1-L1-B8
Method	BLASTX
NCBI GI	g1084349
BLAST score	494
E value	5.0e-50
Match length	129
% identity	78
NCBI Description	aldehyde dehydrogenase homolog btg-26 - rape >gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No.	202405
Seq. ID	LIB3048-039-Q1-L1-C1
Method	BLASTX
NCBI GI	g2076623
BLAST score	152
E value	7.0e-10
Match length	140
% identity	31
NCBI Description	(Z95151) PtrB [Mycobacterium leprae]

Seq. No.	202406
Seq. ID	LIB3048-039-Q1-L1-C10
Method	BLASTX
NCBI GI	g2980641
BLAST score	253
E value	7.0e-22
Match length	109
% identity	45
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	202407
Seq. ID	LIB3048-039-Q1-L1-C12
Method	BLASTX
NCBI GI	g2864609
BLAST score	302
E value	1.0e-27
Match length	100
% identity	59
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	202408
Seq. ID	LIB3048-039-Q1-L1-C2
Method	BLASTX
NCBI GI	g4467145
BLAST score	161
E value	4.0e-16
Match length	54
% identity	83
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	202409
Seq. ID	LIB3048-039-Q1-L1-C4
Method	BLASTX
NCBI GI	g1684857
BLAST score	611
E value	1.0e-63
Match length	125
% identity	39
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	202410
Seq. ID	LIB3048-039-Q1-L1-C5
Method	BLASTX
NCBI GI	g1854581
BLAST score	200
E value	7.0e-16
Match length	73
% identity	56
NCBI Description	(L24120) peroxidase precursor [Linum usitatissimum]

Seq. No.	202411
Seq. ID	LIB3048-039-Q1-L1-C7
Method	BLASTX
NCBI GI	g2499819
BLAST score	521
E value	3.0e-53
Match length	139
% identity	70
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	202412
Seq. ID	LIB3048-039-Q1-L1-C8
Method	BLASTX
NCBI GI	g1778378
BLAST score	220
E value	6.0e-18
Match length	62
% identity	74
NCBI Description	(U81289) NAP1Ps [Pisum sativum]

Seq. No.	202413
Seq. ID	LIB3048-039-Q1-L1-C9
Method	BLASTX
NCBI GI	g2618721
BLAST score	146
E value	2.0e-09
Match length	45
% identity	67
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	202414
Seq. ID	LIB3048-039-Q1-L1-D10

Method	BLASTX
NCBI GI	g3805845
BLAST score	499
E value	1.0e-50
Match length	126
% identity	71
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	202415
Seq. ID	LIB3048-039-Q1-L1-D11
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	71
% identity	87
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202416
Seq. ID	LIB3048-039-Q1-L1-D12
Method	BLASTX
NCBI GI	g4185136
BLAST score	481
E value	2.0e-48
Match length	129
% identity	67
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	202417
Seq. ID	LIB3048-039-Q1-L1-D2
Method	BLASTX
NCBI GI	g2570164
BLAST score	439
E value	1.0e-43
Match length	123
% identity	63
NCBI Description	(D45183) chitinase [Chenopodium amaranticolor]

Seq. No.	202418
Seq. ID	LIB3048-039-Q1-L1-D4
Method	BLASTX
NCBI GI	g285741
BLAST score	455
E value	2.0e-45
Match length	134
% identity	67
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	202419
Seq. ID	LIB3048-039-Q1-L1-D5
Method	BLASTX
NCBI GI	g1175557
BLAST score	161

E value	6.0e-11
Match length	99
% identity	35
NCBI Description	HYPOTHETICAL PROTEIN HI1161 >gi_1073773_pir__A64187 15 kDa protein (P15) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574088 (U32796) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No.	202420
Seq. ID	LIB3048-039-Q1-L1-D8
Method	BLASTX
NCBI GI	g2146797
BLAST score	585
E value	1.0e-60
Match length	141
% identity	77
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	202421
Seq. ID	LIB3048-039-Q1-L1-E1
Method	BLASTX
NCBI GI	g2624383
BLAST score	386
E value	1.0e-62
Match length	143
% identity	78
NCBI Description	(Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]

Seq. No.	202422
Seq. ID	LIB3048-039-Q1-L1-E10
Method	BLASTX
NCBI GI	g2462749
BLAST score	162
E value	3.0e-11
Match length	114
% identity	38
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	202423
Seq. ID	LIB3048-039-Q1-L1-E2
Method	BLASTX
NCBI GI	g2827718
BLAST score	261
E value	1.0e-22
Match length	133
% identity	50
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	202424
Seq. ID	LIB3048-039-Q1-L1-E3
Method	BLASTX
NCBI GI	g2618721

BLAST score	169
E value	6.0e-12
Match length	59
% identity	64
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	202425
Seq. ID	LIB3048-039-Q1-L1-E4
Method	BLASTX
NCBI GI	g1706918
BLAST score	292
E value	3.0e-26
Match length	126
% identity	46
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202426
Seq. ID	LIB3048-039-Q1-L1-E7
Method	BLASTX
NCBI GI	g2244792
BLAST score	312
E value	9.0e-29
Match length	81
% identity	75
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202427
Seq. ID	LIB3048-039-Q1-L1-E8
Method	BLASTX
NCBI GI	g1657621
BLAST score	368
E value	9.0e-38
Match length	116
% identity	71
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	202428
Seq. ID	LIB3048-039-Q1-L1-E9
Method	BLASTX
NCBI GI	g464775
BLAST score	553
E value	5.0e-57
Match length	126
% identity	84
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	202429
Seq. ID	LIB3048-039-Q1-L1-F1
Method	BLASTX
NCBI GI	g2290683
BLAST score	455
E value	2.0e-45
Match length	98

% identity	84
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	202430
Seq. ID	LIB3048-039-Q1-L1-F3
Method	BLASTX
NCBI GI	g1335862
BLAST score	514
E value	2.0e-52
Match length	134
% identity	76
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	202431
Seq. ID	LIB3048-039-Q1-L1-F4
Method	BLASTX
NCBI GI	g2119362
BLAST score	180
E value	2.0e-13
Match length	58
% identity	32
NCBI Description	calmodulin - mouse >gi_469422 (M19381) calmodulin [Mus musculus]

Seq. No.	202432
Seq. ID	LIB3048-039-Q1-L1-F6
Method	BLASTX
NCBI GI	g3024756
BLAST score	176
E value	4.0e-13
Match length	83
% identity	42
NCBI Description	TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi_1926403_emb_CAA71604_ (Y10582) type II DNA topoisomerase subunit B [Sulfolobus shibatae]

Seq. No.	202433
Seq. ID	LIB3048-039-Q1-L1-F7
Method	BLASTX
NCBI GI	g132939
BLAST score	520
E value	5.0e-53
Match length	143
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	202434
Seq. ID	LIB3048-039-Q1-L1-F9
Method	BLASTX
NCBI GI	g2244806
BLAST score	203
E value	6.0e-16
Match length	123
% identity	42
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202435
Seq. ID	LIB3048-039-Q1-L1-G1
Method	BLASTX
NCBI GI	g4544454
BLAST score	563
E value	4.0e-58
Match length	138
% identity	77
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	202436
Seq. ID	LIB3048-039-Q1-L1-G10
Method	BLASTX
NCBI GI	g1658197
BLAST score	160
E value	3.0e-11
Match length	74
% identity	46
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	202437
Seq. ID	LIB3048-039-Q1-L1-G11
Method	BLASTX
NCBI GI	g4432844
BLAST score	190
E value	2.0e-14
Match length	66
% identity	55
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	202438
Seq. ID	LIB3048-039-Q1-L1-G12
Method	BLASTX
NCBI GI	g3420906
BLAST score	237
E value	3.0e-22
Match length	72
% identity	59
NCBI Description	(AF080595) zinc finger protein; WRKY1 [Pimpinella brachycarpa]

Seq. No.	202439
Seq. ID	LIB3048-039-Q1-L1-G3
Method	BLASTX
NCBI GI	g1572819
BLAST score	237
E value	7.0e-20
Match length	98
% identity	49
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	202440
Seq. ID	LIB3048-039-Q1-L1-G4
Method	BLASTX

NCBI GI	g4455317
BLAST score	176
E value	9.0e-13
Match length	123
% identity	12
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	202441
Seq. ID	LIB3048-039-Q1-L1-G5
Method	BLASTX
NCBI GI	g515503
BLAST score	398
E value	1.0e-38
Match length	146
% identity	52
NCBI Description	(U12013) 4-coumarate-CoA ligase enzyme [Pinus taeda] >gi_1143308 (U39404) 4-coumarate:CoA ligase [Pinus taeda] >gi_1143310 (U39405) 4-coumarate:CoA ligase [Pinus taeda]

Seq. No.	202442
Seq. ID	LIB3048-039-Q1-L1-G6
Method	BLASTX
NCBI GI	g1076655
BLAST score	209
E value	9.0e-17
Match length	84
% identity	51
NCBI Description	dioxygenase - eggplant >gi_607190_emb_CAA54557_ (X77368) dioxygenase [Solanum melongena]

Seq. No.	202443
Seq. ID	LIB3048-039-Q1-L1-G9
Method	BLASTX
NCBI GI	g1335862
BLAST score	457
E value	1.0e-45
Match length	126
% identity	72
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	202444
Seq. ID	LIB3048-039-Q1-L1-H10
Method	BLASTX
NCBI GI	g2739381
BLAST score	394
E value	2.0e-38
Match length	110
% identity	68
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202445
Seq. ID	LIB3048-039-Q1-L1-H11
Method	BLASTX
NCBI GI	g478389
BLAST score	231
E value	1.0e-19

Match length	69
% identity	64
NCBI Description	peroxidase (EC 1.11.1.7) precursor, anionic - Japanese aspen x large-toothed aspen >gi_217997_dbj_BAA01877_ (D11102) peroxidase [Populus kitakamiensis] >gi_444801_prf__1908234A anionic peroxidase [Populus kitakamiensis]

Seq. No.	202446
Seq. ID	LIB3048-039-Q1-L1-H12
Method	BLASTX
NCBI GI	g478389
BLAST score	142
E value	2.0e-09
Match length	60
% identity	50
NCBI Description	peroxidase (EC 1.11.1.7) precursor, anionic - Japanese aspen x large-toothed aspen >gi_217997_dbj_BAA01877_ (D11102) peroxidase [Populus kitakamiensis] >gi_444801_prf__1908234A anionic peroxidase [Populus kitakamiensis]

Seq. No.	202447
Seq. ID	LIB3048-039-Q1-L1-H2
Method	BLASTX
NCBI GI	g3193316
BLAST score	652
E value	2.0e-68
Match length	143
% identity	85
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	202448
Seq. ID	LIB3048-039-Q1-L1-H3
Method	BLASTX
NCBI GI	g2326372
BLAST score	530
E value	3.0e-54
Match length	134
% identity	71
NCBI Description	(Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No.	202449
Seq. ID	LIB3048-039-Q1-L1-H4
Method	BLASTX
NCBI GI	g2258414
BLAST score	162
E value	3.0e-11
Match length	64
% identity	55
NCBI Description	(AF007873) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe] >gi_2388967_emb_CAB11700_ (Z98979) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe]

Seq. No.	202450

Seq. ID	LIB3048-039-Q1-L1-H6
Method	BLASTX
NCBI GI	g2258418
BLAST score	262
E value	7.0e-23
Match length	78
% identity	62
NCBI Description	(AF007875) dolichol monophosphate mannose synthase [Homo sapiens]

Seq. No.	202451
Seq. ID	LIB3048-040-Q1-L1-A10
Method	BLASTX
NCBI GI	g2864624
BLAST score	349
E value	5.0e-33
Match length	137
% identity	26
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	202452
Seq. ID	LIB3048-040-Q1-L1-A12
Method	BLASTX
NCBI GI	g119640
BLAST score	283
E value	2.0e-25
Match length	103
% identity	52
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir__S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	202453
Seq. ID	LIB3048-040-Q1-L1-A2
Method	BLASTX
NCBI GI	g1556429
BLAST score	397
E value	1.0e-38
Match length	112
% identity	70
NCBI Description	(X84226) citrate synthase [Nicotiana tabacum]

Seq. No.	202454
Seq. ID	LIB3048-040-Q1-L1-A3
Method	BLASTX
NCBI GI	g3785974
BLAST score	190
E value	2.0e-14
Match length	87
% identity	48
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	202455
Seq. ID	LIB3048-040-Q1-L1-A4
Method	BLASTN
NCBI GI	g1769890

BLAST score 40
E value 4.0e-13
Match length 72
% identity 89
NCBI Description A.thaliana ATB2 gene

Seq. No. 202456
Seq. ID LIB3048-040-Q1-L1-A6
Method BLASTX
NCBI GI g4098129
BLAST score 614
E value 3.0e-64
Match length 119
% identity 97
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 202457
Seq. ID LIB3048-040-Q1-L1-B1
Method BLASTX
NCBI GI g1361983
BLAST score 366
E value 3.0e-35
Match length 102
% identity 72
NCBI Description ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 202458
Seq. ID LIB3048-040-Q1-L1-B10
Method BLASTX
NCBI GI g2618699
BLAST score 183
E value 7.0e-30
Match length 119
% identity 62
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 202459
Seq. ID LIB3048-040-Q1-L1-B12
Method BLASTX
NCBI GI g4406818
BLAST score 426
E value 4.0e-42
Match length 101
% identity 73
NCBI Description (AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 202460
Seq. ID LIB3048-040-Q1-L1-B6
Method BLASTX
NCBI GI g1076386
BLAST score 496
E value 2.0e-50
Match length 113
% identity 85
NCBI Description protein kinase ADK1 - Arabidopsis thaliana >gi_1216484

(U48779) dual specificity kinase 1 [Arabidopsis thaliana]

Seq. No.	202461
Seq. ID	LIB3048-040-Q1-L1-B7
Method	BLASTX
NCBI GI	g3281851
BLAST score	174
E value	1.0e-12
Match length	110
% identity	25
NCBI Description	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]

Seq. No.	202462
Seq. ID	LIB3048-040-Q1-L1-B8
Method	BLASTX
NCBI GI	g3643608
BLAST score	292
E value	2.0e-26
Match length	109
% identity	52
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202463
Seq. ID	LIB3048-040-Q1-L1-C11
Method	BLASTX
NCBI GI	g4056489
BLAST score	224
E value	1.0e-18
Match length	109
% identity	46
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	202464
Seq. ID	LIB3048-040-Q1-L1-C7
Method	BLASTX
NCBI GI	g1346387
BLAST score	516
E value	1.0e-52
Match length	114
% identity	88
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	202465
Seq. ID	LIB3048-040-Q1-L1-C8
Method	BLASTX
NCBI GI	g482230
BLAST score	305
E value	7.0e-28
Match length	133
% identity	49
NCBI Description	hypothetical protein K03H1.2 - Caenorhabditis elegans

Seq. No.	202466

Seq. ID	LIB3048-040-Q1-L1-C9
Method	BLASTX
NCBI GI	g3885329
BLAST score	152
E value	4.0e-10
Match length	48
% identity	60
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	202467
Seq. ID	LIB3048-040-Q1-L1-D10
Method	BLASTN
NCBI GI	g13192
BLAST score	130
E value	5.0e-67
Match length	278
% identity	87
NCBI Description	Oenothera berteriana mitDNA with part of plastid rRNA operon

Seq. No.	202468
Seq. ID	LIB3048-040-Q1-L1-D11
Method	BLASTX
NCBI GI	g3450842
BLAST score	445
E value	2.0e-44
Match length	113
% identity	74
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	202469
Seq. ID	LIB3048-040-Q1-L1-D12
Method	BLASTX
NCBI GI	g3641837
BLAST score	174
E value	2.0e-12
Match length	83
% identity	57
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	202470
Seq. ID	LIB3048-040-Q1-L1-D2
Method	BLASTX
NCBI GI	g4539423
BLAST score	559
E value	1.0e-57
Match length	132
% identity	82
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202471
Seq. ID	LIB3048-040-Q1-L1-D5
Method	BLASTX
NCBI GI	g2541896

BLAST score	147
E value	6.0e-10
Match length	46
% identity	63
NCBI Description	(D63676) acetolactate synthase [Cyanidium caldarium]

Seq. No.	202472
Seq. ID	LIB3048-040-Q1-L1-D6
Method	BLASTX
NCBI GI	g1176658
BLAST score	172
E value	3.0e-12
Match length	65
% identity	52
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	202473
Seq. ID	LIB3048-040-Q1-L1-E10
Method	BLASTX
NCBI GI	g1143322
BLAST score	564
E value	3.0e-58
Match length	126
% identity	82
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	202474
Seq. ID	LIB3048-040-Q1-L1-E11
Method	BLASTX
NCBI GI	g1142619
BLAST score	289
E value	4.0e-26
Match length	111
% identity	56
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	202475
Seq. ID	LIB3048-040-Q1-L1-E12
Method	BLASTX
NCBI GI	g2739381
BLAST score	423
E value	8.0e-42
Match length	120
% identity	67
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202476
Seq. ID	LIB3048-040-Q1-L1-E3
Method	BLASTX
NCBI GI	g1345642
BLAST score	234
E value	1.0e-19
Match length	130
% identity	34

NCBI Description	FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 75A1) (CYPLXXVA1) >gi_629710_pir__S38985 flavonoid 3',5'-hydroxylase Hf1 - garden petunia >gi_311656_emb_CAA80266_ (Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_1853972_dbj_BAA03438_ (D14588) flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738772_prf__2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No.	202477
Seq. ID	LIB3048-040-Q1-L1-E4
Method	BLASTX
NCBI GI	g4455210
BLAST score	321
E value	1.0e-29
Match length	127
% identity	51
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	202478
Seq. ID	LIB3048-040-Q1-L1-E5
Method	BLASTX
NCBI GI	g2245060
BLAST score	182
E value	2.0e-13
Match length	52
% identity	62
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	202479
Seq. ID	LIB3048-040-Q1-L1-E6
Method	BLASTX
NCBI GI	g1002800
BLAST score	370
E value	1.0e-35
Match length	116
% identity	61
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	202480
Seq. ID	LIB3048-040-Q1-L1-F10
Method	BLASTX
NCBI GI	g3175990
BLAST score	256
E value	8.0e-23
Match length	61
% identity	92
NCBI Description	(AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No.	202481
Seq. ID	LIB3048-040-Q1-L1-F12
Method	BLASTX
NCBI GI	g1002800
BLAST score	370

E value	9.0e-36
Match length	96
% identity	66
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	202482
Seq. ID	LIB3048-040-Q1-L1-F3
Method	BLASTX
NCBI GI	g464849
BLAST score	665
E value	4.0e-70
Match length	128
% identity	98
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202483
Seq. ID	LIB3048-040-Q1-L1-F7
Method	BLASTX
NCBI GI	g4406818
BLAST score	427
E value	3.0e-42
Match length	101
% identity	73
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	202484
Seq. ID	LIB3048-040-Q1-L1-F8
Method	BLASTX
NCBI GI	g1943751
BLAST score	194
E value	7.0e-15
Match length	45
% identity	89
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	202485
Seq. ID	LIB3048-040-Q1-L1-F9
Method	BLASTX
NCBI GI	g3882081
BLAST score	517
E value	8.0e-53
Match length	105
% identity	33
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	202486
Seq. ID	LIB3048-040-Q1-L1-G11
Method	BLASTX
NCBI GI	g2462746
BLAST score	446
E value	2.0e-44
Match length	106

% identity	79
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	202487
Seq. ID	LIB3048-040-Q1-L1-G2
Method	BLASTX
NCBI GI	g1001135
BLAST score	192
E value	1.0e-14
Match length	51
% identity	75
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	202488
Seq. ID	LIB3048-040-Q1-L1-H2
Method	BLASTX
NCBI GI	g2829896
BLAST score	248
E value	3.0e-21
Match length	97
% identity	47
NCBI Description	(AC002311) highly similar to auxin-regulated protein GH3, gp_X60033_18591 [Arabidopsis thaliana]

Seq. No.	202489
Seq. ID	LIB3048-040-Q1-L1-H3
Method	BLASTX
NCBI GI	g4220533
BLAST score	327
E value	2.0e-30
Match length	108
% identity	66
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	202490
Seq. ID	LIB3048-040-Q1-L1-H8
Method	BLASTX
NCBI GI	g2507422
BLAST score	321
E value	1.0e-29
Match length	124
% identity	74
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202491
Seq. ID	LIB3048-041-Q1-L1-A1
Method	BLASTX
NCBI GI	g529353
BLAST score	138
E value	8.0e-11
Match length	96
% identity	50

NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	202492
Seq. ID	LIB3048-041-Q1-L1-A11
Method	BLASTX
NCBI GI	g2791834
BLAST score	529
E value	1.0e-57
Match length	130
% identity	89
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	202493
Seq. ID	LIB3048-041-Q1-L1-A12
Method	BLASTX
NCBI GI	g99688
BLAST score	147
E value	4.0e-11
Match length	73
% identity	55
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	202494
Seq. ID	LIB3048-041-Q1-L1-A2
Method	BLASTX
NCBI GI	g1709498
BLAST score	511
E value	5.0e-52
Match length	110
% identity	84
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202495
Seq. ID	LIB3048-041-Q1-L1-A3
Method	BLASTX
NCBI GI	g169989
BLAST score	397
E value	9.0e-39
Match length	115
% identity	72
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine max]

Seq. No.	202496
Seq. ID	LIB3048-041-Q1-L1-A4
Method	BLASTX
NCBI GI	g169989
BLAST score	315
E value	3.0e-29
Match length	100
% identity	66
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine

max]

Seq. No.	202497
Seq. ID	LIB3048-041-Q1-L1-A5
Method	BLASTX
NCBI GI	g4468978
BLAST score	250
E value	5.0e-22
Match length	65
% identity	75
NCBI Description	(AL035605) peroxidase-like protein [Arabidopsis thaliana]

Seq. No.	202498
Seq. ID	LIB3048-041-Q1-L1-A7
Method	BLASTX
NCBI GI	g2444178
BLAST score	295
E value	3.0e-27
Match length	76
% identity	79
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	202499
Seq. ID	LIB3048-041-Q1-L1-B1
Method	BLASTX
NCBI GI	g1155261
BLAST score	393
E value	3.0e-38
Match length	107
% identity	74
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	202500
Seq. ID	LIB3048-041-Q1-L1-B10
Method	BLASTX
NCBI GI	g4432844
BLAST score	194
E value	7.0e-15
Match length	84
% identity	51
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	202501
Seq. ID	LIB3048-041-Q1-L1-B11
Method	BLASTX
NCBI GI	g1174592
BLAST score	705
E value	9.0e-75
Match length	135
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	202502
Seq. ID	LIB3048-041-Q1-L1-B3

Method	BLASTX
NCBI GI	g3763933
BLAST score	303
E value	1.0e-27
Match length	102
% identity	75
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	202503
Seq. ID	LIB3048-041-Q1-L1-B4
Method	BLASTX
NCBI GI	g1703200
BLAST score	370
E value	1.0e-35
Match length	93
% identity	76
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	202504
Seq. ID	LIB3048-041-Q1-L1-B5
Method	BLASTX
NCBI GI	g4262167
BLAST score	482
E value	1.0e-48
Match length	121
% identity	71
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	202505
Seq. ID	LIB3048-041-Q1-L1-B6
Method	BLASTN
NCBI GI	g2264311
BLAST score	53
E value	6.0e-21
Match length	167
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	202506
Seq. ID	LIB3048-041-Q1-L1-B9
Method	BLASTX
NCBI GI	g2213619
BLAST score	179
E value	2.0e-13
Match length	79
% identity	46
NCBI Description	(AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No.	202507
Seq. ID	LIB3048-041-Q1-L1-C11
Method	BLASTX

NCBI GI	g2499553
BLAST score	655
E value	6.0e-69
Match length	134
% identity	90
NCBI Description	CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_629524_pir__S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi_442529_bbs_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa] [Arabidopsis thaliana]

Seq. No.	202508
Seq. ID	LIB3048-041-Q1-L1-C12
Method	BLASTX
NCBI GI	g2213540
BLAST score	167
E value	9.0e-12
Match length	104
% identity	39
NCBI Description	(X98744) chloroplast DNA-binding protein PD3 [Pisum sativum]

Seq. No.	202509
Seq. ID	LIB3048-041-Q1-L1-C2
Method	BLASTX
NCBI GI	g3493172
BLAST score	332
E value	1.0e-31
Match length	74
% identity	89
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	202510
Seq. ID	LIB3048-041-Q1-L1-C6
Method	BLASTX
NCBI GI	g4455365
BLAST score	133
E value	3.0e-10
Match length	51
% identity	63
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202511
Seq. ID	LIB3048-041-Q1-L1-C7
Method	BLASTX
NCBI GI	g2935298
BLAST score	150
E value	7.0e-19
Match length	112
% identity	59
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	202512
Seq. ID	LIB3048-041-Q1-L1-C8

Method	BLASTX
NCBI GI	g3319355
BLAST score	647
E value	6.0e-68
Match length	139
% identity	88
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	202513
Seq. ID	LIB3048-041-Q1-L1-C9
Method	BLASTX
NCBI GI	g479386
BLAST score	282
E value	6.0e-49
Match length	127
% identity	85
NCBI Description	isocitrate dehydrogenase - soybean

Seq. No.	202514
Seq. ID	LIB3048-041-Q1-L1-D1
Method	BLASTX
NCBI GI	g2245070
BLAST score	318
E value	1.0e-29
Match length	93
% identity	65
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202515
Seq. ID	LIB3048-041-Q1-L1-D10
Method	BLASTX
NCBI GI	g2739381
BLAST score	424
E value	8.0e-42
Match length	127
% identity	64
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202516
Seq. ID	LIB3048-041-Q1-L1-D11
Method	BLASTX
NCBI GI	g2129597
BLAST score	271
E value	2.0e-24
Match length	54
% identity	94
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	202517
Seq. ID	LIB3048-041-Q1-L1-D12
Method	BLASTX
NCBI GI	g629592
BLAST score	313

E value	8.0e-29
Match length	125
% identity	51
NCBI Description	hypothetical protein - rape

Seq. No.	202518
Seq. ID	LIB3048-041-Q1-L1-D4
Method	BLASTX
NCBI GI	g4558549
BLAST score	183
E value	5.0e-14
Match length	80
% identity	51
NCBI Description	(AC007138) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana]

Seq. No.	202519
Seq. ID	LIB3048-041-Q1-L1-D5
Method	BLASTX
NCBI GI	g2462826
BLAST score	354
E value	1.0e-33
Match length	124
% identity	53
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	202520
Seq. ID	LIB3048-041-Q1-L1-D6
Method	BLASTX
NCBI GI	g4263778
BLAST score	199
E value	6.0e-16
Match length	55
% identity	67
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	202521
Seq. ID	LIB3048-041-Q1-L1-E10
Method	BLASTN
NCBI GI	g825556
BLAST score	33
E value	6.0e-09
Match length	51
% identity	16
NCBI Description	S.cerevisiae chromosome XIII cosmid

Seq. No.	202522
Seq. ID	LIB3048-041-Q1-L1-E11
Method	BLASTX
NCBI GI	g2398521
BLAST score	339
E value	7.0e-32
Match length	125
% identity	58
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	202523
Seq. ID	LIB3048-041-Q1-L1-E12
Method	BLASTX
NCBI GI	g2316016
BLAST score	257
E value	3.0e-22
Match length	125
% identity	49
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	202524
Seq. ID	LIB3048-041-Q1-L1-E4
Method	BLASTX
NCBI GI	g2499946
BLAST score	493
E value	6.0e-50
Match length	120
% identity	78
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	202525
Seq. ID	LIB3048-041-Q1-L1-E6
Method	BLASTX
NCBI GI	g629602
BLAST score	263
E value	5.0e-23
Match length	104
% identity	56
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	202526
Seq. ID	LIB3048-041-Q1-L1-E7
Method	BLASTX
NCBI GI	g1706918
BLAST score	274
E value	3.0e-24
Match length	115
% identity	46
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202527
Seq. ID	LIB3048-041-Q1-L1-E8
Method	BLASTX
NCBI GI	g3549691
BLAST score	593
E value	1.0e-61
Match length	138
% identity	74
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No. 202528

Seq. ID	LIB3048-041-Q1-L1-F1
Method	BLASTX
NCBI GI	g3158376
BLAST score	442
E value	6.0e-44
Match length	120
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202529
Seq. ID	LIB3048-041-Q1-L1-F11
Method	BLASTX
NCBI GI	g3123745
BLAST score	218
E value	1.0e-17
Match length	67
% identity	66
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	202530
Seq. ID	LIB3048-041-Q1-L1-F2
Method	BLASTX
NCBI GI	g3831455
BLAST score	175
E value	1.0e-12
Match length	68
% identity	79
NCBI Description	(AC005700) putative ubiquitin activating enzyme [Arabidopsis thaliana]

Seq. No.	202531
Seq. ID	LIB3048-041-Q1-L1-F7
Method	BLASTX
NCBI GI	g4454012
BLAST score	459
E value	6.0e-46
Match length	135
% identity	65
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	202532
Seq. ID	LIB3048-041-Q1-L1-F9
Method	BLASTX
NCBI GI	g4567260
BLAST score	456
E value	1.0e-45
Match length	122
% identity	70
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	202533
Seq. ID	LIB3048-041-Q1-L1-G1
Method	BLASTN
NCBI GI	g4388705
BLAST score	39

E value	2.0e-12
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	202534
Seq. ID	LIB3048-041-Q1-L1-G10
Method	BLASTX
NCBI GI	g2622920
BLAST score	250
E value	2.0e-21
Match length	112
% identity	42
NCBI Description	(AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium thermoautotrophicum]

Seq. No.	202535
Seq. ID	LIB3048-041-Q1-L1-G12
Method	BLASTX
NCBI GI	g4432844
BLAST score	188
E value	4.0e-14
Match length	117
% identity	42
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	202536
Seq. ID	LIB3048-041-Q1-L1-G6
Method	BLASTX
NCBI GI	g1407705
BLAST score	579
E value	6.0e-60
Match length	140
% identity	79
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	202537
Seq. ID	LIB3048-041-Q1-L1-G9
Method	BLASTX
NCBI GI	g3386611
BLAST score	259
E value	1.0e-22
Match length	107
% identity	48
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	202538
Seq. ID	LIB3048-041-Q1-L1-H10
Method	BLASTX
NCBI GI	g3236249
BLAST score	256
E value	4.0e-22
Match length	86
% identity	53
NCBI Description	(AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202539
Seq. ID	LIB3048-041-Q1-L1-H3
Method	BLASTX
NCBI GI	g1709449
BLAST score	512
E value	3.0e-52
Match length	113
% identity	86
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No.	202540
Seq. ID	LIB3048-041-Q1-L1-H4
Method	BLASTX
NCBI GI	g4204281
BLAST score	228
E value	8.0e-19
Match length	68
% identity	63
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	202541
Seq. ID	LIB3048-041-Q1-L1-H5
Method	BLASTX
NCBI GI	g1107526
BLAST score	388
E value	1.0e-37
Match length	103
% identity	73
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	202542
Seq. ID	LIB3048-041-Q1-L1-H7
Method	BLASTN
NCBI GI	g3046854
BLAST score	51
E value	1.0e-19
Match length	67
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	202543
Seq. ID	LIB3048-041-Q1-L1-H8
Method	BLASTX
NCBI GI	g4204281
BLAST score	182
E value	2.0e-13
Match length	54
% identity	63
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	202544
Seq. ID	LIB3048-041-Q1-L1-H9
Method	BLASTX
NCBI GI	g1572819

BLAST score	237
E value	6.0e-20
Match length	98
% identity	49
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	202545
Seq. ID	LIB3048-042-Q1-L1-A1
Method	BLASTX
NCBI GI	g2465923
BLAST score	189
E value	3.0e-14
Match length	114
% identity	22
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	202546
Seq. ID	LIB3048-042-Q1-L1-A10
Method	BLASTX
NCBI GI	g116923
BLAST score	267
E value	2.0e-23
Match length	111
% identity	56
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	202547
Seq. ID	LIB3048-042-Q1-L1-A2
Method	BLASTX
NCBI GI	g1486472
BLAST score	355
E value	6.0e-34
Match length	83
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	202548
Seq. ID	LIB3048-042-Q1-L1-A6
Method	BLASTX
NCBI GI	g82131
BLAST score	241
E value	2.0e-20
Match length	113
% identity	50
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi_829281_emb_CAA30261_ (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	202549
Seq. ID	LIB3048-042-Q1-L1-A8
Method	BLASTX

NCBI GI	g1856971
BLAST score	313
E value	2.0e-29
Match length	71
% identity	86
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	202550
Seq. ID	LIB3048-042-Q1-L1-A9
Method	BLASTX
NCBI GI	g116923
BLAST score	241
E value	2.0e-20
Match length	107
% identity	54
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	202551
Seq. ID	LIB3048-042-Q1-L1-B10
Method	BLASTX
NCBI GI	g2052510
BLAST score	586
E value	8.0e-61
Match length	133
% identity	80
NCBI Description	(U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No.	202552
Seq. ID	LIB3048-042-Q1-L1-B11
Method	BLASTX
NCBI GI	g1518540
BLAST score	519
E value	6.0e-53
Match length	123
% identity	81
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	202553
Seq. ID	LIB3048-042-Q1-L1-B12
Method	BLASTX
NCBI GI	g3445238
BLAST score	157
E value	2.0e-10
Match length	45
% identity	78
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana] >gi_3451059_emb_CAA20455.1_ (AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	202554
Seq. ID	LIB3048-042-Q1-L1-B2

Method	BLASTX
NCBI GI	g1856971
BLAST score	312
E value	5.0e-29
Match length	87
% identity	66
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	202555
Seq. ID	LIB3048-042-Q1-L1-C1
Method	BLASTX
NCBI GI	g3063699
BLAST score	325
E value	3.0e-30
Match length	135
% identity	47
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	202556
Seq. ID	LIB3048-042-Q1-L1-C10
Method	BLASTX
NCBI GI	g2262173
BLAST score	351
E value	2.0e-33
Match length	79
% identity	81
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	202557
Seq. ID	LIB3048-042-Q1-L1-C4
Method	BLASTX
NCBI GI	g1483218
BLAST score	293
E value	1.0e-26
Match length	90
% identity	60
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	202558
Seq. ID	LIB3048-042-Q1-L1-C7
Method	BLASTX
NCBI GI	g2583120
BLAST score	164
E value	1.0e-11
Match length	94
% identity	8
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	202559
Seq. ID	LIB3048-042-Q1-L1-C9
Method	BLASTX
NCBI GI	g3687223

BLAST score	156
E value	2.0e-10
Match length	117
% identity	59
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202560
Seq. ID	LIB3048-042-Q1-L1-D1
Method	BLASTX
NCBI GI	g2827555
BLAST score	350
E value	3.0e-33
Match length	120
% identity	62
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	202561
Seq. ID	LIB3048-042-Q1-L1-D11
Method	BLASTX
NCBI GI	g4038056
BLAST score	164
E value	8.0e-17
Match length	115
% identity	45
NCBI Description	(AC005897) putative transposon [Arabidopsis thaliana]

Seq. No.	202562
Seq. ID	LIB3048-042-Q1-L1-D2
Method	BLASTX
NCBI GI	g4539423
BLAST score	382
E value	5.0e-37
Match length	90
% identity	82
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202563
Seq. ID	LIB3048-042-Q1-L1-D3
Method	BLASTX
NCBI GI	g477819
BLAST score	518
E value	7.0e-53
Match length	132
% identity	73
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	202564
Seq. ID	LIB3048-042-Q1-L1-D9
Method	BLASTX
NCBI GI	g1572819
BLAST score	219

E value	8.0e-18
Match length	107
% identity	42
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	202565
Seq. ID	LIB3048-042-Q1-L1-E4
Method	BLASTX
NCBI GI	g4262228
BLAST score	237
E value	5.0e-20
Match length	94
% identity	29
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	202566
Seq. ID	LIB3048-042-Q1-L1-E8
Method	BLASTX
NCBI GI	g4239845
BLAST score	257
E value	3.0e-22
Match length	136
% identity	46
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202567
Seq. ID	LIB3048-042-Q1-L1-F1
Method	BLASTX
NCBI GI	g462013
BLAST score	563
E value	3.0e-58
Match length	124
% identity	90
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	202568
Seq. ID	LIB3048-042-Q1-L1-F10
Method	BLASTX
NCBI GI	g3738316
BLAST score	217
E value	1.0e-17
Match length	64
% identity	67
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	202569
Seq. ID	LIB3048-042-Q1-L1-F11
Method	BLASTX
NCBI GI	g3393062
BLAST score	352
E value	2.0e-33
Match length	100

% identity	58
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202570
Seq. ID	LIB3048-042-Q1-L1-F12
Method	BLASTX
NCBI GI	g4558664
BLAST score	232
E value	2.0e-19
Match length	118
% identity	9
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202571
Seq. ID	LIB3048-042-Q1-L1-F2
Method	BLASTX
NCBI GI	g1575556
BLAST score	423
E value	5.0e-42
Match length	94
% identity	87
NCBI Description	(U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']

Seq. No.	202572
Seq. ID	LIB3048-042-Q1-L1-F3
Method	BLASTX
NCBI GI	g1709498
BLAST score	493
E value	7.0e-50
Match length	122
% identity	75
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202573
Seq. ID	LIB3048-042-Q1-L1-F4
Method	BLASTX
NCBI GI	g3421090
BLAST score	221
E value	5.0e-18
Match length	48
% identity	94
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	202574
Seq. ID	LIB3048-042-Q1-L1-F9
Method	BLASTX
NCBI GI	g2290683
BLAST score	195
E value	4.0e-15
Match length	85
% identity	55
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	202575
Seq. ID	LIB3048-042-Q1-L1-G10
Method	BLASTX
NCBI GI	g3377803
BLAST score	384
E value	3.0e-37
Match length	117
% identity	74
NCBI Description	(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No.	202576
Seq. ID	LIB3048-042-Q1-L1-G11
Method	BLASTX
NCBI GI	g3335366
BLAST score	269
E value	3.0e-24
Match length	71
% identity	69
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	202577
Seq. ID	LIB3048-042-Q1-L1-G12
Method	BLASTX
NCBI GI	g2642158
BLAST score	159
E value	4.0e-20
Match length	78
% identity	69
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202578
Seq. ID	LIB3048-042-Q1-L1-G3
Method	BLASTX
NCBI GI	g3281853
BLAST score	216
E value	2.0e-17
Match length	45
% identity	91
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	202579
Seq. ID	LIB3048-042-Q1-L1-G4
Method	BLASTN
NCBI GI	g167336
BLAST score	100
E value	5.0e-49
Match length	212
% identity	87
NCBI Description	Gossypium hirsutum Lea4-A gene, complete CDS

Seq. No.	202580
Seq. ID	LIB3048-042-Q1-L1-G9
Method	BLASTX
NCBI GI	g2832623
BLAST score	204

E value	1.0e-16
Match length	56
% identity	73
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	202581
Seq. ID	LIB3048-042-Q1-L1-H1
Method	BLASTX
NCBI GI	g3334147
BLAST score	538
E value	2.0e-55
Match length	105
% identity	91
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202582
Seq. ID	LIB3048-042-Q1-L1-H12
Method	BLASTX
NCBI GI	g3077640
BLAST score	169
E value	2.0e-12
Match length	55
% identity	60
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No.	202583
Seq. ID	LIB3048-042-Q1-L1-H2
Method	BLASTX
NCBI GI	g4239845
BLAST score	250
E value	1.0e-21
Match length	72
% identity	67
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202584
Seq. ID	LIB3048-042-Q1-L1-H3
Method	BLASTX
NCBI GI	g4006829
BLAST score	238
E value	2.0e-20
Match length	64
% identity	77
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	202585
Seq. ID	LIB3048-042-Q1-L1-H6
Method	BLASTX
NCBI GI	g322752
BLAST score	156
E value	1.0e-10
Match length	91
% identity	36
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	202586
Seq. ID	LIB3048-042-Q1-L1-H9
Method	BLASTX
NCBI GI	g3450842
BLAST score	251
E value	1.0e-21
Match length	101
% identity	52
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	202587
Seq. ID	LIB3048-043-Q1-L1-B10
Method	BLASTX
NCBI GI	g3643611
BLAST score	272
E value	3.0e-28
Match length	99
% identity	69
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	202588
Seq. ID	LIB3048-043-Q1-L1-B8
Method	BLASTX
NCBI GI	g4263795
BLAST score	301
E value	2.0e-27
Match length	87
% identity	63
NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	202589
Seq. ID	LIB3048-043-Q1-L1-D1
Method	BLASTX
NCBI GI	g347527
BLAST score	376
E value	2.0e-36
Match length	88
% identity	89
NCBI Description	(L16016) ribosomal protein S3 [Homo sapiens]

Seq. No.	202590
Seq. ID	LIB3048-043-Q1-L1-D7
Method	BLASTX
NCBI GI	g1001309
BLAST score	190
E value	2.0e-14
Match length	128
% identity	34
NCBI Description	(D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No.	202591
Seq. ID	LIB3048-043-Q1-L1-E11
Method	BLASTX
NCBI GI	g464849

BLAST score	553
E value	4.0e-57
Match length	114
% identity	93
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202592
Seq. ID	LIB3048-043-Q1-L1-E6
Method	BLASTX
NCBI GI	g3947733
BLAST score	319
E value	1.0e-29
Match length	99
% identity	60
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	202593
Seq. ID	LIB3048-043-Q1-L1-E8
Method	BLASTX
NCBI GI	g3334147
BLAST score	402
E value	3.0e-39
Match length	124
% identity	63
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202594
Seq. ID	LIB3048-043-Q1-L1-F3
Method	BLASTX
NCBI GI	g3492803
BLAST score	269
E value	1.0e-23
Match length	124
% identity	48
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	202595
Seq. ID	LIB3048-043-Q1-L1-F6
Method	BLASTX
NCBI GI	g2262105
BLAST score	256
E value	4.0e-22
Match length	83
% identity	61
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	202596
Seq. ID	LIB3048-043-Q1-L1-F8
Method	BLASTX
NCBI GI	g2088647
BLAST score	283
E value	2.0e-25
Match length	102
% identity	62

NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
Seq. No.	202597
Seq. ID	LIB3048-043-Q1-L1-F9
Method	BLASTN
NCBI GI	g556421
BLAST score	40
E value	3.0e-13
Match length	44
% identity	98
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds
Seq. No.	202598
Seq. ID	LIB3048-043-Q1-L1-G5
Method	BLASTX
NCBI GI	g3892712
BLAST score	145
E value	6.0e-13
Match length	95
% identity	53
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]
Seq. No.	202599
Seq. ID	LIB3048-043-Q1-L1-H2
Method	BLASTX
NCBI GI	g1703200
BLAST score	554
E value	4.0e-57
Match length	120
% identity	88
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]
Seq. No.	202600
Seq. ID	LIB3048-043-Q1-L2-A9
Method	BLASTX
NCBI GI	g2262173
BLAST score	140
E value	3.0e-11
Match length	98
% identity	37
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]
Seq. No.	202601
Seq. ID	LIB3048-043-Q1-L2-C2
Method	BLASTX
NCBI GI	g3152609
BLAST score	352
E value	2.0e-33

Match length	119
% identity	55
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	202602
Seq. ID	LIB3048-043-Q1-L2-C7
Method	BLASTX
NCBI GI	g1173253
BLAST score	562
E value	6.0e-58
Match length	125
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_543317_pir__S41170 ribosomal protein S3 - mouse >gi_57728_emb_CAA35916_ (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi_439522_emb_CAA54167_ (X76772) ribosomal protein S3 [Mus musculus]

Seq. No.	202603
Seq. ID	LIB3048-043-Q1-L2-D5
Method	BLASTX
NCBI GI	g1363325
BLAST score	303
E value	9.0e-28
Match length	111
% identity	59
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	202604
Seq. ID	LIB3048-043-Q1-L2-D6
Method	BLASTX
NCBI GI	g1361983
BLAST score	469
E value	4.0e-47
Match length	129
% identity	74
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	202605
Seq. ID	LIB3048-043-Q1-L2-F10
Method	BLASTX
NCBI GI	g2827537
BLAST score	250
E value	2.0e-21
Match length	68
% identity	66
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	202606
Seq. ID	LIB3048-043-Q1-L2-F9
Method	BLASTX
NCBI GI	g3309243
BLAST score	313

E value	4.0e-29
Match length	77
% identity	79
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	202607
Seq. ID	LIB3048-043-Q1-L2-H2
Method	BLASTX
NCBI GI	g3080424
BLAST score	527
E value	2.0e-66
Match length	144
% identity	88
NCBI Description	(AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	202608
Seq. ID	LIB3048-043-Q1-L2-H6
Method	BLASTX
NCBI GI	g1703200
BLAST score	549
E value	1.0e-56
Match length	119
% identity	87
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	202609
Seq. ID	LIB3048-044-Q1-L1-D10
Method	BLASTX
NCBI GI	g2642158
BLAST score	469
E value	4.0e-47
Match length	127
% identity	69
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202610
Seq. ID	LIB3048-044-Q1-L2-A7
Method	BLASTN
NCBI GI	g303731
BLAST score	32
E value	9.0e-09
Match length	48
% identity	92
NCBI Description	Pea mRNA for GTP-binding protein, complete cds

Seq. No.	202611
Seq. ID	LIB3048-044-Q1-L2-C3
Method	BLASTX
NCBI GI	g2317729
BLAST score	254
E value	3.0e-22

Match length	66
% identity	76
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	202612
Seq. ID	LIB3048-044-Q1-L2-D3
Method	BLASTN
NCBI GI	g2829146
BLAST score	34
E value	8.0e-10
Match length	98
% identity	84
NCBI Description	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-5 allele, partial cds

Seq. No.	202613
Seq. ID	LIB3048-044-Q1-L2-E3
Method	BLASTX
NCBI GI	g1777579
BLAST score	142
E value	2.0e-09
Match length	46
% identity	63
NCBI Description	(U40826) WW-domain binding protein 2 [Mus musculus]

Seq. No.	202614
Seq. ID	LIB3048-044-Q1-L2-E9
Method	BLASTX
NCBI GI	g464849
BLAST score	655
E value	6.0e-69
Match length	124
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202615
Seq. ID	LIB3048-045-G5T3A
Method	BLASTX
NCBI GI	g4454012
BLAST score	734
E value	8.0e-78
Match length	220
% identity	63
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	202616
Seq. ID	LIB3048-045-Q1-L1-A1
Method	BLASTX
NCBI GI	g3859594
BLAST score	165
E value	6.0e-12
Match length	53
% identity	60

NCBI Description	(AF104919) contains similarity to ribosomal protein L7Ae (Pfam: PF01248, E=0.0017, N=1) [Arabidopsis thaliana]

Seq. No.	202617
Seq. ID	LIB3048-045-Q1-L1-A12
Method	BLASTX
NCBI GI	g4204303
BLAST score	289
E value	5.0e-26
Match length	59
% identity	81
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	202618
Seq. ID	LIB3048-045-Q1-L1-B10
Method	BLASTX
NCBI GI	g1619300
BLAST score	162
E value	5.0e-17
Match length	59
% identity	68
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	202619
Seq. ID	LIB3048-045-Q1-L1-B11
Method	BLASTX
NCBI GI	g3242705
BLAST score	238
E value	4.0e-20
Match length	60
% identity	72
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	202620
Seq. ID	LIB3048-045-Q1-L1-B2
Method	BLASTX
NCBI GI	g2864624
BLAST score	258
E value	2.0e-22
Match length	110
% identity	46
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	202621
Seq. ID	LIB3048-045-Q1-L1-B3
Method	BLASTX
NCBI GI	g4508068
BLAST score	210
E value	9.0e-17
Match length	130
% identity	45
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	202622
Seq. ID	LIB3048-045-Q1-L1-B5

Method	BLASTX
NCBI GI	g2642158
BLAST score	186
E value	3.0e-14
Match length	85
% identity	48
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202623
Seq. ID	LIB3048-045-Q1-L1-C1
Method	BLASTX
NCBI GI	g3402693
BLAST score	149
E value	1.0e-09
Match length	88
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	202624
Seq. ID	LIB3048-045-Q1-L1-C10
Method	BLASTX
NCBI GI	g3790587
BLAST score	363
E value	6.0e-35
Match length	92
% identity	70
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	202625
Seq. ID	LIB3048-045-Q1-L1-C2
Method	BLASTX
NCBI GI	g1345979
BLAST score	162
E value	3.0e-11
Match length	89
% identity	42
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No.	202626
Seq. ID	LIB3048-045-Q1-L1-D10
Method	BLASTX
NCBI GI	g1304227
BLAST score	443
E value	4.0e-44
Match length	119
% identity	66
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	202627
Seq. ID	LIB3048-045-Q1-L1-D11
Method	BLASTX
NCBI GI	g3738257

BLAST score	365
E value	3.0e-35
Match length	76
% identity	93
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202628
Seq. ID	LIB3048-045-Q1-L1-D6
Method	BLASTX
NCBI GI	g3746059
BLAST score	183
E value	4.0e-14
Match length	69
% identity	51
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	202629
Seq. ID	LIB3048-045-Q1-L1-D8
Method	BLASTX
NCBI GI	g4539335
BLAST score	182
E value	1.0e-13
Match length	104
% identity	36
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	202630
Seq. ID	LIB3048-045-Q1-L1-E1
Method	BLASTX
NCBI GI	g4240207
BLAST score	163
E value	2.0e-11
Match length	59
% identity	49
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]

Seq. No.	202631
Seq. ID	LIB3048-045-Q1-L1-E10
Method	BLASTX
NCBI GI	g1076280
BLAST score	141
E value	5.0e-09
Match length	63
% identity	48
NCBI Description	dihydrodipicolinate synthase (EC 4.2.1.52) precursor - western balsam poplar x cottonwood

Seq. No.	202632
Seq. ID	LIB3048-045-Q1-L1-E11
Method	BLASTX
NCBI GI	g3334147
BLAST score	407
E value	6.0e-40
Match length	91

% identity	84
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202633
Seq. ID	LIB3048-045-Q1-L1-E5
Method	BLASTX
NCBI GI	g1399275
BLAST score	216
E value	5.0e-18
Match length	59
% identity	69
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	202634
Seq. ID	LIB3048-045-Q1-L1-E8
Method	BLASTX
NCBI GI	g1107526
BLAST score	281
E value	1.0e-25
Match length	75
% identity	69
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	202635
Seq. ID	LIB3048-045-Q1-L1-E9
Method	BLASTX
NCBI GI	g4567251
BLAST score	387
E value	1.0e-37
Match length	95
% identity	74
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	202636
Seq. ID	LIB3048-045-Q1-L1-F12
Method	BLASTX
NCBI GI	g4508068
BLAST score	188
E value	3.0e-14
Match length	58
% identity	69
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	202637
Seq. ID	LIB3048-045-Q1-L1-F4
Method	BLASTX
NCBI GI	g119354
BLAST score	418
E value	3.0e-41
Match length	99
% identity	84
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185

phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	202638
Seq. ID	LIB3048-045-Q1-L1-F6
Method	BLASTX
NCBI GI	g3402693
BLAST score	159
E value	7.0e-11
Match length	88
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	202639
Seq. ID	LIB3048-045-Q1-L1-F8
Method	BLASTX
NCBI GI	g3334147
BLAST score	371
E value	7.0e-36
Match length	97
% identity	72
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202640
Seq. ID	LIB3048-045-Q1-L1-G10
Method	BLASTX
NCBI GI	g4263695
BLAST score	188
E value	3.0e-14
Match length	102
% identity	23
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	202641
Seq. ID	LIB3048-045-Q1-L1-G12
Method	BLASTX
NCBI GI	g3393062
BLAST score	378
E value	2.0e-36
Match length	126
% identity	53
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202642
Seq. ID	LIB3048-045-Q1-L1-G3
Method	BLASTX
NCBI GI	g4455155
BLAST score	341
E value	2.0e-32
Match length	69
% identity	90
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	202643
Seq. ID	LIB3048-045-Q1-L1-G4
Method	BLASTX
NCBI GI	g3355465
BLAST score	151
E value	3.0e-12
Match length	85
% identity	54
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	202644
Seq. ID	LIB3048-045-Q1-L1-G9
Method	BLASTX
NCBI GI	g3320462
BLAST score	227
E value	1.0e-37
Match length	129
% identity	57
NCBI Description	(AF062467) polygalacturonase precursor [Cucumis melo]

Seq. No.	202645
Seq. ID	LIB3048-045-Q1-L1-H12
Method	BLASTX
NCBI GI	g3393062
BLAST score	358
E value	2.0e-34
Match length	96
% identity	61
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202646
Seq. ID	LIB3048-045-Q1-L1-H2
Method	BLASTX
NCBI GI	g3763933
BLAST score	252
E value	3.0e-27
Match length	130
% identity	65
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	202647
Seq. ID	LIB3048-045-Q1-L1-H4
Method	BLASTX
NCBI GI	g119354
BLAST score	470
E value	3.0e-47
Match length	104
% identity	88
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	202648
Seq. ID	LIB3048-045-Q1-L1-H6

Method	BLASTX
NCBI GI	g2978452
BLAST score	158
E value	4.0e-11
Match length	66
% identity	48
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	202649
Seq. ID	LIB3048-046-Q1-L1-A12
Method	BLASTX
NCBI GI	g729620
BLAST score	591
E value	2.0e-61
Match length	130
% identity	90
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 4 PRECURSOR (GRP 78-4) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 4) (BIP 4) >gi_82174_pir__JQ1360 luminal binding protein BLP-4 precursor - common tobacco >gi_100339_pir__S21879 heat shock protein BiP homolog blp4 - common tobacco >gi_19811_emb_CAA42659_ (X60057) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	202650
Seq. ID	LIB3048-046-Q1-L1-A5
Method	BLASTX
NCBI GI	g3367522
BLAST score	297
E value	5.0e-27
Match length	100
% identity	60
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	202651
Seq. ID	LIB3048-046-Q1-L1-A8
Method	BLASTX
NCBI GI	g765203
BLAST score	484
E value	5.0e-49
Match length	113
% identity	82
NCBI Description	(S73865) linoleate:oxygen oxidoreductase, lipoxygenase, LOX {EC 1.13.11.12} [Solanum tuberosum, cv. Desiree, roots, Peptide, 857 aa] [Solanum tuberosum]

Seq. No.	202652
Seq. ID	LIB3048-046-Q1-L1-B10
Method	BLASTX
NCBI GI	g1946364
BLAST score	271
E value	5.0e-24
Match length	105
% identity	44
NCBI Description	(U93215) lipase isolog [Arabidopsis thaliana]

Seq. No.	202653
Seq. ID	LIB3048-046-Q1-L1-B3
Method	BLASTX
NCBI GI	g4204265
BLAST score	229
E value	6.0e-19
Match length	121
% identity	46
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	202654
Seq. ID	LIB3048-046-Q1-L1-B4
Method	BLASTX
NCBI GI	g3643611
BLAST score	338
E value	4.0e-32
Match length	89
% identity	75
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	202655
Seq. ID	LIB3048-046-Q1-L1-C10
Method	BLASTX
NCBI GI	g4262174
BLAST score	476
E value	5.0e-48
Match length	115
% identity	70
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	202656
Seq. ID	LIB3048-046-Q1-L1-C11
Method	BLASTX
NCBI GI	g1477428
BLAST score	589
E value	3.0e-61
Match length	113
% identity	95
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	202657
Seq. ID	LIB3048-046-Q1-L1-C2
Method	BLASTX
NCBI GI	g4567267
BLAST score	263
E value	5.0e-23
Match length	52
% identity	87
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	202658
Seq. ID	LIB3048-046-Q1-L1-C3
Method	BLASTX
NCBI GI	g1498731
BLAST score	309
E value	3.0e-28

Match length	86
% identity	63
NCBI Description	(U64806) pathogenesis-related protein PR1 [Brassica napus]

Seq. No.	202659
Seq. ID	LIB3048-046-Q1-L1-C5
Method	BLASTX
NCBI GI	g4454026
BLAST score	295
E value	7.0e-27
Match length	108
% identity	55
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	202660
Seq. ID	LIB3048-046-Q1-L1-C6
Method	BLASTX
NCBI GI	g2642158
BLAST score	545
E value	4.0e-56
Match length	118
% identity	80
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202661
Seq. ID	LIB3048-046-Q1-L1-C9
Method	BLASTX
NCBI GI	g1143188
BLAST score	512
E value	3.0e-52
Match length	115
% identity	34
NCBI Description	(U32627) ubiquitin precursor [Candida albicans]

Seq. No.	202662
Seq. ID	LIB3048-046-Q1-L1-D1
Method	BLASTX
NCBI GI	g3183570
BLAST score	252
E value	9.0e-22
Match length	97
% identity	52
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN IN DINF-QOR INTERGENIC REGION

Seq. No.	202663
Seq. ID	LIB3048-046-Q1-L1-D2
Method	BLASTX
NCBI GI	g3183570
BLAST score	156
E value	1.0e-10
Match length	64
% identity	47
NCBI Description	HYPOTHETICAL 36.8 KD PROTEIN IN DINF-QOR INTERGENIC REGION

Seq. No.	202664
Seq. ID	LIB3048-046-Q1-L1-D3
Method	BLASTX

NCBI GI	g1778370
BLAST score	468
E value	4.0e-47
Match length	113
% identity	78
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	202665
Seq. ID	LIB3048-046-Q1-L1-D4
Method	BLASTX
NCBI GI	g2978452
BLAST score	167
E value	8.0e-15
Match length	66
% identity	51
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	202666
Seq. ID	LIB3048-046-Q1-L1-D7
Method	BLASTX
NCBI GI	g625509
BLAST score	251
E value	7.0e-22
Match length	68
% identity	21
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No.	202667
Seq. ID	LIB3048-046-Q1-L1-D9
Method	BLASTX
NCBI GI	g1256509
BLAST score	327
E value	2.0e-31
Match length	86
% identity	78
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	202668
Seq. ID	LIB3048-046-Q1-L1-E1
Method	BLASTX
NCBI GI	g3603456
BLAST score	206
E value	8.0e-17
Match length	45
% identity	31
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	202669
Seq. ID	LIB3048-046-Q1-L1-E2
Method	BLASTX
NCBI GI	g1449179
BLAST score	177
E value	8.0e-16
Match length	92
% identity	61
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	202670
Seq. ID	LIB3048-046-Q1-L1-E8
Method	BLASTX
NCBI GI	g1769901
BLAST score	221
E value	3.0e-18
Match length	94
% identity	50
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No.	202671
Seq. ID	LIB3048-046-Q1-L1-E9
Method	BLASTX
NCBI GI	g3334146
BLAST score	147
E value	6.0e-10
Match length	69
% identity	51
NCBI Description	ENDOCHITINASE 2 PRECURSOR >gi_1791007 (U78888) class I endochitinase [Gossypium hirsutum]

Seq. No.	202672
Seq. ID	LIB3048-046-Q1-L1-F1
Method	BLASTX
NCBI GI	g1723239
BLAST score	341
E value	3.0e-32
Match length	112
% identity	59
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	202673
Seq. ID	LIB3048-046-Q1-L1-F10
Method	BLASTX
NCBI GI	g3811007
BLAST score	515
E value	2.0e-52
Match length	104
% identity	94
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	202674
Seq. ID	LIB3048-046-Q1-L1-F11
Method	BLASTX
NCBI GI	g100525
BLAST score	469
E value	3.0e-47
Match length	106
% identity	21
NCBI Description	ubiquitin precursor UbB2 - common sunflower (fragment) >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein

[Helianthus annuus]

Seq. No.	202675
Seq. ID	LIB3048-046-Q1-L1-F12
Method	BLASTX
NCBI GI	g2129950
BLAST score	601
E value	1.0e-62
Match length	134
% identity	91
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco

Seq. No.	202676
Seq. ID	LIB3048-046-Q1-L1-F5
Method	BLASTX
NCBI GI	g541847
BLAST score	326
E value	1.0e-30
Match length	76
% identity	82
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	202677
Seq. ID	LIB3048-046-Q1-L1-G10
Method	BLASTX
NCBI GI	g4262147
BLAST score	256
E value	4.0e-22
Match length	113
% identity	49
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	202678
Seq. ID	LIB3048-046-Q1-L1-G11
Method	BLASTX
NCBI GI	g1350988
BLAST score	158
E value	7.0e-11
Match length	78
% identity	50
NCBI Description	40S RIBOSOMAL PROTEIN S3B (S1B) >gi_2119058_pir__I51635 ribosomal protein S1 - African clawed frog >gi_587600_emb_CAA84291_ (Z34530) ribosomal protein S1 [Xenopus laevis] >gi_587602_emb_CAA84290_ (Z34529) ribosomal protein [Xenopus laevis]

Seq. No.	202679
Seq. ID	LIB3048-046-Q1-L1-G12
Method	BLASTX
NCBI GI	g3393062
BLAST score	358
E value	3.0e-34
Match length	102
% identity	58
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202680
Seq. ID	LIB3048-046-Q1-L1-G5
Method	BLASTX
NCBI GI	g4572674
BLAST score	284
E value	2.0e-25
Match length	75
% identity	72
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	202681
Seq. ID	LIB3048-046-Q1-L1-G9
Method	BLASTX
NCBI GI	g548488
BLAST score	187
E value	1.0e-28
Match length	100
% identity	59
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	202682
Seq. ID	LIB3048-046-Q1-L1-H10
Method	BLASTX
NCBI GI	g3393062
BLAST score	350
E value	3.0e-33
Match length	102
% identity	57
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	202683
Seq. ID	LIB3048-046-Q1-L1-H2
Method	BLASTX
NCBI GI	g4262142
BLAST score	270
E value	8.0e-24
Match length	92
% identity	52
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	202684
Seq. ID	LIB3048-046-Q1-L1-H3
Method	BLASTX
NCBI GI	g1709498
BLAST score	224
E value	2.0e-33
Match length	110
% identity	66
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202685

Seq. ID	LIB3048-046-Q1-L1-H5
Method	BLASTX
NCBI GI	g1486472
BLAST score	489
E value	2.0e-49
Match length	111
% identity	85
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	202686
Seq. ID	LIB3048-047-Q1-L1-A1
Method	BLASTX
NCBI GI	g485742
BLAST score	426
E value	1.0e-44
Match length	102
% identity	97
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	202687
Seq. ID	LIB3048-047-Q1-L1-A10
Method	BLASTX
NCBI GI	g3450842
BLAST score	185
E value	8.0e-14
Match length	63
% identity	60
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	202688
Seq. ID	LIB3048-047-Q1-L1-A2
Method	BLASTX
NCBI GI	g3608155
BLAST score	304
E value	9.0e-28
Match length	133
% identity	45
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	202689
Seq. ID	LIB3048-047-Q1-L1-A3
Method	BLASTX
NCBI GI	g3298474
BLAST score	389
E value	8.0e-50
Match length	130
% identity	74
NCBI Description	(AB012765) ovp1 [Oryza sativa]

Seq. No.	202690
Seq. ID	LIB3048-047-Q1-L1-A5
Method	BLASTX
NCBI GI	g4539423
BLAST score	551
E value	1.0e-56

Match length	129
% identity	82
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202691
Seq. ID	LIB3048-047-Q1-L1-A6
Method	BLASTX
NCBI GI	g2880043
BLAST score	328
E value	1.0e-30
Match length	132
% identity	48
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	202692
Seq. ID	LIB3048-047-Q1-L1-A7
Method	BLASTX
NCBI GI	g3925703
BLAST score	583
E value	2.0e-60
Match length	129
% identity	88
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	202693
Seq. ID	LIB3048-047-Q1-L1-A8
Method	BLASTX
NCBI GI	g1841475
BLAST score	349
E value	5.0e-33
Match length	110
% identity	59
NCBI Description	(Y11105) Myb26 [Pisum sativum]

Seq. No.	202694
Seq. ID	LIB3048-047-Q1-L1-B11
Method	BLASTX
NCBI GI	g2435395
BLAST score	236
E value	9.0e-20
Match length	101
% identity	57
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	202695
Seq. ID	LIB3048-047-Q1-L1-B2
Method	BLASTX
NCBI GI	g2130149
BLAST score	621
E value	5.0e-65
Match length	119
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	202696
Seq. ID	LIB3048-047-Q1-L1-B4
Method	BLASTX
NCBI GI	g3395432
BLAST score	327
E value	2.0e-30
Match length	97
% identity	65
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	202697
Seq. ID	LIB3048-047-Q1-L1-B5
Method	BLASTX
NCBI GI	g3080400
BLAST score	515
E value	2.0e-52
Match length	123
% identity	79
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	202698
Seq. ID	LIB3048-047-Q1-L1-B6
Method	BLASTX
NCBI GI	g606942
BLAST score	142
E value	9.0e-09
Match length	74
% identity	49
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	202699
Seq. ID	LIB3048-047-Q1-L1-B7
Method	BLASTX
NCBI GI	g2981167
BLAST score	142
E value	8.0e-09
Match length	70
% identity	50
NCBI Description	(AF053076) late embryogenis abundant protein 5 [Nicotiana tabacum]

Seq. No.	202700
Seq. ID	LIB3048-047-Q1-L1-B8
Method	BLASTX
NCBI GI	g421954
BLAST score	332
E value	5.0e-31
Match length	132
% identity	46
NCBI Description	hypothetical protein 3 - potato transposon Tst1 >gi_21433_emb_CAA36615_ (X52387) ORF3 [Solanum tuberosum]

Seq. No.	202701
Seq. ID	LIB3048-047-Q1-L1-B9
Method	BLASTX

NCBI GI	g2465923
BLAST score	187
E value	5.0e-14
Match length	98
% identity	13
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	202702
Seq. ID	LIB3048-047-Q1-L1-C11
Method	BLASTX
NCBI GI	g3894159
BLAST score	172
E value	3.0e-12
Match length	80
% identity	41
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202703
Seq. ID	LIB3048-047-Q1-L1-C4
Method	BLASTX
NCBI GI	g2739381
BLAST score	447
E value	1.0e-44
Match length	126
% identity	67
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202704
Seq. ID	LIB3048-047-Q1-L1-C6
Method	BLASTX
NCBI GI	g136057
BLAST score	361
E value	2.0e-34
Match length	113
% identity	64
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	202705
Seq. ID	LIB3048-047-Q1-L1-C8
Method	BLASTX
NCBI GI	g2244851
BLAST score	292
E value	2.0e-26
Match length	135
% identity	43
NCBI Description	(Z97337) amine oxidase [Arabidopsis thaliana]

Seq. No.	202706
Seq. ID	LIB3048-047-Q1-L1-D11
Method	BLASTX
NCBI GI	g1408460
BLAST score	345
E value	1.0e-32

Match length	132
% identity	55
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No.	202707
Seq. ID	LIB3048-047-Q1-L1-D12
Method	BLASTX
NCBI GI	g4433048
BLAST score	390
E value	7.0e-38
Match length	123
% identity	61
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	202708
Seq. ID	LIB3048-047-Q1-L1-D2
Method	BLASTX
NCBI GI	g1729760
BLAST score	762
E value	2.0e-81
Match length	135
% identity	99
NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	202709
Seq. ID	LIB3048-047-Q1-L1-D4
Method	BLASTX
NCBI GI	g629562
BLAST score	604
E value	6.0e-63
Match length	135
% identity	83
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	202710
Seq. ID	LIB3048-047-Q1-L1-D7
Method	BLASTX
NCBI GI	g1399275
BLAST score	453
E value	2.0e-45
Match length	102
% identity	82
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	202711

Seq. ID	LIB3048-047-Q1-L1-D8
Method	BLASTX
NCBI GI	g2454182
BLAST score	150
E value	1.0e-09
Match length	93
% identity	44
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	202712
Seq. ID	LIB3048-047-Q1-L1-D9
Method	BLASTX
NCBI GI	g3413716
BLAST score	355
E value	4.0e-40
Match length	130
% identity	49
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643589 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	202713
Seq. ID	LIB3048-047-Q1-L1-E1
Method	BLASTX
NCBI GI	g4115913
BLAST score	439
E value	1.0e-43
Match length	126
% identity	60
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_ (AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	202714
Seq. ID	LIB3048-047-Q1-L1-E10
Method	BLASTX
NCBI GI	g120669
BLAST score	457
E value	9.0e-46
Match length	92
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	202715
Seq. ID	LIB3048-047-Q1-L1-E11
Method	BLASTX
NCBI GI	g4138647
BLAST score	531
E value	2.0e-54
Match length	129

% identity	77
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	202716
Seq. ID	LIB3048-047-Q1-L1-E12
Method	BLASTX
NCBI GI	g1220196
BLAST score	461
E value	3.0e-46
Match length	90
% identity	97
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	202717
Seq. ID	LIB3048-047-Q1-L1-E2
Method	BLASTX
NCBI GI	g4508068
BLAST score	222
E value	4.0e-18
Match length	135
% identity	44
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	202718
Seq. ID	LIB3048-047-Q1-L1-E3
Method	BLASTX
NCBI GI	g4406818
BLAST score	425
E value	6.0e-42
Match length	101
% identity	73
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	202719
Seq. ID	LIB3048-047-Q1-L1-E4
Method	BLASTX
NCBI GI	g4249382
BLAST score	495
E value	4.0e-50
Match length	120
% identity	74
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	202720
Seq. ID	LIB3048-047-Q1-L1-E6
Method	BLASTX
NCBI GI	g3435196
BLAST score	444
E value	3.0e-44
Match length	136
% identity	65
NCBI Description	(AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	202721

Seq. ID	LIB3048-047-Q1-L1-E9
Method	BLASTX
NCBI GI	g3608495
BLAST score	326
E value	2.0e-30
Match length	93
% identity	70
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No.	202722
Seq. ID	LIB3048-047-Q1-L1-F1
Method	BLASTX
NCBI GI	g3329294
BLAST score	152
E value	6.0e-10
Match length	115
% identity	30
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	202723
Seq. ID	LIB3048-047-Q1-L1-F10
Method	BLASTX
NCBI GI	g3790102
BLAST score	369
E value	2.0e-35
Match length	82
% identity	82
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	202724
Seq. ID	LIB3048-047-Q1-L1-F11
Method	BLASTX
NCBI GI	g2462762
BLAST score	303
E value	1.0e-27
Match length	118
% identity	55
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	202725
Seq. ID	LIB3048-047-Q1-L1-F12
Method	BLASTX
NCBI GI	g1332579
BLAST score	593
E value	1.0e-61
Match length	120
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	202726
Seq. ID	LIB3048-047-Q1-L1-F2
Method	BLASTX

NCBI GI	g4454052
BLAST score	144
E value	5.0e-09
Match length	89
% identity	42
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202727
Seq. ID	LIB3048-047-Q1-L1-F3
Method	BLASTX
NCBI GI	g431144
BLAST score	141
E value	5.0e-09
Match length	80
% identity	45
NCBI Description	(D21824) HSP70 [Lilium longiflorum]

Seq. No.	202728
Seq. ID	LIB3048-047-Q1-L1-F9
Method	BLASTX
NCBI GI	g2911044
BLAST score	479
E value	3.0e-48
Match length	124
% identity	74
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	202729
Seq. ID	LIB3048-047-Q1-L1-G10
Method	BLASTX
NCBI GI	g2739046
BLAST score	190
E value	2.0e-14
Match length	53
% identity	68
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	202730
Seq. ID	LIB3048-047-Q1-L1-G11
Method	BLASTX
NCBI GI	g1076511
BLAST score	517
E value	9.0e-53
Match length	128
% identity	80
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	202731
Seq. ID	LIB3048-047-Q1-L1-G12
Method	BLASTX
NCBI GI	g3395432
BLAST score	287
E value	8.0e-26
Match length	91

% identity	62
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	202732
Seq. ID	LIB3048-047-Q1-L1-G3
Method	BLASTX
NCBI GI	g861112
BLAST score	341
E value	3.0e-32
Match length	100
% identity	62
NCBI Description	(Z49853) alpha-tubulin [Stentor coeruleus]

Seq. No.	202733
Seq. ID	LIB3048-047-Q1-L1-G4
Method	BLASTX
NCBI GI	g3924597
BLAST score	141
E value	1.0e-08
Match length	72
% identity	42
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	202734
Seq. ID	LIB3048-047-Q1-L1-G7
Method	BLASTX
NCBI GI	g416758
BLAST score	612
E value	7.0e-64
Match length	137
% identity	79
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	202735
Seq. ID	LIB3048-047-Q1-L1-G8
Method	BLASTX
NCBI GI	g4262250
BLAST score	167
E value	8.0e-12
Match length	52
% identity	62
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	202736
Seq. ID	LIB3048-047-Q1-L1-H11
Method	BLASTX
NCBI GI	g464849
BLAST score	660
E value	1.0e-69
Match length	124
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202737
Seq. ID	LIB3048-047-Q1-L1-H12
Method	BLASTX
NCBI GI	g1477428
BLAST score	706
E value	7.0e-75
Match length	134
% identity	97
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	202738
Seq. ID	LIB3048-047-Q1-L1-H2
Method	BLASTX
NCBI GI	g300265
BLAST score	145
E value	2.0e-09
Match length	53
% identity	62
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	202739
Seq. ID	LIB3048-047-Q1-L1-H4
Method	BLASTX
NCBI GI	g3738257
BLAST score	475
E value	7.0e-48
Match length	100
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	202740
Seq. ID	LIB3048-047-Q1-L1-H6
Method	BLASTX
NCBI GI	g300265
BLAST score	651
E value	2.0e-68
Match length	135
% identity	96
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	202741
Seq. ID	LIB3048-047-Q1-L1-H7
Method	BLASTX
NCBI GI	g2570164
BLAST score	423
E value	1.0e-41
Match length	123
% identity	61
NCBI Description	(D45183) chitinase [Chenopodium amaranticolor]

Seq. No.	202742
Seq. ID	LIB3048-047-Q1-L1-H8
Method	BLASTX

NCBI GI	g483057
BLAST score	183
E value	1.0e-13
Match length	104
% identity	40
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	202743
Seq. ID	LIB3048-048-Q1-L1-A10
Method	BLASTX
NCBI GI	g4539423
BLAST score	229
E value	2.0e-19
Match length	55
% identity	75
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202744
Seq. ID	LIB3048-048-Q1-L1-A12
Method	BLASTX
NCBI GI	g4432866
BLAST score	261
E value	8.0e-23
Match length	117
% identity	38
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	202745
Seq. ID	LIB3048-048-Q1-L1-A2
Method	BLASTX
NCBI GI	g1709498
BLAST score	384
E value	3.0e-37
Match length	100
% identity	74
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202746
Seq. ID	LIB3048-048-Q1-L1-A3
Method	BLASTX
NCBI GI	g2264373
BLAST score	207
E value	2.0e-16
Match length	50
% identity	74
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Seq. No.	202747
Seq. ID	LIB3048-048-Q1-L1-A4

Method	BLASTX
NCBI GI	g3287835
BLAST score	351
E value	2.0e-33
Match length	77
% identity	87
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME A (D-CADINENE SYNTHASE) >gi_1002523 (U27535) (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi_1217956_emb_CAA65289_ (X96429) (+)-delta-cadinene synthase [Gossypium arboreum]

Seq. No.	202748
Seq. ID	LIB3048-048-Q1-L1-A5
Method	BLASTX
NCBI GI	g4239845
BLAST score	171
E value	3.0e-12
Match length	47
% identity	72
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202749
Seq. ID	LIB3048-048-Q1-L1-A6
Method	BLASTX
NCBI GI	g464849
BLAST score	294
E value	6.0e-27
Match length	89
% identity	65
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202750
Seq. ID	LIB3048-048-Q1-L1-B10
Method	BLASTX
NCBI GI	g3355626
BLAST score	520
E value	3.0e-53
Match length	110
% identity	87
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]

Seq. No.	202751
Seq. ID	LIB3048-048-Q1-L1-B12
Method	BLASTX
NCBI GI	g2244905
BLAST score	246
E value	3.0e-21
Match length	80
% identity	56
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	202752
Seq. ID	LIB3048-048-Q1-L1-B4

Method	BLASTX
NCBI GI	g2244851
BLAST score	182
E value	4.0e-14
Match length	103
% identity	38
NCBI Description	(Z97337) amine oxidase [Arabidopsis thaliana]

Seq. No.	202753
Seq. ID	LIB3048-048-Q1-L1-B6
Method	BLASTX
NCBI GI	g2245077
BLAST score	207
E value	7.0e-17
Match length	72
% identity	61
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	202754
Seq. ID	LIB3048-048-Q1-L1-B7
Method	BLASTX
NCBI GI	g2642158
BLAST score	393
E value	2.0e-38
Match length	89
% identity	79
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202755
Seq. ID	LIB3048-048-Q1-L1-B9
Method	BLASTX
NCBI GI	g3687223
BLAST score	200
E value	1.0e-15
Match length	116
% identity	47
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202756
Seq. ID	LIB3048-048-Q1-L1-C1
Method	BLASTX
NCBI GI	g1483230
BLAST score	325
E value	2.0e-30
Match length	76
% identity	87
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	202757
Seq. ID	LIB3048-048-Q1-L1-C12
Method	BLASTX
NCBI GI	g1399275
BLAST score	309
E value	1.0e-43
Match length	102
% identity	85
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6

[Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	202758
Seq. ID	LIB3048-048-Q1-L1-C3
Method	BLASTX
NCBI GI	g3062801
BLAST score	351
E value	2.0e-33
Match length	77
% identity	83
NCBI Description	(AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No.	202759
Seq. ID	LIB3048-048-Q1-L1-C5
Method	BLASTX
NCBI GI	g2244759
BLAST score	391
E value	3.0e-38
Match length	98
% identity	69
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	202760
Seq. ID	LIB3048-048-Q1-L1-C7
Method	BLASTX
NCBI GI	g439489
BLAST score	103
E value	7.0e-10
Match length	67
% identity	66
NCBI Description	(D26084) zinc-finger DNA binding protein [Petunia x hybrida]

Seq. No.	202761
Seq. ID	LIB3048-048-Q1-L1-C9
Method	BLASTX
NCBI GI	g3885329
BLAST score	490
E value	1.0e-49
Match length	96
% identity	96
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	202762
Seq. ID	LIB3048-048-Q1-L1-D10
Method	BLASTX
NCBI GI	g3132696
BLAST score	315
E value	4.0e-29
Match length	85
% identity	78
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	202763
Seq. ID	LIB3048-048-Q1-L1-D12

Method	BLASTX
NCBI GI	g2244760
BLAST score	184
E value	6.0e-14
Match length	95
% identity	16
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	202764
Seq. ID	LIB3048-048-Q1-L1-D2
Method	BLASTX
NCBI GI	g4539423
BLAST score	290
E value	1.0e-26
Match length	70
% identity	77
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202765
Seq. ID	LIB3048-048-Q1-L1-D3
Method	BLASTX
NCBI GI	g4544443
BLAST score	170
E value	1.0e-12
Match length	55
% identity	71
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	202766
Seq. ID	LIB3048-048-Q1-L1-D5
Method	BLASTX
NCBI GI	g2191183
BLAST score	283
E value	2.0e-25
Match length	113
% identity	45
NCBI Description	(AF007271) similar to the ligand-gated ionic channels family [Arabidopsis thaliana]

Seq. No.	202767
Seq. ID	LIB3048-048-Q1-L1-D8
Method	BLASTN
NCBI GI	g4388705
BLAST score	39
E value	1.0e-12
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	202768
Seq. ID	LIB3048-048-Q1-L1-D9
Method	BLASTX
NCBI GI	g2642158
BLAST score	453

E value	3.0e-45
Match length	133
% identity	68
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202769
Seq. ID	LIB3048-048-Q1-L1-E1
Method	BLASTX
NCBI GI	g3075398
BLAST score	302
E value	8.0e-28
Match length	62
% identity	87
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	202770
Seq. ID	LIB3048-048-Q1-L1-E12
Method	BLASTX
NCBI GI	g1486472
BLAST score	396
E value	1.0e-38
Match length	92
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	202771
Seq. ID	LIB3048-048-Q1-L1-E3
Method	BLASTX
NCBI GI	g119010
BLAST score	277
E value	9.0e-25
Match length	71
% identity	73
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM GGIB50 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE, BASIC) (GLUCANASE GLA) >gi_100329_pir__A38257 glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) basic precursor (clone ggIb50) - common tobacco (cv. Samsun NN)

Seq. No.	202772
Seq. ID	LIB3048-048-Q1-L1-E4
Method	BLASTX
NCBI GI	g167367
BLAST score	494
E value	3.0e-50
Match length	100
% identity	96
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	202773
Seq. ID	LIB3048-048-Q1-L1-E5
Method	BLASTX
NCBI GI	g4185599
BLAST score	187
E value	4.0e-14

Match length	113
% identity	45
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	202774
Seq. ID	LIB3048-048-Q1-L1-E8
Method	BLASTX
NCBI GI	g4240207
BLAST score	165
E value	1.0e-11
Match length	59
% identity	49
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]

Seq. No.	202775
Seq. ID	LIB3048-048-Q1-L1-F1
Method	BLASTX
NCBI GI	g2134962
BLAST score	207
E value	2.0e-16
Match length	83
% identity	52
NCBI Description	cyclophilin-like protein CyP-60 - human >gi_1199598 (U37219) cyclophilin-like protein CyP-60 [Homo sapiens] >gi_1587642_prf__2207180A cyclophilin:ISOTYPE=CyP-60 [Homo sapiens]

Seq. No.	202776
Seq. ID	LIB3048-048-Q1-L1-F10
Method	BLASTX
NCBI GI	g483057
BLAST score	210
E value	7.0e-17
Match length	109
% identity	44
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	202777
Seq. ID	LIB3048-048-Q1-L1-F11
Method	BLASTX
NCBI GI	g3785974
BLAST score	162
E value	3.0e-11
Match length	78
% identity	46
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	202778
Seq. ID	LIB3048-048-Q1-L1-F2
Method	BLASTX
NCBI GI	g3176687
BLAST score	442
E value	5.0e-44
Match length	114

% identity	72
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	202779
Seq. ID	LIB3048-048-Q1-L1-F3
Method	BLASTX
NCBI GI	g2088651
BLAST score	194
E value	3.0e-15
Match length	53
% identity	70
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	202780
Seq. ID	LIB3048-048-Q1-L1-F9
Method	BLASTX
NCBI GI	g3850579
BLAST score	263
E value	3.0e-23
Match length	86
% identity	63
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	202781
Seq. ID	LIB3048-048-Q1-L1-G4
Method	BLASTX
NCBI GI	g135060
BLAST score	365
E value	4.0e-35
Match length	98
% identity	65
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]

Seq. No.	202782
Seq. ID	LIB3048-048-Q1-L1-G5
Method	BLASTX
NCBI GI	g4239845
BLAST score	194
E value	3.0e-15
Match length	83
% identity	54
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	202783
Seq. ID	LIB3048-048-Q1-L1-G8

D95-4P0-5P0-4P0-5P0-4P0-5P0

Method	BLASTX
NCBI GI	g2529703
BLAST score	229
E value	3.0e-19
Match length	98
% identity	55
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	202784
Seq. ID	LIB3048-048-Q1-L1-G9
Method	BLASTX
NCBI GI	g1142621
BLAST score	235
E value	6.0e-20
Match length	87
% identity	54
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No.	202785
Seq. ID	LIB3048-048-Q1-L1-H1
Method	BLASTX
NCBI GI	g629561
BLAST score	237
E value	6.0e-20
Match length	101
% identity	43
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	202786
Seq. ID	LIB3048-048-Q1-L1-H10
Method	BLASTX
NCBI GI	g3885329
BLAST score	538
E value	2.0e-55
Match length	107
% identity	93
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	202787
Seq. ID	LIB3048-048-Q1-L1-H11
Method	BLASTX
NCBI GI	g131276
BLAST score	363
E value	3.0e-35
Match length	73
% identity	93
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	202788
Seq. ID	LIB3048-048-Q1-L1-H3
Method	BLASTX
NCBI GI	g529353
BLAST score	165
E value	7.0e-12
Match length	57
% identity	58
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	202789
Seq. ID	LIB3048-048-Q1-L1-H4
Method	BLASTX
NCBI GI	g1762148
BLAST score	576
E value	9.0e-60
Match length	113
% identity	94
NCBI Description	(U48695) glutamate dehydrogenase [Solanum lycopersicum]

Seq. No.	202790
Seq. ID	LIB3048-048-Q1-L1-H6
Method	BLASTX
NCBI GI	g2244771
BLAST score	376
E value	2.0e-36
Match length	92
% identity	80
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	202791
Seq. ID	LIB3048-048-Q1-L1-H8
Method	BLASTX
NCBI GI	g4454012
BLAST score	290
E value	2.0e-26
Match length	76
% identity	72
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	202792
Seq. ID	LIB3048-048-Q1-L1-H9
Method	BLASTX
NCBI GI	g3493367
BLAST score	307
E value	2.0e-28
Match length	82
% identity	73
NCBI Description	(AB017159) citrate synthase [Daucus carota]

Seq. No.	202793
Seq. ID	LIB3048-049-Q1-L1-A2
Method	BLASTX
NCBI GI	g3821793
BLAST score	663
E value	7.0e-70

Match length	127
% identity	96
NCBI Description	(Y11526) casein kinase II alpha subunit [Zea mays]

Seq. No.	202794
Seq. ID	LIB3048-049-Q1-L1-A4
Method	BLASTX
NCBI GI	g4455365
BLAST score	218
E value	9.0e-18
Match length	57
% identity	68
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202795
Seq. ID	LIB3048-049-Q1-L1-A5
Method	BLASTX
NCBI GI	g1361983
BLAST score	337
E value	9.0e-32
Match length	110
% identity	64
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	202796
Seq. ID	LIB3048-049-Q1-L1-A8
Method	BLASTX
NCBI GI	g133940
BLAST score	371
E value	9.0e-36
Match length	86
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	202797
Seq. ID	LIB3048-049-Q1-L1-A9
Method	BLASTX
NCBI GI	g4115371
BLAST score	311
E value	5.0e-29
Match length	82
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	202798
Seq. ID	LIB3048-049-Q1-L1-B1
Method	BLASTX
NCBI GI	g4335751
BLAST score	295
E value	5.0e-27
Match length	93
% identity	55
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis

thaliana]

Seq. No.	202799
Seq. ID	LIB3048-049-Q1-L1-B3
Method	BLASTX
NCBI GI	g100484
BLAST score	377
E value	2.0e-36
Match length	102
% identity	62
NCBI Description	hypothetical protein - garden snapdragon

Seq. No.	202800
Seq. ID	LIB3048-049-Q1-L1-B4
Method	BLASTX
NCBI GI	g3738306
BLAST score	403
E value	1.0e-39
Match length	99
% identity	81
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	202801
Seq. ID	LIB3048-049-Q1-L1-B5
Method	BLASTX
NCBI GI	g4455365
BLAST score	257
E value	2.0e-22
Match length	57
% identity	77
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202802
Seq. ID	LIB3048-049-Q1-L1-B6
Method	BLASTX
NCBI GI	g3763921
BLAST score	310
E value	2.0e-28
Match length	92
% identity	67
NCBI Description	(AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No.	202803
Seq. ID	LIB3048-049-Q1-L1-B7
Method	BLASTX
NCBI GI	g2827715
BLAST score	322
E value	3.0e-30
Match length	79
% identity	8
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	202804
Seq. ID	LIB3048-049-Q1-L1-B8
Method	BLASTX
NCBI GI	g4335751

BLAST score	395
E value	1.0e-38
Match length	114
% identity	61
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	202805
Seq. ID	LIB3048-049-Q1-L1-C11
Method	BLASTX
NCBI GI	g2864624
BLAST score	147
E value	7.0e-10
Match length	71
% identity	45
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	202806
Seq. ID	LIB3048-049-Q1-L1-C2
Method	BLASTX
NCBI GI	g2244987
BLAST score	232
E value	2.0e-19
Match length	103
% identity	46
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No.	202807
Seq. ID	LIB3048-049-Q1-L1-C5
Method	BLASTX
NCBI GI	g3201627
BLAST score	200
E value	5.0e-16
Match length	58
% identity	64
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	202808
Seq. ID	LIB3048-049-Q1-L1-C6
Method	BLASTX
NCBI GI	g2739376
BLAST score	259
E value	2.0e-25
Match length	84
% identity	76
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	202809
Seq. ID	LIB3048-049-Q1-L1-C7
Method	BLASTX
NCBI GI	g3068713
BLAST score	273
E value	2.0e-24
Match length	87
% identity	70
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	202810
Seq. ID	LIB3048-049-Q1-L1-C9
Method	BLASTX
NCBI GI	g1778370
BLAST score	414
E value	5.0e-41
Match length	84
% identity	92
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	202811
Seq. ID	LIB3048-049-Q1-L1-D12
Method	BLASTX
NCBI GI	g2316016
BLAST score	147
E value	9.0e-16
Match length	124
% identity	44
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	202812
Seq. ID	LIB3048-049-Q1-L1-D3
Method	BLASTX
NCBI GI	g3582021
BLAST score	183
E value	8.0e-14
Match length	98
% identity	43
NCBI Description	(Y09423) cytochrome P450 [Nepeta racemosa]

Seq. No.	202813
Seq. ID	LIB3048-049-Q1-L1-D4
Method	BLASTX
NCBI GI	g3522938
BLAST score	188
E value	3.0e-14
Match length	107
% identity	36
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	202814
Seq. ID	LIB3048-049-Q1-L1-D5
Method	BLASTX
NCBI GI	g4432860
BLAST score	418
E value	3.0e-41
Match length	115
% identity	13
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	202815
Seq. ID	LIB3048-049-Q1-L1-D6
Method	BLASTN
NCBI GI	g1293094
BLAST score	39

E value	5.0e-13
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana glutamate dehydrogenase 1 (GDH1) mRNA, complete cds

Seq. No.	202816
Seq. ID	LIB3048-049-Q1-L1-D7
Method	BLASTX
NCBI GI	g3297827
BLAST score	172
E value	1.0e-12
Match length	51
% identity	69
NCBI Description	(AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	202817
Seq. ID	LIB3048-049-Q1-L1-D8
Method	BLASTX
NCBI GI	g3176708
BLAST score	253
E value	7.0e-22
Match length	87
% identity	56
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	202818
Seq. ID	LIB3048-049-Q1-L1-E12
Method	BLASTX
NCBI GI	g3152609
BLAST score	383
E value	5.0e-37
Match length	115
% identity	60
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	202819
Seq. ID	LIB3048-049-Q1-L1-E3
Method	BLASTX
NCBI GI	g167367
BLAST score	594
E value	7.0e-62
Match length	118
% identity	96
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	202820
Seq. ID	LIB3048-049-Q1-L1-E6
Method	BLASTX
NCBI GI	g3687237
BLAST score	516
E value	8.0e-53
Match length	96
% identity	86

NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	202821
Seq. ID	LIB3048-049-Q1-L1-E7
Method	BLASTX
NCBI GI	g4433048
BLAST score	214
E value	6.0e-29
Match length	114
% identity	62
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	202822
Seq. ID	LIB3048-049-Q1-L1-E9
Method	BLASTX
NCBI GI	g2980770
BLAST score	259
E value	8.0e-23
Match length	58
% identity	83
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	202823
Seq. ID	LIB3048-049-Q1-L1-F11
Method	BLASTX
NCBI GI	g2462826
BLAST score	288
E value	3.0e-26
Match length	95
% identity	57
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	202824
Seq. ID	LIB3048-049-Q1-L1-F12
Method	BLASTX
NCBI GI	g1174592
BLAST score	637
E value	8.0e-67
Match length	121
% identity	98
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	202825
Seq. ID	LIB3048-049-Q1-L1-F2
Method	BLASTX
NCBI GI	g2739381
BLAST score	363
E value	9.0e-35
Match length	117
% identity	61
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	202826
Seq. ID	LIB3048-049-Q1-L1-F5

Method	BLASTX
NCBI GI	g2245023
BLAST score	274
E value	2.0e-24
Match length	118
% identity	48
NCBI Description	(Z97341) RNA helicase [Arabidopsis thaliana]

Seq. No.	202827
Seq. ID	LIB3048-049-Q1-L1-F6
Method	BLASTX
NCBI GI	g2642158
BLAST score	274
E value	1.0e-24
Match length	83
% identity	66
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202828
Seq. ID	LIB3048-049-Q1-L1-F9
Method	BLASTX
NCBI GI	g2499819
BLAST score	306
E value	5.0e-28
Match length	87
% identity	72
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	202829
Seq. ID	LIB3048-049-Q1-L1-G10
Method	BLASTX
NCBI GI	g4204259
BLAST score	331
E value	4.0e-31
Match length	103
% identity	65
NCBI Description	(AC005223) 18074 [Arabidopsis thaliana]

Seq. No.	202830
Seq. ID	LIB3048-049-Q1-L1-G11
Method	BLASTX
NCBI GI	g2981439
BLAST score	118
E value	7.0e-10
Match length	67
% identity	66
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]

Seq. No.	202831
Seq. ID	LIB3048-049-Q1-L1-G2
Method	BLASTX
NCBI GI	g2369714
BLAST score	565

E value	2.0e-58
Match length	118
% identity	89
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	202832
Seq. ID	LIB3048-049-Q1-L1-G6
Method	BLASTX
NCBI GI	g3183247
BLAST score	368
E value	3.0e-35
Match length	120
% identity	56
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB

Seq. No.	202833
Seq. ID	LIB3048-049-Q1-L1-G7
Method	BLASTX
NCBI GI	g1946359
BLAST score	251
E value	9.0e-22
Match length	86
% identity	57
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	202834
Seq. ID	LIB3048-049-Q1-L1-G9
Method	BLASTX
NCBI GI	g3738319
BLAST score	278
E value	4.0e-25
Match length	66
% identity	79
NCBI Description	(AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202835
Seq. ID	LIB3048-049-Q1-L1-H2
Method	BLASTX
NCBI GI	g1532050
BLAST score	172
E value	6.0e-13
Match length	80
% identity	48
NCBI Description	(X82542) farnesyl diphosphate synthase [Parthenium argentatum]

Seq. No.	202836
Seq. ID	LIB3048-049-Q1-L1-H3
Method	BLASTX
NCBI GI	g464734
BLAST score	518
E value	6.0e-53

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Match length	115
% identity	88
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No.	202837
Seq. ID	LIB3048-049-Q1-L1-H9
Method	BLASTX
NCBI GI	g3924597
BLAST score	164
E value	1.0e-11
Match length	72
% identity	43
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	202838
Seq. ID	LIB3048-050-Q1-L1-A10
Method	BLASTN
NCBI GI	g4220643
BLAST score	39
E value	1.0e-12
Match length	155
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	202839
Seq. ID	LIB3048-050-Q1-L1-A11
Method	BLASTX
NCBI GI	g1332579
BLAST score	535
E value	6.0e-55
Match length	109
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	202840
Seq. ID	LIB3048-050-Q1-L1-A12
Method	BLASTX
NCBI GI	g3461820
BLAST score	226
E value	1.0e-18
Match length	61
% identity	62
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	202841
Seq. ID	LIB3048-050-Q1-L1-A2
Method	BLASTX
NCBI GI	g3687230
BLAST score	473
E value	1.0e-47
Match length	132
% identity	71

NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202842
Seq. ID	LIB3048-050-Q1-L1-A4
Method	BLASTX
NCBI GI	g4309698
BLAST score	467
E value	7.0e-47
Match length	115
% identity	83
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	202843
Seq. ID	LIB3048-050-Q1-L1-A5
Method	BLASTX
NCBI GI	g1346029
BLAST score	490
E value	1.0e-49
Match length	110
% identity	82
NCBI Description	FARNESYL PYROPHOSPHATE SYNTHETASE 2 (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE / GERANYLTRANSTRANSFERASE >gi_2129850_pir__S66471 farnesyl pyrophosphate synthase 2 - white lupine >gi_710350 (U20771) farnesyl pyrophosphate synthase [Lupinus albus]

Seq. No.	202844
Seq. ID	LIB3048-050-Q1-L1-A6
Method	BLASTX
NCBI GI	g1518540
BLAST score	554
E value	4.0e-57
Match length	124
% identity	85
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	202845
Seq. ID	LIB3048-050-Q1-L1-A7
Method	BLASTX
NCBI GI	g1364161
BLAST score	631
E value	4.0e-66
Match length	137
% identity	89
NCBI Description	thiolase precursor, peroxisomal - ripe mango

Seq. No.	202846
Seq. ID	LIB3048-050-Q1-L1-A8
Method	BLASTX
NCBI GI	g4235646
BLAST score	266
E value	3.0e-23
Match length	130
% identity	11
NCBI Description	(AF119041) SC0A [Lycopersicon esculentum]

Seq. No.	202847
Seq. ID	LIB3048-050-Q1-L1-B10
Method	BLASTX
NCBI GI	g3928097
BLAST score	561
E value	6.0e-58
Match length	126
% identity	81
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	202848
Seq. ID	LIB3048-050-Q1-L1-B11
Method	BLASTX
NCBI GI	g4432860
BLAST score	363
E value	9.0e-35
Match length	120
% identity	16
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	202849
Seq. ID	LIB3048-050-Q1-L1-B12
Method	BLASTX
NCBI GI	g1931642
BLAST score	403
E value	2.0e-39
Match length	124
% identity	60
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	202850
Seq. ID	LIB3048-050-Q1-L1-B3
Method	BLASTX
NCBI GI	g4309698
BLAST score	527
E value	6.0e-54
Match length	117
% identity	90
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	202851
Seq. ID	LIB3048-050-Q1-L1-B4
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	99
% identity	83
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202852
Seq. ID	LIB3048-050-Q1-L1-B5
Method	BLASTX
NCBI GI	g3367522
BLAST score	402
E value	3.0e-39
Match length	120
% identity	66
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	202853
Seq. ID	LIB3048-050-Q1-L1-B6
Method	BLASTX
NCBI GI	g3128180
BLAST score	322
E value	5.0e-30
Match length	91
% identity	76
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	202854
Seq. ID	LIB3048-050-Q1-L1-C1
Method	BLASTX
NCBI GI	g2129550
BLAST score	383
E value	2.0e-37
Match length	90
% identity	79
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	202855
Seq. ID	LIB3048-050-Q1-L1-C12
Method	BLASTX
NCBI GI	g2129759
BLAST score	405
E value	1.0e-39
Match length	111
% identity	74
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	202856
Seq. ID	LIB3048-050-Q1-L1-C2
Method	BLASTX
NCBI GI	g1841468
BLAST score	558
E value	1.0e-57
Match length	122

% identity	86
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	202857
Seq. ID	LIB3048-050-Q1-L1-C3
Method	BLASTX
NCBI GI	g3377848
BLAST score	411
E value	3.0e-40
Match length	136
% identity	58
NCBI Description	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No.	202858
Seq. ID	LIB3048-050-Q1-L1-C4
Method	BLASTX
NCBI GI	g2499553
BLAST score	487
E value	3.0e-49
Match length	128
% identity	72
NCBI Description	CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_629524_pir__S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi_442529_bbs_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa] [Arabidopsis thaliana]

Seq. No.	202859
Seq. ID	LIB3048-050-Q1-L1-C5
Method	BLASTX
NCBI GI	g4056462
BLAST score	200
E value	4.0e-16
Match length	71
% identity	56
NCBI Description	(AC005990) Strong similarity to gb_Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]

Seq. No.	202860
Seq. ID	LIB3048-050-Q1-L1-C6
Method	BLASTX
NCBI GI	g4454052
BLAST score	149
E value	1.0e-09
Match length	102
% identity	24
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202861
Seq. ID	LIB3048-050-Q1-L1-C8
Method	BLASTX

NCBI GI	g4567095
BLAST score	252
E value	7.0e-26
Match length	114
% identity	53
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	202862
Seq. ID	LIB3048-050-Q1-L1-C9
Method	BLASTX
NCBI GI	g2290683
BLAST score	461
E value	3.0e-46
Match length	99
% identity	84
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	202863
Seq. ID	LIB3048-050-Q1-L1-D1
Method	BLASTX
NCBI GI	g2317906
BLAST score	463
E value	2.0e-46
Match length	104
% identity	85
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	202864
Seq. ID	LIB3048-050-Q1-L1-D10
Method	BLASTX
NCBI GI	g3033375
BLAST score	184
E value	1.0e-13
Match length	94
% identity	41
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	202865
Seq. ID	LIB3048-050-Q1-L1-D11
Method	BLASTX
NCBI GI	g1729760
BLAST score	719
E value	2.0e-76
Match length	127
% identity	98
NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	202866
Seq. ID	LIB3048-050-Q1-L1-D2
Method	BLASTX
NCBI GI	g4138647
BLAST score	402
E value	2.0e-39
Match length	101
% identity	77

NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	202867
Seq. ID	LIB3048-050-Q1-L1-D3
Method	BLASTX
NCBI GI	g3549691
BLAST score	202
E value	8.0e-24
Match length	97
% identity	61
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	202868
Seq. ID	LIB3048-050-Q1-L1-D4
Method	BLASTX
NCBI GI	g2388580
BLAST score	233
E value	1.0e-19
Match length	54
% identity	70
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	202869
Seq. ID	LIB3048-050-Q1-L1-D5
Method	BLASTX
NCBI GI	g3461814
BLAST score	517
E value	1.0e-52
Match length	135
% identity	72
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202870
Seq. ID	LIB3048-050-Q1-L1-D8
Method	BLASTX
NCBI GI	g2827546
BLAST score	328
E value	1.0e-30
Match length	131
% identity	47
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	202871
Seq. ID	LIB3048-050-Q1-L1-D9
Method	BLASTX
NCBI GI	g1657374
BLAST score	414
E value	9.0e-41
Match length	89
% identity	87
NCBI Description	(X96853) endo-beta-1,4-glucanase [Prunus persica] >gi_1657380_emb_CAA65600_ (X96856) endo-beta-1,4-glucanase [Prunus persica]

Seq. No.	202872

Seq. ID	LIB3048-050-Q1-L1-E2
Method	BLASTX
NCBI GI	g4539423
BLAST score	286
E value	1.0e-25
Match length	114
% identity	46
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	202873
Seq. ID	LIB3048-050-Q1-L1-E4
Method	BLASTX
NCBI GI	g4455365
BLAST score	208
E value	2.0e-16
Match length	57
% identity	55
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202874
Seq. ID	LIB3048-050-Q1-L1-E5
Method	BLASTX
NCBI GI	g3687223
BLAST score	253
E value	5.0e-22
Match length	92
% identity	63
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202875
Seq. ID	LIB3048-050-Q1-L1-E8
Method	BLASTX
NCBI GI	g132944
BLAST score	565
E value	2.0e-58
Match length	120
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	202876
Seq. ID	LIB3048-050-Q1-L1-F1
Method	BLASTX
NCBI GI	g2499946
BLAST score	571
E value	4.0e-59
Match length	121
% identity	88
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	202877
Seq. ID	LIB3048-050-Q1-L1-F11

Method	BLASTX
NCBI GI	g4468979
BLAST score	208
E value	1.0e-16
Match length	57
% identity	70
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	202878
Seq. ID	LIB3048-050-Q1-L1-F12
Method	BLASTX
NCBI GI	g3821793
BLAST score	667
E value	2.0e-70
Match length	127
% identity	97
NCBI Description	(Y11526) casein kinase II alpha subunit [Zea mays]

Seq. No.	202879
Seq. ID	LIB3048-050-Q1-L1-F3
Method	BLASTX
NCBI GI	g2865437
BLAST score	266
E value	3.0e-23
Match length	133
% identity	42
NCBI Description	(AF039376) polyprotein [Arabidopsis arenosa]

Seq. No.	202880
Seq. ID	LIB3048-050-Q1-L1-F4
Method	BLASTX
NCBI GI	g2996096
BLAST score	718
E value	3.0e-76
Match length	136
% identity	100
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	202881
Seq. ID	LIB3048-050-Q1-L1-F7
Method	BLASTX
NCBI GI	g1172903
BLAST score	148
E value	2.0e-09
Match length	58
% identity	47
NCBI Description	GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi_1073884_pir__D64062 ATP--GTP 3'-pyrophosphotransferase (relA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573303 (U32718) GTP pyrophosphokinase (relA) [Haemophilus influenzae Rd]

Seq. No.	202882
Seq. ID	LIB3048-050-Q1-L1-F8
Method	BLASTX
NCBI GI	g3075392

BLAST score	234
E value	4.0e-20
Match length	62
% identity	71
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	202883
Seq. ID	LIB3048-050-Q1-L1-F9
Method	BLASTX
NCBI GI	g1617272
BLAST score	530
E value	3.0e-54
Match length	121
% identity	80
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	202884
Seq. ID	LIB3048-050-Q1-L1-G1
Method	BLASTN
NCBI GI	g2804257
BLAST score	51
E value	9.0e-20
Match length	135
% identity	84
NCBI Description	Arabidopsis thaliana DNA for phosphoglycerate dehydrogenase, complete cds

Seq. No.	202885
Seq. ID	LIB3048-050-Q1-L1-G11
Method	BLASTX
NCBI GI	g3668093
BLAST score	550
E value	1.0e-56
Match length	123
% identity	82
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	202886
Seq. ID	LIB3048-050-Q1-L1-G2
Method	BLASTX
NCBI GI	g464775
BLAST score	458
E value	2.0e-56
Match length	136
% identity	75
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	202887
Seq. ID	LIB3048-050-Q1-L1-G3
Method	BLASTX
NCBI GI	g862931
BLAST score	416
E value	7.0e-41
Match length	126

% identity	69
NCBI Description	(U27179) acidic glucanase [Medicago sativa subsp. sativa]

Seq. No.	202888
Seq. ID	LIB3048-050-Q1-L1-G9
Method	BLASTX
NCBI GI	g1572819
BLAST score	238
E value	5.0e-20
Match length	98
% identity	49
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	202889
Seq. ID	LIB3048-050-Q1-L1-H1
Method	BLASTX
NCBI GI	g4239889
BLAST score	158
E value	1.0e-21
Match length	103
% identity	50
NCBI Description	(AB016802) MAP kinase 5 [Zea mays]

Seq. No.	202890
Seq. ID	LIB3048-050-Q1-L1-H10
Method	BLASTX
NCBI GI	g1076511
BLAST score	504
E value	3.0e-51
Match length	124
% identity	80
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	202891
Seq. ID	LIB3048-050-Q1-L1-H12
Method	BLASTX
NCBI GI	g4512617
BLAST score	204
E value	4.0e-16
Match length	83
% identity	51
NCBI Description	(AC004793) F28K20.16 [Arabidopsis thaliana]

Seq. No.	202892
Seq. ID	LIB3048-050-Q1-L1-H2
Method	BLASTX
NCBI GI	g3355626
BLAST score	328
E value	1.0e-30
Match length	126
% identity	47
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]

Seq. No.	202893
Seq. ID	LIB3048-050-Q1-L1-H3
Method	BLASTX
NCBI GI	g2947060
BLAST score	212
E value	2.0e-17
Match length	73
% identity	63
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	202894
Seq. ID	LIB3048-050-Q1-L1-H6
Method	BLASTX
NCBI GI	g1729760
BLAST score	149
E value	4.0e-10
Match length	35
% identity	83
NCBI Description	(Z68152) chitinase [Gossypium hirsutum]

Seq. No.	202895
Seq. ID	LIB3048-050-Q1-L1-H9
Method	BLASTX
NCBI GI	g2811025
BLAST score	316
E value	9.0e-30
Match length	72
% identity	82
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	202896
Seq. ID	LIB3048-051-Q1-L1-A10
Method	BLASTX
NCBI GI	g4206122
BLAST score	172
E value	8.0e-13
Match length	44
% identity	66
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	202897
Seq. ID	LIB3048-051-Q1-L1-A11
Method	BLASTX
NCBI GI	g1619300
BLAST score	187
E value	4.0e-14
Match length	45
% identity	78
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	202898
Seq. ID	LIB3048-051-Q1-L1-A2
Method	BLASTX
NCBI GI	g3643611
BLAST score	472

E value	2.0e-47
Match length	124
% identity	73
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	202899
Seq. ID	LIB3048-051-Q1-L1-A4
Method	BLASTX
NCBI GI	g544250
BLAST score	348
E value	4.0e-33
Match length	87
% identity	77
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	202900
Seq. ID	LIB3048-051-Q1-L1-B2
Method	BLASTX
NCBI GI	g4558547
BLAST score	207
E value	2.0e-16
Match length	95
% identity	47
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202901
Seq. ID	LIB3048-051-Q1-L1-B4
Method	BLASTN
NCBI GI	g19784
BLAST score	53
E value	5.0e-21
Match length	136
% identity	89
NCBI Description	N.tabacum atpC mRNA for gamma subunit of ATP synthase

Seq. No.	202902
Seq. ID	LIB3048-051-Q1-L1-B9
Method	BLASTX
NCBI GI	g2498706
BLAST score	150
E value	1.0e-09
Match length	42
% identity	67
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	202903
Seq. ID	LIB3048-051-Q1-L1-C1
Method	BLASTX
NCBI GI	g2497538
BLAST score	157
E value	9.0e-11
Match length	61

% identity	56
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	202904
Seq. ID	LIB3048-051-Q1-L1-C3
Method	BLASTX
NCBI GI	g2244792
BLAST score	417
E value	5.0e-41
Match length	121
% identity	64
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202905
Seq. ID	LIB3048-051-Q1-L1-C7
Method	BLASTX
NCBI GI	g2244792
BLAST score	641
E value	3.0e-67
Match length	137
% identity	81
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202906
Seq. ID	LIB3048-051-Q1-L1-D1
Method	BLASTX
NCBI GI	g2244792
BLAST score	251
E value	3.0e-38
Match length	107
% identity	66
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	202907
Seq. ID	LIB3048-051-Q1-L1-D11
Method	BLASTX
NCBI GI	g3334147
BLAST score	576
E value	1.0e-59
Match length	118
% identity	88
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202908
Seq. ID	LIB3048-051-Q1-L1-D12
Method	BLASTX
NCBI GI	g1363325
BLAST score	282
E value	3.0e-25
Match length	108
% identity	58
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	202909

Seq. ID	LIB3048-051-Q1-L1-D3
Method	BLASTX
NCBI GI	g464840
BLAST score	302
E value	6.0e-28
Match length	79
% identity	72
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	202910
Seq. ID	LIB3048-051-Q1-L1-D7
Method	BLASTX
NCBI GI	g464849
BLAST score	492
E value	5.0e-50
Match length	96
% identity	98
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	202911
Seq. ID	LIB3048-051-Q1-L1-D9
Method	BLASTX
NCBI GI	g3462614
BLAST score	460
E value	4.0e-46
Match length	121
% identity	77
NCBI Description	(AF080105) knotted I class homeodomain protein [Pisum sativum]

Seq. No.	202912
Seq. ID	LIB3048-051-Q1-L1-E1
Method	BLASTX
NCBI GI	g1895084
BLAST score	296
E value	2.0e-27
Match length	68
% identity	82
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	202913
Seq. ID	LIB3048-051-Q1-L1-E12
Method	BLASTX
NCBI GI	g2766452
BLAST score	200
E value	9.0e-16
Match length	60
% identity	62
NCBI Description	(AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No.	202914
Seq. ID	LIB3048-051-Q1-L1-E3

Method	BLASTX
NCBI GI	g3687223
BLAST score	150
E value	3.0e-10
Match length	49
% identity	67
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202915
Seq. ID	LIB3048-051-Q1-L1-E4
Method	BLASTX
NCBI GI	g4558547
BLAST score	262
E value	7.0e-23
Match length	108
% identity	50
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202916
Seq. ID	LIB3048-051-Q1-L1-E7
Method	BLASTX
NCBI GI	g2811025
BLAST score	295
E value	4.0e-27
Match length	85
% identity	65
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	202917
Seq. ID	LIB3048-051-Q1-L1-E8
Method	BLASTX
NCBI GI	g3915737
BLAST score	344
E value	1.0e-33
Match length	83
% identity	33
NCBI Description	IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon esculentum]

Seq. No.	202918
Seq. ID	LIB3048-051-Q1-L1-E9
Method	BLASTX
NCBI GI	g1709498
BLAST score	420
E value	2.0e-41
Match length	104
% identity	75
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202919
Seq. ID	LIB3048-051-Q1-L1-F10
Method	BLASTX

NCBI GI	g2243118
BLAST score	248
E value	3.0e-21
Match length	62
% identity	73
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	202920
Seq. ID	LIB3048-051-Q1-L1-F11
Method	BLASTX
NCBI GI	g3687237
BLAST score	491
E value	8.0e-50
Match length	96
% identity	83
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	202921
Seq. ID	LIB3048-051-Q1-L1-F3
Method	BLASTX
NCBI GI	g4432844
BLAST score	180
E value	3.0e-13
Match length	66
% identity	52
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	202922
Seq. ID	LIB3048-051-Q1-L1-F5
Method	BLASTX
NCBI GI	g2258414
BLAST score	265
E value	3.0e-23
Match length	84
% identity	63
NCBI Description	(AF007873) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe] >gi_2388967_emb_CAB11700_ (Z98979) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe]

Seq. No.	202923
Seq. ID	LIB3048-051-Q1-L1-G12
Method	BLASTX
NCBI GI	g1361983
BLAST score	475
E value	8.0e-48
Match length	129
% identity	74
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	202924
Seq. ID	LIB3048-051-Q1-L1-G3
Method	BLASTX
NCBI GI	g3603456
BLAST score	410

E value	2.0e-40
Match length	88
% identity	26
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	202925
Seq. ID	LIB3048-051-Q1-L1-G5
Method	BLASTX
NCBI GI	g3549691
BLAST score	402
E value	1.0e-39
Match length	90
% identity	78
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	202926
Seq. ID	LIB3048-051-Q1-L1-G6
Method	BLASTX
NCBI GI	g2980641
BLAST score	252
E value	8.0e-22
Match length	109
% identity	46
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	202927
Seq. ID	LIB3048-051-Q1-L1-H1
Method	BLASTX
NCBI GI	g1895084
BLAST score	321
E value	2.0e-30
Match length	68
% identity	90
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	202928
Seq. ID	LIB3048-051-Q1-L1-H11
Method	BLASTX
NCBI GI	g4185136
BLAST score	236
E value	4.0e-20
Match length	73
% identity	60
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	202929
Seq. ID	LIB3048-051-Q1-L1-H3
Method	BLASTX
NCBI GI	g3212865
BLAST score	303
E value	6.0e-28
Match length	92
% identity	66
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	202930

Seq. ID	LIB3048-051-Q1-L1-H4
Method	BLASTX
NCBI GI	g3193292
BLAST score	215
E value	3.0e-34
Match length	105
% identity	79
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	202931
Seq. ID	LIB3048-051-Q1-L1-H5
Method	BLASTX
NCBI GI	g2342724
BLAST score	252
E value	2.0e-27
Match length	130
% identity	65
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	202932
Seq. ID	LIB3048-051-Q1-L1-H7
Method	BLASTX
NCBI GI	g1361983
BLAST score	423
E value	1.0e-41
Match length	129
% identity	69
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	202933
Seq. ID	LIB3048-051-Q1-L1-H9
Method	BLASTX
NCBI GI	g2281085
BLAST score	292
E value	2.0e-26
Match length	129
% identity	51
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	202934
Seq. ID	LIB3048-052-Q1-L1-A10
Method	BLASTX
NCBI GI	g3461844
BLAST score	292
E value	2.0e-26
Match length	137
% identity	42
NCBI Description	(AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202935
Seq. ID	LIB3048-052-Q1-L1-A11
Method	BLASTX
NCBI GI	g1707857

BLAST score	627
E value	1.0e-65
Match length	135
% identity	88
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	202936
Seq. ID	LIB3048-052-Q1-L1-A12
Method	BLASTX
NCBI GI	g2827711
BLAST score	691
E value	4.0e-73
Match length	145
% identity	87
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	202937
Seq. ID	LIB3048-052-Q1-L1-A2
Method	BLASTX
NCBI GI	g1946364
BLAST score	168
E value	2.0e-12
Match length	63
% identity	44
NCBI Description	(U93215) lipase isolog [Arabidopsis thaliana]

Seq. No.	202938
Seq. ID	LIB3048-052-Q1-L1-A4
Method	BLASTX
NCBI GI	g1350680
BLAST score	322
E value	4.0e-30
Match length	83
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	202939
Seq. ID	LIB3048-052-Q1-L1-A6
Method	BLASTX
NCBI GI	g4455365
BLAST score	240
E value	2.0e-20
Match length	57
% identity	74
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	202940
Seq. ID	LIB3048-052-Q1-L1-A7
Method	BLASTX
NCBI GI	g3242705
BLAST score	253
E value	6.0e-27
Match length	76
% identity	66
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase

[Arabidopsis thaliana]

Seq. No.	202941
Seq. ID	LIB3048-052-Q1-L1-A8
Method	BLASTX
NCBI GI	g4220462
BLAST score	202
E value	9.0e-16
Match length	48
% identity	75
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	202942
Seq. ID	LIB3048-052-Q1-L1-A9
Method	BLASTX
NCBI GI	g483057
BLAST score	174
E value	1.0e-12
Match length	68
% identity	49
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]

Seq. No.	202943
Seq. ID	LIB3048-052-Q1-L1-B1
Method	BLASTX
NCBI GI	g3242705
BLAST score	318
E value	2.0e-29
Match length	83
% identity	69
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	202944
Seq. ID	LIB3048-052-Q1-L1-B10
Method	BLASTX
NCBI GI	g3334147
BLAST score	604
E value	6.0e-63
Match length	125
% identity	86
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	202945
Seq. ID	LIB3048-052-Q1-L1-B4
Method	BLASTX
NCBI GI	g2894612
BLAST score	559
E value	1.0e-57
Match length	125
% identity	84
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	202946
Seq. ID	LIB3048-052-Q1-L1-B7
Method	BLASTX
NCBI GI	g1041706
BLAST score	315
E value	2.0e-42
Match length	103
% identity	83
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	202947
Seq. ID	LIB3048-052-Q1-L1-B8
Method	BLASTX
NCBI GI	g3297816
BLAST score	492
E value	8.0e-50
Match length	128
% identity	77
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	202948
Seq. ID	LIB3048-052-Q1-L1-B9
Method	BLASTX
NCBI GI	g4455340
BLAST score	199
E value	1.0e-15
Match length	67
% identity	61
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	202949
Seq. ID	LIB3048-052-Q1-L1-C10
Method	BLASTX
NCBI GI	g1209756
BLAST score	344
E value	8.0e-33
Match length	86
% identity	78
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	202950
Seq. ID	LIB3048-052-Q1-L1-C11
Method	BLASTX
NCBI GI	g3421090
BLAST score	221
E value	5.0e-18
Match length	48
% identity	94
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	202951
Seq. ID	LIB3048-052-Q1-L1-C12
Method	BLASTX
NCBI GI	g627468
BLAST score	321

E value	9.0e-30
Match length	124
% identity	54
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	202952
Seq. ID	LIB3048-052-Q1-L1-C2
Method	BLASTX
NCBI GI	g4567267
BLAST score	263
E value	5.0e-23
Match length	52
% identity	87
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	202953
Seq. ID	LIB3048-052-Q1-L1-C3
Method	BLASTX
NCBI GI	g2499946
BLAST score	525
E value	1.0e-53
Match length	121
% identity	84
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	202954
Seq. ID	LIB3048-052-Q1-L1-C4
Method	BLASTX
NCBI GI	g4098129
BLAST score	649
E value	3.0e-68
Match length	135
% identity	90
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	202955
Seq. ID	LIB3048-052-Q1-L1-C5
Method	BLASTX
NCBI GI	g4512685
BLAST score	184
E value	8.0e-14
Match length	66
% identity	50
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202956
Seq. ID	LIB3048-052-Q1-L1-C9
Method	BLASTX
NCBI GI	g2739279
BLAST score	372

E value	1.0e-35
Match length	126
% identity	59
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	202957
Seq. ID	LIB3048-052-Q1-L1-D1
Method	BLASTX
NCBI GI	g1706918
BLAST score	238
E value	5.0e-20
Match length	107
% identity	46
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202958
Seq. ID	LIB3048-052-Q1-L1-D2
Method	BLASTX
NCBI GI	g3763933
BLAST score	330
E value	8.0e-31
Match length	103
% identity	77
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	202959
Seq. ID	LIB3048-052-Q1-L1-D3
Method	BLASTX
NCBI GI	g2244898
BLAST score	529
E value	2.0e-56
Match length	141
% identity	78
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	202960
Seq. ID	LIB3048-052-Q1-L1-D4
Method	BLASTX
NCBI GI	g2739046
BLAST score	144
E value	5.0e-09
Match length	42
% identity	67
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	202961
Seq. ID	LIB3048-052-Q1-L1-D5
Method	BLASTX
NCBI GI	g2244898
BLAST score	153
E value	2.0e-10
Match length	66

% identity	50
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	202962
Seq. ID	LIB3048-052-Q1-L1-D9
Method	BLASTX
NCBI GI	g4567260
BLAST score	572
E value	4.0e-59
Match length	143
% identity	75
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	202963
Seq. ID	LIB3048-052-Q1-L1-E5
Method	BLASTX
NCBI GI	g1709498
BLAST score	506
E value	2.0e-51
Match length	112
% identity	81
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	202964
Seq. ID	LIB3048-052-Q1-L1-E6
Method	BLASTN
NCBI GI	g2829205
BLAST score	134
E value	3.0e-69
Match length	411
% identity	18
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	202965
Seq. ID	LIB3048-052-Q1-L1-F10
Method	BLASTX
NCBI GI	g3047114
BLAST score	191
E value	2.0e-14
Match length	94
% identity	44
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	202966
Seq. ID	LIB3048-052-Q1-L1-F11
Method	BLASTX
NCBI GI	g1001135
BLAST score	191
E value	2.0e-14
Match length	51
% identity	75

NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]
Seq. No.	202967
Seq. ID	LIB3048-052-Q1-L1-F2
Method	BLASTX
NCBI GI	g2739046
BLAST score	148
E value	2.0e-09
Match length	42
% identity	69
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]
Seq. No.	202968
Seq. ID	LIB3048-052-Q1-L1-F4
Method	BLASTX
NCBI GI	g2244760
BLAST score	353
E value	7.0e-34
Match length	84
% identity	71
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	202969
Seq. ID	LIB3048-052-Q1-L1-F9
Method	BLASTX
NCBI GI	g2137603
BLAST score	197
E value	4.0e-15
Match length	87
% identity	25
NCBI Description	nuclear receptor co-repressor N-CoR - mouse >gi_1022718 (U35312) nuclear receptor co-repressor [Mus musculus] >gi_1583865_prf__2121436A thyroid hormone receptor co-repressor [Mus musculus]
Seq. No.	202970
Seq. ID	LIB3048-052-Q1-L1-G1
Method	BLASTX
NCBI GI	g4106061
BLAST score	168
E value	9.0e-12
Match length	61
% identity	54
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]
Seq. No.	202971
Seq. ID	LIB3048-052-Q1-L1-G10
Method	BLASTX
NCBI GI	g1777386
BLAST score	277
E value	1.0e-24
Match length	114
% identity	45
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]
Seq. No.	202972

Seq. ID	LIB3048-052-Q1-L1-G11
Method	BLASTX
NCBI GI	g3047114
BLAST score	438
E value	2.0e-43
Match length	113
% identity	73
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	202973
Seq. ID	LIB3048-052-Q1-L1-G2
Method	BLASTX
NCBI GI	g4006827
BLAST score	536
E value	6.0e-55
Match length	134
% identity	75
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	202974
Seq. ID	LIB3048-052-Q1-L1-G4
Method	BLASTX
NCBI GI	g132944
BLAST score	333
E value	1.0e-31
Match length	64
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	202975
Seq. ID	LIB3048-052-Q1-L1-H10
Method	BLASTX
NCBI GI	g1483230
BLAST score	448
E value	1.0e-44
Match length	121
% identity	78
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	202976
Seq. ID	LIB3048-052-Q1-L1-H11
Method	BLASTX
NCBI GI	g1723832
BLAST score	149
E value	2.0e-09
Match length	58
% identity	50
NCBI Description	HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION >gi_2132531_pir__S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) >gi_1322550_emb_CAA96756_ (Z72576) ORF YGL054c [Saccharomyces cerevisiae]

Seq. No.	202977
Seq. ID	LIB3048-052-Q1-L1-H12
Method	BLASTX

NCBI GI	g1363325
BLAST score	294
E value	9.0e-27
Match length	107
% identity	58
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	202978
Seq. ID	LIB3048-052-Q1-L1-H2
Method	BLASTX
NCBI GI	g267196
BLAST score	339
E value	5.0e-32
Match length	98
% identity	62
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359_ (X58453) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	202979
Seq. ID	LIB3048-052-Q1-L1-H6
Method	BLASTX
NCBI GI	g2507422
BLAST score	254
E value	3.0e-22
Match length	55
% identity	93
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	202980
Seq. ID	LIB3048-053-H10T3A
Method	BLASTX
NCBI GI	g1483230
BLAST score	622
E value	9.0e-65
Match length	189
% identity	69
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	202981
Seq. ID	LIB3048-053-Q1-L1-A1
Method	BLASTX
NCBI GI	g4235430
BLAST score	438
E value	2.0e-43
Match length	110
% identity	76
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	202982
Seq. ID	LIB3048-053-Q1-L1-A10
Method	BLASTX

NCBI GI	g4455288
BLAST score	348
E value	7.0e-33
Match length	86
% identity	78
NCBI Description	(AL035527) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	202983
Seq. ID	LIB3048-053-Q1-L1-A12
Method	BLASTX
NCBI GI	g2275204
BLAST score	205
E value	4.0e-16
Match length	122
% identity	37
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	202984
Seq. ID	LIB3048-053-Q1-L1-A7
Method	BLASTX
NCBI GI	g3450842
BLAST score	264
E value	5.0e-23
Match length	141
% identity	50
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	202985
Seq. ID	LIB3048-053-Q1-L1-A9
Method	BLASTX
NCBI GI	g2062167
BLAST score	286
E value	1.0e-25
Match length	146
% identity	43
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	202986
Seq. ID	LIB3048-053-Q1-L1-B10
Method	BLASTX
NCBI GI	g3158376
BLAST score	253
E value	6.0e-22
Match length	99
% identity	53
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	202987
Seq. ID	LIB3048-053-Q1-L1-B12
Method	BLASTX
NCBI GI	g2252863
BLAST score	229
E value	2.0e-19

Match length	85
% identity	54
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	202988
Seq. ID	LIB3048-053-Q1-L1-B4
Method	BLASTX
NCBI GI	g2766452
BLAST score	217
E value	1.0e-17
Match length	67
% identity	60
NCBI Description	(AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No.	202989
Seq. ID	LIB3048-053-Q1-L1-B6
Method	BLASTX
NCBI GI	g4262153
BLAST score	165
E value	8.0e-12
Match length	73
% identity	52
NCBI Description	(AC005275) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	202990
Seq. ID	LIB3048-053-Q1-L1-B7
Method	BLASTX
NCBI GI	g1706918
BLAST score	295
E value	1.0e-26
Match length	121
% identity	45
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	202991
Seq. ID	LIB3048-053-Q1-L1-B8
Method	BLASTX
NCBI GI	g2956783
BLAST score	241
E value	2.0e-20
Match length	115
% identity	47
NCBI Description	(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq. No.	202992
Seq. ID	LIB3048-053-Q1-L1-C1
Method	BLASTX
NCBI GI	g1709449
BLAST score	631
E value	4.0e-66
Match length	135
% identity	87
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT

PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No.	202993
Seq. ID	LIB3048-053-Q1-L1-C2
Method	BLASTX
NCBI GI	g627468
BLAST score	261
E value	7.0e-23
Match length	98
% identity	55
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	202994
Seq. ID	LIB3048-053-Q1-L1-C3
Method	BLASTX
NCBI GI	g3738285
BLAST score	471
E value	3.0e-47
Match length	121
% identity	74
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	202995
Seq. ID	LIB3048-053-Q1-L1-C4
Method	BLASTX
NCBI GI	g1666096
BLAST score	183
E value	9.0e-14
Match length	81
% identity	49
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	202996
Seq. ID	LIB3048-053-Q1-L1-C5
Method	BLASTN
NCBI GI	g1865678
BLAST score	40
E value	4.0e-13
Match length	72
% identity	89
NCBI Description	A.thaliana ATB2 gene

Seq. No.	202997
Seq. ID	LIB3048-053-Q1-L1-C6
Method	BLASTX
NCBI GI	g2642158
BLAST score	530
E value	2.0e-54
Match length	113
% identity	81
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	202998
Seq. ID	LIB3048-053-Q1-L1-C7
Method	BLASTX

NCBI GI	g3288823
BLAST score	413
E value	2.0e-44
Match length	140
% identity	61
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]

Seq. No.	202999
Seq. ID	LIB3048-053-Q1-L1-C8
Method	BLASTX
NCBI GI	g1706918
BLAST score	262
E value	7.0e-23
Match length	95
% identity	49
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	203000
Seq. ID	LIB3048-053-Q1-L1-C9
Method	BLASTX
NCBI GI	g3687230
BLAST score	513
E value	3.0e-52
Match length	117
% identity	81
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203001
Seq. ID	LIB3048-053-Q1-L1-D11
Method	BLASTN
NCBI GI	g3212102
BLAST score	53
E value	7.0e-21
Match length	129
% identity	85
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	203002
Seq. ID	LIB3048-053-Q1-L1-D2
Method	BLASTX
NCBI GI	g3402693
BLAST score	151
E value	5.0e-10
Match length	86
% identity	44
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	203003
Seq. ID	LIB3048-053-Q1-L1-D8
Method	BLASTX
NCBI GI	g2129495
BLAST score	188
E value	3.0e-14
Match length	62
% identity	63

NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]

Seq. No.	203004
Seq. ID	LIB3048-053-Q1-L1-D9
Method	BLASTX
NCBI GI	g4512617
BLAST score	205
E value	4.0e-16
Match length	95
% identity	48
NCBI Description	(AC004793) F28K20.16 [Arabidopsis thaliana]

Seq. No.	203005
Seq. ID	LIB3048-053-Q1-L1-E10
Method	BLASTX
NCBI GI	g3377848
BLAST score	321
E value	8.0e-30
Match length	109
% identity	57
NCBI Description	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No.	203006
Seq. ID	LIB3048-053-Q1-L1-E11
Method	BLASTX
NCBI GI	g4490332
BLAST score	242
E value	2.0e-20
Match length	89
% identity	56
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	203007
Seq. ID	LIB3048-053-Q1-L1-E12
Method	BLASTX
NCBI GI	g3047114
BLAST score	420
E value	3.0e-41
Match length	106
% identity	75
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	203008
Seq. ID	LIB3048-053-Q1-L1-E2
Method	BLASTX
NCBI GI	g4567095
BLAST score	333
E value	2.0e-31
Match length	90
% identity	67
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	203009

Seq. ID	LIB3048-053-Q1-L1-E3
Method	BLASTX
NCBI GI	g3766368
BLAST score	149
E value	8.0e-10
Match length	73
% identity	49
NCBI Description	(AL031907) putative trascription factor, ccr4-associated factor homolog [Schizosaccharomyces pombe]

Seq. No.	203010
Seq. ID	LIB3048-053-Q1-L1-E6
Method	BLASTN
NCBI GI	g2656025
BLAST score	45
E value	4.0e-16
Match length	69
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	203011
Seq. ID	LIB3048-053-Q1-L1-E8
Method	BLASTX
NCBI GI	g1076685
BLAST score	244
E value	5.0e-23
Match length	70
% identity	60
NCBI Description	SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No.	203012
Seq. ID	LIB3048-053-Q1-L1-F12
Method	BLASTX
NCBI GI	g1777386
BLAST score	437
E value	3.0e-43
Match length	141
% identity	56
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	203013
Seq. ID	LIB3048-053-Q1-L1-F2
Method	BLASTX
NCBI GI	g2911044
BLAST score	479
E value	3.0e-48
Match length	124
% identity	74
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	203014
Seq. ID	LIB3048-053-Q1-L1-F3
Method	BLASTX
NCBI GI	g3335375
BLAST score	358

E value	1.0e-34
Match length	76
% identity	89
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	203015
Seq. ID	LIB3048-053-Q1-L1-F4
Method	BLASTX
NCBI GI	g4455225
BLAST score	630
E value	6.0e-66
Match length	143
% identity	75
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	203016
Seq. ID	LIB3048-053-Q1-L1-F6
Method	BLASTX
NCBI GI	g4106061
BLAST score	216
E value	2.0e-17
Match length	63
% identity	63
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	203017
Seq. ID	LIB3048-053-Q1-L1-F7
Method	BLASTX
NCBI GI	g133940
BLAST score	323
E value	3.0e-30
Match length	75
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	203018
Seq. ID	LIB3048-053-Q1-L1-F9
Method	BLASTX
NCBI GI	g2864610
BLAST score	189
E value	3.0e-14
Match length	68
% identity	53
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	203019
Seq. ID	LIB3048-053-Q1-L1-G10
Method	BLASTX
NCBI GI	g3549691
BLAST score	391
E value	3.0e-38
Match length	83

% identity	81
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	203020
Seq. ID	LIB3048-053-Q1-L1-G12
Method	BLASTX
NCBI GI	g2463509
BLAST score	220
E value	3.0e-18
Match length	51
% identity	75
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	203021
Seq. ID	LIB3048-053-Q1-L1-G3
Method	BLASTX
NCBI GI	g3492803
BLAST score	260
E value	1.0e-22
Match length	110
% identity	51
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	203022
Seq. ID	LIB3048-053-Q1-L1-G4
Method	BLASTX
NCBI GI	g2213619
BLAST score	261
E value	9.0e-23
Match length	125
% identity	47
NCBI Description	(AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No.	203023
Seq. ID	LIB3048-053-Q1-L1-G7
Method	BLASTX
NCBI GI	g4185136
BLAST score	324
E value	2.0e-30
Match length	84
% identity	68
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	203024
Seq. ID	LIB3048-053-Q1-L1-G8
Method	BLASTX
NCBI GI	g1263291
BLAST score	519
E value	5.0e-53
Match length	98
% identity	100
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	203025
Seq. ID	LIB3048-053-Q1-L1-H1
Method	BLASTX

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NCBI GI	g2244971
BLAST score	334
E value	3.0e-34
Match length	90
% identity	71
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203026
Seq. ID	LIB3048-053-Q1-L1-H10
Method	BLASTX
NCBI GI	g1483230
BLAST score	457
E value	1.0e-45
Match length	125
% identity	77
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	203027
Seq. ID	LIB3048-053-Q1-L1-H11
Method	BLASTX
NCBI GI	g1352439
BLAST score	151
E value	6.0e-10
Match length	102
% identity	42
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1008881 (L47221) eukaryotic initiation factor 5 [Phaseolus vulgaris]

Seq. No.	203028
Seq. ID	LIB3048-053-Q1-L1-H3
Method	BLASTX
NCBI GI	g2462745
BLAST score	223
E value	2.0e-18
Match length	105
% identity	38
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	203029
Seq. ID	LIB3048-053-Q1-L1-H7
Method	BLASTX
NCBI GI	g2827718
BLAST score	182
E value	1.0e-13
Match length	106
% identity	48
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	203030
Seq. ID	LIB3048-053-Q1-L1-H8
Method	BLASTX
NCBI GI	g3892712
BLAST score	628
E value	1.0e-65
Match length	145

% identity	83
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	203031
Seq. ID	LIB3048-054-Q1-L1-A10
Method	BLASTX
NCBI GI	g167367
BLAST score	646
E value	7.0e-68
Match length	133
% identity	86
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	203032
Seq. ID	LIB3048-054-Q1-L1-A11
Method	BLASTX
NCBI GI	g2252830
BLAST score	233
E value	2.0e-19
Match length	77
% identity	62
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	203033
Seq. ID	LIB3048-054-Q1-L1-A3
Method	BLASTX
NCBI GI	g1086252
BLAST score	232
E value	2.0e-19
Match length	89
% identity	56
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	203034
Seq. ID	LIB3048-054-Q1-L1-A6
Method	BLASTX
NCBI GI	g1199772
BLAST score	372
E value	1.0e-35
Match length	124
% identity	65
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	203035
Seq. ID	LIB3048-054-Q1-L1-A7
Method	BLASTX
NCBI GI	g2980770
BLAST score	336
E value	1.0e-31
Match length	125

% identity	58
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203036
Seq. ID	LIB3048-054-Q1-L1-A8
Method	BLASTX
NCBI GI	g2864624
BLAST score	302
E value	1.0e-27
Match length	127
% identity	25
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	203037
Seq. ID	LIB3048-054-Q1-L1-B12
Method	BLASTX
NCBI GI	g1352681
BLAST score	407
E value	7.0e-40
Match length	128
% identity	65
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	203038
Seq. ID	LIB3048-054-Q1-L1-B2
Method	BLASTX
NCBI GI	g1841464
BLAST score	285
E value	2.0e-25
Match length	55
% identity	48
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	203039
Seq. ID	LIB3048-054-Q1-L1-B3
Method	BLASTX
NCBI GI	g4262174
BLAST score	498
E value	1.0e-50
Match length	122
% identity	70
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	203040
Seq. ID	LIB3048-054-Q1-L1-B4
Method	BLASTX
NCBI GI	g3334659
BLAST score	272
E value	5.0e-24
Match length	138
% identity	43
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	203041

Seq. ID	LIB3048-054-Q1-L1-B6
Method	BLASTX
NCBI GI	g1698548
BLAST score	608
E value	2.0e-63
Match length	136
% identity	83
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	203042
Seq. ID	LIB3048-054-Q1-L1-B7
Method	BLASTX
NCBI GI	g3811359
BLAST score	187
E value	5.0e-14
Match length	100
% identity	37
NCBI Description	(AF099920) contains similarity to E1-E2 ATPases (Pfam: E1-E2_ATPase.hmm, score: 19.98 and 11.87) partial CDS [Caenorhabditis elegans]

Seq. No.	203043
Seq. ID	LIB3048-054-Q1-L1-B8
Method	BLASTX
NCBI GI	g1619300
BLAST score	220
E value	7.0e-18
Match length	56
% identity	73
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	203044
Seq. ID	LIB3048-054-Q1-L1-B9
Method	BLASTX
NCBI GI	g3738257
BLAST score	501
E value	7.0e-51
Match length	107
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	203045
Seq. ID	LIB3048-054-Q1-L1-C1
Method	BLASTX
NCBI GI	g136057
BLAST score	456
E value	1.0e-45
Match length	117
% identity	74
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	203046
Seq. ID	LIB3048-054-Q1-L1-C10

Method	BLASTX
NCBI GI	g1854581
BLAST score	171
E value	2.0e-13
Match length	70
% identity	61
NCBI Description	(L24120) peroxidase precursor [Linum usitatissimum]

Seq. No.	203047
Seq. ID	LIB3048-054-Q1-L1-C12
Method	BLASTX
NCBI GI	g4539399
BLAST score	322
E value	7.0e-30
Match length	75
% identity	85
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	203048
Seq. ID	LIB3048-054-Q1-L1-C2
Method	BLASTX
NCBI GI	g1169782
BLAST score	515
E value	2.0e-52
Match length	128
% identity	74
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	203049
Seq. ID	LIB3048-054-Q1-L1-C5
Method	BLASTX
NCBI GI	g3135274
BLAST score	232
E value	2.0e-19
Match length	120
% identity	44
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	203050
Seq. ID	LIB3048-054-Q1-L1-C6
Method	BLASTX
NCBI GI	g4100433
BLAST score	172
E value	3.0e-12
Match length	89
% identity	40
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	203051
Seq. ID	LIB3048-054-Q1-L1-C8
Method	BLASTX
NCBI GI	g4336426
BLAST score	431
E value	1.0e-42

Match length	124
% identity	66
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	203052
Seq. ID	LIB3048-054-Q1-L1-D1
Method	BLASTX
NCBI GI	g3419681
BLAST score	335
E value	2.0e-31
Match length	124
% identity	49
NCBI Description	(U37371) chaperonin [Candida albicans]

Seq. No.	203053
Seq. ID	LIB3048-054-Q1-L1-D2
Method	BLASTX
NCBI GI	g1346387
BLAST score	633
E value	3.0e-66
Match length	138
% identity	88
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No.	203054
Seq. ID	LIB3048-054-Q1-L1-D4
Method	BLASTX
NCBI GI	g119748
BLAST score	416
E value	7.0e-41
Match length	94
% identity	88
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No.	203055
Seq. ID	LIB3048-054-Q1-L1-D5
Method	BLASTX
NCBI GI	g2102691
BLAST score	266
E value	2.0e-23
Match length	99
% identity	57
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	203056
Seq. ID	LIB3048-054-Q1-L1-D6
Method	BLASTX
NCBI GI	g2275204
BLAST score	182

E value	2.0e-13
Match length	117
% identity	36
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	203057
Seq. ID	LIB3048-054-Q1-L1-D7
Method	BLASTX
NCBI GI	g872116
BLAST score	277
E value	6.0e-25
Match length	87
% identity	38
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	203058
Seq. ID	LIB3048-054-Q1-L1-D8
Method	BLASTX
NCBI GI	g4138647
BLAST score	559
E value	1.0e-57
Match length	136
% identity	77
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	203059
Seq. ID	LIB3048-054-Q1-L1-D9
Method	BLASTX
NCBI GI	g571519
BLAST score	221
E value	4.0e-18
Match length	97
% identity	10
NCBI Description	(U16852) polyubiquitin [Gracilaria verrucosa] >gi_1095488_prf__2109223A poly-ubiquitin [Gracilaria verrucosa]

Seq. No.	203060
Seq. ID	LIB3048-054-Q1-L1-E1
Method	BLASTX
NCBI GI	g2062167
BLAST score	202
E value	5.0e-32
Match length	106
% identity	67
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	203061
Seq. ID	LIB3048-054-Q1-L1-E10
Method	BLASTX
NCBI GI	g623586
BLAST score	256
E value	2.0e-22
Match length	57
% identity	89

NCBI Description	(L29273) putative [Nicotiana tabacum]

Seq. No.	203062
Seq. ID	LIB3048-054-Q1-L1-E11
Method	BLASTX
NCBI GI	g1708401
BLAST score	580
E value	4.0e-60
Match length	128
% identity	89
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)

Seq. No.	203063
Seq. ID	LIB3048-054-Q1-L1-E12
Method	BLASTX
NCBI GI	g1708401
BLAST score	192
E value	8.0e-15
Match length	102
% identity	46
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)

Seq. No.	203064
Seq. ID	LIB3048-054-Q1-L1-E2
Method	BLASTX
NCBI GI	g1777386
BLAST score	362
E value	2.0e-34
Match length	138
% identity	48
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	203065
Seq. ID	LIB3048-054-Q1-L1-E4
Method	BLASTX
NCBI GI	g2506139
BLAST score	289
E value	6.0e-26
Match length	74
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	203066
Seq. ID	LIB3048-054-Q1-L1-E5
Method	BLASTX
NCBI GI	g2129597
BLAST score	554
E value	4.0e-57
Match length	109
% identity	95
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1

[Arabidopsis thaliana]

Seq. No.	203067
Seq. ID	LIB3048-054-Q1-L1-E6
Method	BLASTX
NCBI GI	g3785978
BLAST score	185
E value	8.0e-14
Match length	40
% identity	75
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	203068
Seq. ID	LIB3048-054-Q1-L1-E7
Method	BLASTX
NCBI GI	g417103
BLAST score	140
E value	3.0e-19
Match length	60
% identity	80
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	203069
Seq. ID	LIB3048-054-Q1-L1-E8
Method	BLASTX
NCBI GI	g2911052
BLAST score	517
E value	8.0e-53
Match length	122
% identity	82
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	203070
Seq. ID	LIB3048-054-Q1-L1-F1
Method	BLASTX
NCBI GI	g3435196
BLAST score	427
E value	3.0e-42
Match length	131

% identity	66
NCBI Description	(AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	203071
Seq. ID	LIB3048-054-Q1-L1-F10
Method	BLASTX
NCBI GI	g3077640
BLAST score	294
E value	1.0e-26
Match length	109
% identity	56
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No.	203072
Seq. ID	LIB3048-054-Q1-L1-F11
Method	BLASTX
NCBI GI	g1001955
BLAST score	549
E value	2.0e-56
Match length	131
% identity	82
NCBI Description	(U19099) unknown protein [Lycopersicon chilense]

Seq. No.	203073
Seq. ID	LIB3048-054-Q1-L1-F12
Method	BLASTX
NCBI GI	g3204134
BLAST score	586
E value	8.0e-61
Match length	131
% identity	78
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	203074
Seq. ID	LIB3048-054-Q1-L1-F2
Method	BLASTX
NCBI GI	g3264767
BLAST score	266
E value	3.0e-23
Match length	138
% identity	43
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	203075
Seq. ID	LIB3048-054-Q1-L1-F5
Method	BLASTX
NCBI GI	g133940
BLAST score	502
E value	6.0e-51
Match length	115
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	203076

Seq. ID	LIB3048-054-Q1-L1-F6
Method	BLASTX
NCBI GI	g629562
BLAST score	594
E value	9.0e-62
Match length	136
% identity	82
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	203077
Seq. ID	LIB3048-054-Q1-L1-F7
Method	BLASTX
NCBI GI	g464707
BLAST score	529
E value	4.0e-54
Match length	110
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	203078
Seq. ID	LIB3048-054-Q1-L1-F8
Method	BLASTX
NCBI GI	g464707
BLAST score	143
E value	2.0e-10
Match length	70
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

	>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	203079
Seq. ID	LIB3048-054-Q1-L1-F9
Method	BLASTX
NCBI GI	g3297816
BLAST score	264
E value	4.0e-23
Match length	80
% identity	65
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	203080
Seq. ID	LIB3048-054-Q1-L1-G1
Method	BLASTX
NCBI GI	g2492782
BLAST score	496
E value	3.0e-50
Match length	130
% identity	72
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]
Seq. No.	203081
Seq. ID	LIB3048-054-Q1-L1-G10
Method	BLASTX
NCBI GI	g1929056
BLAST score	503
E value	3.0e-51
Match length	118
% identity	82
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]
Seq. No.	203082
Seq. ID	LIB3048-054-Q1-L1-G11
Method	BLASTX
NCBI GI	g1766046
BLAST score	577
E value	8.0e-60
Match length	124
% identity	86
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]
Seq. No.	203083
Seq. ID	LIB3048-054-Q1-L1-G12
Method	BLASTX
NCBI GI	g1401268
BLAST score	140

E value	1.0e-08
Match length	54
% identity	46
NCBI Description	(U59812) ornithine decarboxylase [Nicotiana tabacum]

Seq. No.	203084
Seq. ID	LIB3048-054-Q1-L1-G2
Method	BLASTX
NCBI GI	g1172874
BLAST score	145
E value	2.0e-09
Match length	76
% identity	49
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	203085
Seq. ID	LIB3048-054-Q1-L1-G4
Method	BLASTX
NCBI GI	g2920706
BLAST score	211
E value	8.0e-17
Match length	139
% identity	42
NCBI Description	(Y13568) beta-xylosidase [Emericella nidulans]

Seq. No.	203086
Seq. ID	LIB3048-054-Q1-L1-G5
Method	BLASTX
NCBI GI	g1174592
BLAST score	719
E value	2.0e-76
Match length	135
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203087
Seq. ID	LIB3048-054-Q1-L1-G6
Method	BLASTX
NCBI GI	g976402
BLAST score	510
E value	6.0e-52
Match length	120
% identity	80
NCBI Description	(U31932) amino acid permease 1 [Nicotiana sylvestris] >gi_1906549 (U64823) amino acid permease [Nicotiana sylvestris]

Seq. No.	203088
Seq. ID	LIB3048-054-Q1-L1-G9
Method	BLASTX
NCBI GI	g285741

BLAST score	377
E value	2.0e-36
Match length	130
% identity	58
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	203089
Seq. ID	LIB3048-054-Q1-L1-H10
Method	BLASTX
NCBI GI	g4432859
BLAST score	212
E value	4.0e-17
Match length	126
% identity	45
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	203090
Seq. ID	LIB3048-054-Q1-L1-H4
Method	BLASTX
NCBI GI	g1351722
BLAST score	151
E value	8.0e-10
Match length	71
% identity	45
NCBI Description	HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	203091
Seq. ID	LIB3048-054-Q1-L1-H5
Method	BLASTX
NCBI GI	g3337361
BLAST score	612
E value	7.0e-64
Match length	136
% identity	79
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	203092
Seq. ID	LIB3048-054-Q1-L1-H7
Method	BLASTX
NCBI GI	g3873807
BLAST score	147
E value	2.0e-09
Match length	60
% identity	45
NCBI Description	(Z49907) B0491.1 [Caenorhabditis elegans]

Seq. No.	203093
Seq. ID	LIB3048-054-Q1-L1-H9
Method	BLASTX
NCBI GI	g1107526
BLAST score	146
E value	3.0e-14
Match length	106
% identity	44
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	203094
Seq. ID	LIB3048-055-Q1-L1-A11
Method	BLASTX
NCBI GI	g4006853
BLAST score	209
E value	1.0e-16
Match length	118
% identity	36
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	203095
Seq. ID	LIB3048-055-Q1-L1-A12
Method	BLASTX
NCBI GI	g3033375
BLAST score	152
E value	1.0e-11
Match length	118
% identity	39
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	203096
Seq. ID	LIB3048-055-Q1-L1-A3
Method	BLASTX
NCBI GI	g2506139
BLAST score	280
E value	6.0e-25
Match length	72
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	203097
Seq. ID	LIB3048-055-Q1-L1-A7
Method	BLASTX
NCBI GI	g4567095
BLAST score	440
E value	1.0e-43
Match length	118
% identity	65
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	203098
Seq. ID	LIB3048-055-Q1-L1-A8
Method	BLASTX
NCBI GI	g627468
BLAST score	321
E value	9.0e-30
Match length	124
% identity	54
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	203099
Seq. ID	LIB3048-055-Q1-L1-B1
Method	BLASTN
NCBI GI	g3869068
BLAST score	70
E value	5.0e-31
Match length	223
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	203100
Seq. ID	LIB3048-055-Q1-L1-B3
Method	BLASTX
NCBI GI	g3746059
BLAST score	545
E value	5.0e-56
Match length	136
% identity	69
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	203101
Seq. ID	LIB3048-055-Q1-L1-B5
Method	BLASTX
NCBI GI	g3643611
BLAST score	423
E value	9.0e-42
Match length	124
% identity	65
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	203102
Seq. ID	LIB3048-055-Q1-L1-B6
Method	BLASTX
NCBI GI	g1531758
BLAST score	712
E value	1.0e-75
Match length	136
% identity	93
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	203103
Seq. ID	LIB3048-055-Q1-L1-B7
Method	BLASTX
NCBI GI	g1531758
BLAST score	340
E value	3.0e-36
Match length	130
% identity	62
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	203104
Seq. ID	LIB3048-055-Q1-L1-B9

Method	BLASTX
NCBI GI	g629602
BLAST score	168
E value	3.0e-12
Match length	77
% identity	48
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	203105
Seq. ID	LIB3048-055-Q1-L1-C1
Method	BLASTX
NCBI GI	g3132696
BLAST score	187
E value	4.0e-14
Match length	101
% identity	45
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	203106
Seq. ID	LIB3048-055-Q1-L1-C10
Method	BLASTX
NCBI GI	g1931642
BLAST score	151
E value	7.0e-18
Match length	102
% identity	49
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	203107
Seq. ID	LIB3048-055-Q1-L1-C5
Method	BLASTX
NCBI GI	g2443329
BLAST score	426
E value	4.0e-42
Match length	132
% identity	66
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	203108
Seq. ID	LIB3048-055-Q1-L1-C6
Method	BLASTX
NCBI GI	g4539315
BLAST score	269
E value	1.0e-23
Match length	141
% identity	45
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	203109
Seq. ID	LIB3048-055-Q1-L1-C7
Method	BLASTN
NCBI GI	g3873174
BLAST score	37

E value	2.0e-11
Match length	93
% identity	85
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	203110
Seq. ID	LIB3048-055-Q1-L1-D1
Method	BLASTX
NCBI GI	g1169586
BLAST score	398
E value	8.0e-39
Match length	89
% identity	85
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946) fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No.	203111
Seq. ID	LIB3048-055-Q1-L1-D11
Method	BLASTX
NCBI GI	g3158376
BLAST score	160
E value	5.0e-11
Match length	94
% identity	43
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	203112
Seq. ID	LIB3048-055-Q1-L1-D12
Method	BLASTX
NCBI GI	g3413700
BLAST score	164
E value	2.0e-11
Match length	41
% identity	78
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	203113
Seq. ID	LIB3048-055-Q1-L1-D3
Method	BLASTX
NCBI GI	g417073
BLAST score	540
E value	2.0e-55
Match length	137
% identity	75
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	203114
Seq. ID	LIB3048-055-Q1-L1-D4
Method	BLASTX
NCBI GI	g132944

BLAST score	550
E value	1.0e-56
Match length	110
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	203115
Seq. ID	LIB3048-055-Q1-L1-D5
Method	BLASTX
NCBI GI	g3643611
BLAST score	444
E value	3.0e-44
Match length	124
% identity	70
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	203116
Seq. ID	LIB3048-055-Q1-L1-E1
Method	BLASTX
NCBI GI	g4105798
BLAST score	372
E value	8.0e-36
Match length	89
% identity	69
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	203117
Seq. ID	LIB3048-055-Q1-L1-E12
Method	BLASTX
NCBI GI	g4558547
BLAST score	335
E value	2.0e-31
Match length	109
% identity	60
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203118
Seq. ID	LIB3048-055-Q1-L1-E3
Method	BLASTX
NCBI GI	g3334147
BLAST score	356
E value	7.0e-34
Match length	115
% identity	60
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	203119
Seq. ID	LIB3048-055-Q1-L1-E4
Method	BLASTX
NCBI GI	g1617272
BLAST score	374
E value	2.0e-41
Match length	120
% identity	74

NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	203120
Seq. ID	LIB3048-055-Q1-L1-E5
Method	BLASTX
NCBI GI	g3047082
BLAST score	140
E value	1.0e-08
Match length	81
% identity	41
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	203121
Seq. ID	LIB3048-055-Q1-L1-E6
Method	BLASTX
NCBI GI	g1407705
BLAST score	515
E value	1.0e-52
Match length	117
% identity	83
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	203122
Seq. ID	LIB3048-055-Q1-L1-E8
Method	BLASTX
NCBI GI	g4008037
BLAST score	250
E value	2.0e-21
Match length	131
% identity	44
NCBI Description	(AF104925) 2-oxoglutarate-dependent dioxygenase [Solanum chacoense]

Seq. No.	203123
Seq. ID	LIB3048-055-Q1-L1-E9
Method	BLASTX
NCBI GI	g1709498
BLAST score	336
E value	1.0e-34
Match length	106
% identity	72
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	203124
Seq. ID	LIB3048-055-Q1-L1-F12
Method	BLASTX
NCBI GI	g3329294
BLAST score	147
E value	2.0e-09
Match length	127
% identity	28
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	203125
Seq. ID	LIB3048-055-Q1-L1-F6
Method	BLASTX
NCBI GI	g116923
BLAST score	286
E value	1.0e-25
Match length	113
% identity	58
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	203126
Seq. ID	LIB3048-055-Q1-L1-G12
Method	BLASTX
NCBI GI	g4558547
BLAST score	309
E value	2.0e-28
Match length	108
% identity	55
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203127
Seq. ID	LIB3048-055-Q1-L1-G3
Method	BLASTX
NCBI GI	g4455340
BLAST score	361
E value	2.0e-34
Match length	99
% identity	66
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	203128
Seq. ID	LIB3048-055-Q1-L1-G5
Method	BLASTX
NCBI GI	g1750376
BLAST score	194
E value	6.0e-15
Match length	112
% identity	41
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	203129
Seq. ID	LIB3048-055-Q1-L1-G6
Method	BLASTX
NCBI GI	g1766046
BLAST score	377
E value	1.0e-36
Match length	84
% identity	81
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	203130
Seq. ID	LIB3048-055-Q1-L1-G7
Method	BLASTX
NCBI GI	g481812
BLAST score	161
E value	3.0e-11
Match length	81
% identity	46
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	203131
Seq. ID	LIB3048-055-Q1-L1-G9
Method	BLASTX
NCBI GI	g119748
BLAST score	349
E value	4.0e-33
Match length	84
% identity	82
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No.	203132
Seq. ID	LIB3048-055-Q1-L1-H11
Method	BLASTX
NCBI GI	g3687235
BLAST score	254
E value	5.0e-22
Match length	58
% identity	88
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	203133
Seq. ID	LIB3048-055-Q1-L1-H3
Method	BLASTX
NCBI GI	g2864624
BLAST score	353
E value	2.0e-33
Match length	137
% identity	27
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	203134
Seq. ID	LIB3048-055-Q1-L1-H5
Method	BLASTX
NCBI GI	g1777386
BLAST score	187
E value	9.0e-22
Match length	118
% identity	45
NCBI Description	(U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No.	203135
Seq. ID	LIB3048-055-Q1-L1-H8
Method	BLASTX
NCBI GI	g1943751
BLAST score	168
E value	6.0e-12
Match length	40
% identity	90
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	203136
Seq. ID	LIB3083-001-Q1-L1-B10
Method	BLASTX
NCBI GI	g4098246
BLAST score	172
E value	9.0e-13
Match length	62
% identity	63
NCBI Description	(U76410) homeobox 2 protein [Lycopersicon esculentum]

Seq. No.	203137
Seq. ID	LIB3083-001-Q1-L1-B11
Method	BLASTX
NCBI GI	g4544399
BLAST score	428
E value	2.0e-42
Match length	125
% identity	66
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	203138
Seq. ID	LIB3083-001-Q1-L1-C11
Method	BLASTX
NCBI GI	g1903364
BLAST score	258
E value	1.0e-22
Match length	88
% identity	58
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	203139
Seq. ID	LIB3083-001-Q1-L1-C12
Method	BLASTX
NCBI GI	g1174599
BLAST score	168
E value	5.0e-21
Match length	71
% identity	75
NCBI Description	TUBULIN BETA-2 CHAIN >gi_1076659_pir__S50748 beta-tubulin - potato >gi_609270_emb_CAA83853_ (Z33402) beta-tubulin [Solanum tuberosum]

Seq. No.	203140

Seq. ID	LIB3083-001-Q1-L1-D12
Method	BLASTX
NCBI GI	g2245378
BLAST score	336
E value	1.0e-31
Match length	113
% identity	60
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	203141
Seq. ID	LIB3083-001-Q1-L1-F12
Method	BLASTX
NCBI GI	g3212877
BLAST score	438
E value	2.0e-43
Match length	100
% identity	80
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	203142
Seq. ID	LIB3083-001-Q1-L1-H10
Method	BLASTX
NCBI GI	g4104561
BLAST score	287
E value	8.0e-26
Match length	113
% identity	54
NCBI Description	(AF036960) subtilisin-like protease [Glycine max]

Seq. No.	203143
Seq. ID	LIB3083-001-Q1-L1-H12
Method	BLASTX
NCBI GI	g4056568
BLAST score	237
E value	6.0e-20
Match length	93
% identity	18
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	203144
Seq. ID	LIB3083-001-Q1-L2-A4
Method	BLASTX
NCBI GI	g2129473
BLAST score	295
E value	8.0e-27
Match length	105
% identity	56
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	203145
Seq. ID	LIB3083-001-Q1-L2-A8
Method	BLASTX
NCBI GI	g3805765
BLAST score	162
E value	4.0e-11
Match length	51

% identity	63
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203146
Seq. ID	LIB3083-001-Q1-L2-B1
Method	BLASTX
NCBI GI	g3122785
BLAST score	530
E value	3.0e-54
Match length	132
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No.	203147
Seq. ID	LIB3083-001-Q1-L2-B3
Method	BLASTX
NCBI GI	g1086249
BLAST score	396
E value	1.0e-38
Match length	125
% identity	59
NCBI Description	subtilisin-like protease - Alnus glutinosa >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease [Alnus glutinosa]

Seq. No.	203148
Seq. ID	LIB3083-001-Q1-L2-B7
Method	BLASTX
NCBI GI	g2760330
BLAST score	555
E value	4.0e-57
Match length	139
% identity	74
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	203149
Seq. ID	LIB3083-001-Q1-L2-B8
Method	BLASTX
NCBI GI	g1174592
BLAST score	610
E value	9.0e-64
Match length	113
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203150
Seq. ID	LIB3083-001-Q1-L2-C3
Method	BLASTN
NCBI GI	g2829205
BLAST score	400
E value	0.0e+00
Match length	428
% identity	23
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No.	203151
Seq. ID	LIB3083-001-Q1-L2-C4
Method	BLASTX
NCBI GI	g1174592
BLAST score	598
E value	2.0e-62
Match length	116
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203152
Seq. ID	LIB3083-001-Q1-L2-C6
Method	BLASTX
NCBI GI	g130720
BLAST score	182
E value	1.0e-13
Match length	104
% identity	35
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	203153
Seq. ID	LIB3083-001-Q1-L2-C7
Method	BLASTX
NCBI GI	g464840
BLAST score	371
E value	1.0e-35
Match length	73
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	203154
Seq. ID	LIB3083-001-Q1-L2-D3
Method	BLASTX
NCBI GI	g4337175
BLAST score	447
E value	1.0e-44
Match length	124
% identity	68
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	203155
Seq. ID	LIB3083-001-Q1-L2-D5

Method	BLASTX
NCBI GI	g639722
BLAST score	532
E value	2.0e-54
Match length	136
% identity	50
NCBI Description	(L27484) calcium-dependent protein kinase [Zea mays]

Seq. No.	203156
Seq. ID	LIB3083-001-Q1-L2-D6
Method	BLASTX
NCBI GI	g4572682
BLAST score	211
E value	2.0e-17
Match length	72
% identity	60
NCBI Description	(AC006954) putative APG protein [Arabidopsis thaliana]

Seq. No.	203157
Seq. ID	LIB3083-001-Q1-L2-E1
Method	BLASTX
NCBI GI	g4544412
BLAST score	240
E value	1.0e-23
Match length	112
% identity	45
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203158
Seq. ID	LIB3083-001-Q1-L2-E4
Method	BLASTX
NCBI GI	g1706956
BLAST score	612
E value	5.0e-64
Match length	114
% identity	97
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203159
Seq. ID	LIB3083-001-Q1-L2-E5
Method	BLASTX
NCBI GI	g1706958
BLAST score	314
E value	5.0e-29
Match length	120
% identity	59
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203160
Seq. ID	LIB3083-001-Q1-L2-F1
Method	BLASTX
NCBI GI	g2832625
BLAST score	246
E value	3.0e-26
Match length	85
% identity	74
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	203161
Seq. ID	LIB3083-001-Q1-L2-F2
Method	BLASTX
NCBI GI	g2494620
BLAST score	144
E value	3.0e-09
Match length	38
% identity	61
NCBI Description	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN >gi_975319 (U31902) succinate dehydrogenase iron-sulfur protein subunit [Paracoccus denitrificans]

Seq. No.	203162
Seq. ID	LIB3083-001-Q1-L2-F5
Method	BLASTX
NCBI GI	g1174592
BLAST score	507
E value	1.0e-51
Match length	105
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203163
Seq. ID	LIB3083-001-Q1-L2-F8
Method	BLASTX
NCBI GI	g1710838
BLAST score	166
E value	4.0e-12
Match length	51
% identity	75
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	203164
Seq. ID	LIB3083-001-Q1-L2-G1
Method	BLASTX
NCBI GI	g4406775
BLAST score	184
E value	7.0e-14
Match length	85
% identity	41
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	203165
Seq. ID	LIB3083-001-Q1-L2-G2
Method	BLASTX
NCBI GI	g1706958
BLAST score	355
E value	5.0e-34
Match length	92
% identity	77
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203166
Seq. ID	LIB3083-001-Q1-L2-G4
Method	BLASTX
NCBI GI	g2119278
BLAST score	570
E value	5.0e-59
Match length	109
% identity	99
NCBI Description	tubulin beta-1 chain - rice

Seq. No.	203167
Seq. ID	LIB3083-001-Q1-L2-G7
Method	BLASTX
NCBI GI	g4468999
BLAST score	157
E value	1.0e-10
Match length	71
% identity	25
NCBI Description	(Z97342) unnamed protein product [Arabidopsis thaliana]

Seq. No.	203168
Seq. ID	LIB3083-001-Q1-L2-H1
Method	BLASTX
NCBI GI	g2959324
BLAST score	256
E value	2.0e-22
Match length	72
% identity	72
NCBI Description	(Y15224) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	203169
Seq. ID	LIB3083-001-Q1-L2-H12
Method	BLASTN
NCBI GI	g2267582
BLAST score	61
E value	5.0e-26
Match length	81
% identity	94
NCBI Description	Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, complete cds

Seq. No.	203170
Seq. ID	LIB3083-001-Q1-L2-H3
Method	BLASTX
NCBI GI	g2213628
BLAST score	155
E value	2.0e-10
Match length	112
% identity	38
NCBI Description	(AC000103) F21J9.20 [Arabidopsis thaliana]

Seq. No.	203171
Seq. ID	LIB3083-001-Q1-L2-H4
Method	BLASTN
NCBI GI	g556687
BLAST score	51
E value	5.0e-20

Match length	79
% identity	34
NCBI Description	H.annuus mRNA for seed tetraubiquitin

Seq. No.	203172
Seq. ID	LIB3083-001-Q1-L2-H8
Method	BLASTX
NCBI GI	g2098713
BLAST score	162
E value	2.0e-11
Match length	65
% identity	55
NCBI Description	(U82977) pectinesterase [Citrus sinensis]

Seq. No.	203173
Seq. ID	LIB3083-002-Q1-L1-A1
Method	BLASTX
NCBI GI	g1743277
BLAST score	615
E value	3.0e-64
Match length	123
% identity	94
NCBI Description	(Y09741) beta-tubulin 1 [Hordeum vulgare]

Seq. No.	203174
Seq. ID	LIB3083-002-Q1-L1-A10
Method	BLASTX
NCBI GI	g2829899
BLAST score	309
E value	2.0e-28
Match length	125
% identity	47
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	203175
Seq. ID	LIB3083-002-Q1-L1-A11
Method	BLASTX
NCBI GI	g2129473
BLAST score	292
E value	2.0e-26
Match length	105
% identity	54
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	203176
Seq. ID	LIB3083-002-Q1-L1-A12
Method	BLASTX
NCBI GI	g4510344
BLAST score	175
E value	1.0e-12
Match length	67
% identity	49
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203177
Seq. ID	LIB3083-002-Q1-L1-A2
Method	BLASTX
NCBI GI	g2209358
BLAST score	698
E value	6.0e-74
Match length	134
% identity	95
NCBI Description	(AF004812) beta-D-galactosidase [Mangifera indica]

Seq. No.	203178
Seq. ID	LIB3083-002-Q1-L1-A3
Method	BLASTX
NCBI GI	g2811025
BLAST score	245
E value	7.0e-21
Match length	85
% identity	61
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	203179
Seq. ID	LIB3083-002-Q1-L1-A4
Method	BLASTX
NCBI GI	g4105772
BLAST score	121
E value	3.0e-16
Match length	94
% identity	36
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	203180
Seq. ID	LIB3083-002-Q1-L1-A5
Method	BLASTX
NCBI GI	g543867
BLAST score	437
E value	2.0e-43
Match length	115
% identity	76
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	203181
Seq. ID	LIB3083-002-Q1-L1-A6
Method	BLASTX
NCBI GI	g417360
BLAST score	345
E value	1.0e-32
Match length	103
% identity	61
NCBI Description	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 >gi_2131280_pir__S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae) >gi_666101_emb_CAA40885_ (X57714) high mobility group-like

nuclear protein 2 [Saccharomyces cerevisiae] >gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae] >gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w [Saccharomyces cerevisiae]

Seq. No.	203182
Seq. ID	LIB3083-002-Q1-L1-A7
Method	BLASTX
NCBI GI	g1174592
BLAST score	577
E value	8.0e-60
Match length	108
% identity	98
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203183
Seq. ID	LIB3083-002-Q1-L1-A9
Method	BLASTX
NCBI GI	g1706958
BLAST score	571
E value	4.0e-59
Match length	126
% identity	88
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203184
Seq. ID	LIB3083-002-Q1-L1-B1
Method	BLASTX
NCBI GI	g2827139
BLAST score	681
E value	6.0e-72
Match length	136
% identity	90
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	203185
Seq. ID	LIB3083-002-Q1-L1-B10
Method	BLASTX
NCBI GI	g1477428
BLAST score	598
E value	3.0e-62
Match length	131
% identity	86
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	203186
Seq. ID	LIB3083-002-Q1-L1-B11
Method	BLASTX
NCBI GI	g2529677
BLAST score	182
E value	2.0e-13

Match length	87
% identity	49
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	203187
Seq. ID	LIB3083-002-Q1-L1-B12
Method	BLASTX
NCBI GI	g4098246
BLAST score	597
E value	3.0e-62
Match length	122
% identity	93
NCBI Description	(U76410) homeobox 2 protein [Lycopersicon esculentum]

Seq. No.	203188
Seq. ID	LIB3083-002-Q1-L1-B2
Method	BLASTX
NCBI GI	g3269288
BLAST score	559
E value	1.0e-57
Match length	129
% identity	81
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	203189
Seq. ID	LIB3083-002-Q1-L1-B3
Method	BLASTX
NCBI GI	g2129932
BLAST score	495
E value	3.0e-50
Match length	91
% identity	95
NCBI Description	myb-related transcription factor TMH1 - tomato >gi_1167486_emb_CAA64615_ (X95297) transcription factor [Lycopersicon esculentum]

Seq. No.	203190
Seq. ID	LIB3083-002-Q1-L1-B6
Method	BLASTX
NCBI GI	g4580523
BLAST score	435
E value	4.0e-43
Match length	126
% identity	67
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	203191
Seq. ID	LIB3083-002-Q1-L1-B7
Method	BLASTX
NCBI GI	g267082
BLAST score	575
E value	1.0e-59
Match length	106
% identity	98
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. No.	203192
Seq. ID	LIB3083-002-Q1-L1-B8
Method	BLASTX
NCBI GI	g2459421
BLAST score	222
E value	6.0e-36
Match length	130
% identity	58
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	203193
Seq. ID	LIB3083-002-Q1-L1-C10
Method	BLASTN
NCBI GI	g1419732
BLAST score	128
E value	7.0e-66
Match length	172
% identity	94
NCBI Description	P.sativum mitochondrial DNA for 18S rRNA gene

Seq. No.	203194
Seq. ID	LIB3083-002-Q1-L1-C11
Method	BLASTX
NCBI GI	g4115931
BLAST score	670
E value	1.0e-70
Match length	131
% identity	94
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	203195
Seq. ID	LIB3083-002-Q1-L1-C12
Method	BLASTX
NCBI GI	g2497743
BLAST score	155
E value	1.0e-10
Match length	57
% identity	56
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	203196
Seq. ID	LIB3083-002-Q1-L1-C2
Method	BLASTX
NCBI GI	g3702964
BLAST score	342
E value	3.0e-32
Match length	66
% identity	97
NCBI Description	(AF079485) rac GTP binding protein Arac10 [Arabidopsis thaliana]

Seq. No.	203197
Seq. ID	LIB3083-002-Q1-L1-C3
Method	BLASTX
NCBI GI	g3334405
BLAST score	536
E value	6.0e-55
Match length	112
% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	203198
Seq. ID	LIB3083-002-Q1-L1-C5
Method	BLASTX
NCBI GI	g4126473
BLAST score	582
E value	2.0e-60
Match length	115
% identity	96
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	203199
Seq. ID	LIB3083-002-Q1-L1-C6
Method	BLASTX
NCBI GI	g4218011
BLAST score	356
E value	7.0e-34
Match length	128
% identity	57
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	203200
Seq. ID	LIB3083-002-Q1-L1-C8
Method	BLASTX
NCBI GI	g3868758
BLAST score	319
E value	1.0e-29
Match length	128
% identity	55
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	203201
Seq. ID	LIB3083-002-Q1-L1-C9
Method	BLASTX
NCBI GI	g4544399
BLAST score	547
E value	3.0e-56
Match length	133
% identity	74
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	203202
Seq. ID	LIB3083-002-Q1-L1-D10
Method	BLASTX
NCBI GI	g1351202
BLAST score	533
E value	1.0e-54
Match length	123
% identity	78
NCBI Description	TUBULIN BETA CHAIN >gi_312989_emb_CAA42777_ (X60216) beta-tubulin [Glycine max]

Seq. No.	203203
Seq. ID	LIB3083-002-Q1-L1-D12
Method	BLASTX
NCBI GI	g2245378
BLAST score	525
E value	1.0e-53
Match length	130
% identity	78
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	203204
Seq. ID	LIB3083-002-Q1-L1-D2
Method	BLASTX
NCBI GI	g2997591
BLAST score	595
E value	7.0e-62
Match length	134
% identity	84
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	203205
Seq. ID	LIB3083-002-Q1-L1-D3
Method	BLASTX
NCBI GI	g1684855
BLAST score	454
E value	2.0e-45
Match length	113
% identity	20
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	203206
Seq. ID	LIB3083-002-Q1-L1-D7
Method	BLASTX
NCBI GI	g886100
BLAST score	450
E value	6.0e-45
Match length	103
% identity	83
NCBI Description	(U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No.	203207
Seq. ID	LIB3083-002-Q1-L1-D8
Method	BLASTX

NCBI GI	g4538975
BLAST score	318
E value	2.0e-29
Match length	109
% identity	61
NCBI Description	(AL049487) putative protein [Arabidopsis thaliana]

Seq. No.	203208
Seq. ID	LIB3083-002-Q1-L1-D9
Method	BLASTX
NCBI GI	g1903364
BLAST score	366
E value	5.0e-35
Match length	116
% identity	63
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	203209
Seq. ID	LIB3083-002-Q1-L1-E11
Method	BLASTX
NCBI GI	g4454014
BLAST score	219
E value	8.0e-18
Match length	124
% identity	43
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	203210
Seq. ID	LIB3083-002-Q1-L1-E4
Method	BLASTX
NCBI GI	g2129825
BLAST score	503
E value	4.0e-51
Match length	112
% identity	88
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	203211
Seq. ID	LIB3083-002-Q1-L1-E6
Method	BLASTN
NCBI GI	g1143223
BLAST score	134
E value	3.0e-69
Match length	400
% identity	51
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203212
Seq. ID	LIB3083-002-Q1-L1-E7
Method	BLASTX
NCBI GI	g4115936
BLAST score	298
E value	4.0e-27
Match length	70
% identity	83

NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]
Seq. No.	203213
Seq. ID	LIB3083-002-Q1-L1-E8
Method	BLASTX
NCBI GI	g2058282
BLAST score	354
E value	1.0e-33
Match length	93
% identity	73
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	203214
Seq. ID	LIB3083-002-Q1-L1-F5
Method	BLASTX
NCBI GI	g4490737
BLAST score	348
E value	6.0e-33
Match length	124
% identity	48
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	203215
Seq. ID	LIB3083-002-Q1-L1-F7
Method	BLASTX
NCBI GI	g322492
BLAST score	345
E value	1.0e-32
Match length	101
% identity	71
NCBI Description	photomorphogenesis repressor COP1 - Arabidopsis thaliana
Seq. No.	203216
Seq. ID	LIB3083-002-Q1-L1-F8
Method	BLASTX
NCBI GI	g322492
BLAST score	156
E value	2.0e-10
Match length	71
% identity	52
NCBI Description	photomorphogenesis repressor COP1 - Arabidopsis thaliana
Seq. No.	203217
Seq. ID	LIB3083-002-Q1-L1-G1
Method	BLASTX
NCBI GI	g266945
BLAST score	538
E value	3.0e-55
Match length	123
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi_100065_pir__S19978 ribosomal protein L9 - garden pea >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum] >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]
Seq. No.	203218

Seq. ID	LIB3083-002-Q1-L1-G11
Method	BLASTX
NCBI GI	g2129820
BLAST score	324
E value	4.0e-30
Match length	130
% identity	46
NCBI Description	chitinase (EC 3.2.1.14) class II - peanut >gi_1237025_emb_CAA57773_ (X82329) chitinase (class II) [Arachis hypogaea]

Seq. No.	203219
Seq. ID	LIB3083-002-Q1-L1-G2
Method	BLASTX
NCBI GI	g3249086
BLAST score	171
E value	3.0e-12
Match length	37
% identity	86
NCBI Description	(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb_AF006086 from Homo sapiens. EST gb_Z37222 comes [Arabidopsis thaliana]

Seq. No.	203220
Seq. ID	LIB3083-002-Q1-L1-G6
Method	BLASTX
NCBI GI	g4218011
BLAST score	167
E value	2.0e-21
Match length	114
% identity	60
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	203221
Seq. ID	LIB3083-002-Q1-L1-G8
Method	BLASTX
NCBI GI	g4006886
BLAST score	481
E value	2.0e-48
Match length	108
% identity	80
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	203222
Seq. ID	LIB3083-002-Q1-L1-H1
Method	BLASTX
NCBI GI	g2695711
BLAST score	576
E value	1.0e-59
Match length	122
% identity	84
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	203223
Seq. ID	LIB3083-002-Q1-L1-H11

Method	BLASTX
NCBI GI	g1353157
BLAST score	152
E value	6.0e-10
Match length	100
% identity	30
NCBI Description	HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from this gene; cDNA EST EMBL:D34974 comes from this gene [Caenorhabditis elegans]

Seq. No.	203224
Seq. ID	LIB3083-002-Q1-L1-H2
Method	BLASTX
NCBI GI	g1750376
BLAST score	163
E value	3.0e-11
Match length	40
% identity	82
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	203225
Seq. ID	LIB3083-002-Q1-L1-H3
Method	BLASTX
NCBI GI	g464980
BLAST score	182
E value	1.0e-13
Match length	78
% identity	42
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_166422 (L06967) ubiquitin carrier protein [Medicago sativa]

Seq. No.	203226
Seq. ID	LIB3083-002-Q1-L1-H5
Method	BLASTX
NCBI GI	g3513727
BLAST score	563
E value	4.0e-58
Match length	133
% identity	57
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	203227
Seq. ID	LIB3083-002-Q1-L1-H6
Method	BLASTX
NCBI GI	g3395436
BLAST score	249
E value	3.0e-21
Match length	69

% identity	65
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	203228
Seq. ID	LIB3083-002-Q1-L1-H7
Method	BLASTX
NCBI GI	g464980
BLAST score	298
E value	3.0e-27
Match length	105
% identity	54
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_166422 (L06967) ubiquitin carrier protein [Medicago sativa]

Seq. No.	203229
Seq. ID	LIB3083-006-Q1-L1-A11
Method	BLASTX
NCBI GI	g3213227
BLAST score	162
E value	4.0e-11
Match length	90
% identity	33
NCBI Description	(AF035209) putative v-SNARE Vti1a [Mus musculus] >gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No.	203230
Seq. ID	LIB3083-006-Q1-L1-A4
Method	BLASTX
NCBI GI	g2459429
BLAST score	341
E value	3.0e-32
Match length	93
% identity	67
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	203231
Seq. ID	LIB3083-006-Q1-L1-A6
Method	BLASTX
NCBI GI	g4510383
BLAST score	238
E value	4.0e-20
Match length	72
% identity	68
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	203232
Seq. ID	LIB3083-006-Q1-L1-A8
Method	BLASTX
NCBI GI	g464987
BLAST score	141
E value	5.0e-09
Match length	83
% identity	42
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	203233
Seq. ID	LIB3083-006-Q1-L1-A9
Method	BLASTX
NCBI GI	g4539543
BLAST score	486
E value	3.0e-49
Match length	117
% identity	79
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	203234
Seq. ID	LIB3083-006-Q1-L1-B12
Method	BLASTX
NCBI GI	g2760332
BLAST score	194
E value	5.0e-15
Match length	77
% identity	29
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	203235
Seq. ID	LIB3083-006-Q1-L1-B2
Method	BLASTX
NCBI GI	g1174592
BLAST score	372
E value	5.0e-36
Match length	93
% identity	80
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203236
Seq. ID	LIB3083-006-Q1-L1-B4
Method	BLASTX
NCBI GI	g3158376
BLAST score	239
E value	2.0e-20
Match length	94
% identity	55
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	203237
Seq. ID	LIB3083-006-Q1-L1-B5
Method	BLASTX
NCBI GI	g4512659
BLAST score	337
E value	1.0e-31
Match length	138
% identity	53
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana]

>gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203238
Seq. ID	LIB3083-006-Q1-L1-B7
Method	BLASTX
NCBI GI	g4538911
BLAST score	201
E value	9.0e-16
Match length	99
% identity	40
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203239
Seq. ID	LIB3083-006-Q1-L1-B8
Method	BLASTX
NCBI GI	g2190187
BLAST score	163
E value	8.0e-12
Match length	70
% identity	25
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	203240
Seq. ID	LIB3083-006-Q1-L1-B9
Method	BLASTX
NCBI GI	g3341693
BLAST score	150
E value	7.0e-10
Match length	79
% identity	39
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	203241
Seq. ID	LIB3083-006-Q1-L1-C1
Method	BLASTX
NCBI GI	g2642215
BLAST score	327
E value	2.0e-30
Match length	75
% identity	83
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	203242
Seq. ID	LIB3083-006-Q1-L1-C11
Method	BLASTX
NCBI GI	g421929
BLAST score	525
E value	2.0e-71
Match length	148
% identity	14
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	203243
Seq. ID	LIB3083-006-Q1-L1-C12

Method	BLASTN
NCBI GI	g525331
BLAST score	36
E value	7.0e-11
Match length	48
% identity	94
NCBI Description	Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete cds

Seq. No.	203244
Seq. ID	LIB3083-006-Q1-L1-C4
Method	BLASTX
NCBI GI	g3004565
BLAST score	310
E value	1.0e-28
Match length	104
% identity	61
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203245
Seq. ID	LIB3083-006-Q1-L1-C5
Method	BLASTX
NCBI GI	g1076315
BLAST score	194
E value	4.0e-15
Match length	74
% identity	49
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	203246
Seq. ID	LIB3083-006-Q1-L1-C6
Method	BLASTX
NCBI GI	g2961384
BLAST score	350
E value	3.0e-33
Match length	108
% identity	57
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	203247
Seq. ID	LIB3083-006-Q1-L1-C7
Method	BLASTX
NCBI GI	g3367534
BLAST score	493
E value	5.0e-50
Match length	116
% identity	82
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	203248
Seq. ID	LIB3083-006-Q1-L1-C8

Method	BLASTX
NCBI GI	g3738320
BLAST score	159
E value	5.0e-11
Match length	92
% identity	41
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	203249
Seq. ID	LIB3083-006-Q1-L1-C9
Method	BLASTX
NCBI GI	g2647949
BLAST score	574
E value	2.0e-59
Match length	121
% identity	86
NCBI Description	(AJ001369) cytochrome b5 [Olea europaea]

Seq. No.	203250
Seq. ID	LIB3083-006-Q1-L1-D1
Method	BLASTX
NCBI GI	g4371292
BLAST score	165
E value	9.0e-12
Match length	83
% identity	39
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	203251
Seq. ID	LIB3083-006-Q1-L1-D10
Method	BLASTX
NCBI GI	g2865523
BLAST score	171
E value	3.0e-12
Match length	51
% identity	36
NCBI Description	(AF044584) cold regulated LTCOR18 [Lavatera thuringiaca]

Seq. No.	203252
Seq. ID	LIB3083-006-Q1-L1-D12
Method	BLASTX
NCBI GI	g4262186
BLAST score	427
E value	2.0e-42
Match length	106
% identity	75
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	203253
Seq. ID	LIB3083-006-Q1-L1-D2
Method	BLASTX
NCBI GI	g2493130
BLAST score	351
E value	2.0e-33
Match length	70

% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B [Gossypium hirsutum]
Seq. No.	203254
Seq. ID	LIB3083-006-Q1-L1-D4
Method	BLASTX
NCBI GI	g2739366
BLAST score	175
E value	7.0e-13
Match length	90
% identity	39
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]
Seq. No.	203255
Seq. ID	LIB3083-006-Q1-L1-D5
Method	BLASTN
NCBI GI	g2842474
BLAST score	35
E value	2.0e-10
Match length	91
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)
Seq. No.	203256
Seq. ID	LIB3083-006-Q1-L1-E1
Method	BLASTX
NCBI GI	g584795
BLAST score	149
E value	7.0e-10
Match length	52
% identity	62
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_170295 (M80490) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
Seq. No.	203257
Seq. ID	LIB3083-006-Q1-L1-E10
Method	BLASTN
NCBI GI	g1143223
BLAST score	364
E value	0.0e+00
Match length	380
% identity	34
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.	203258
Seq. ID	LIB3083-006-Q1-L1-E12
Method	BLASTX
NCBI GI	g730463
BLAST score	322
E value	6.0e-30
Match length	105
% identity	59
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast

(Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	203259
Seq. ID	LIB3083-006-Q1-L1-E5
Method	BLASTX
NCBI GI	g2583130
BLAST score	177
E value	6.0e-13
Match length	113
% identity	35
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	203260
Seq. ID	LIB3083-006-Q1-L1-E7
Method	BLASTX
NCBI GI	g2511693
BLAST score	364
E value	9.0e-35
Match length	132
% identity	54
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	203261
Seq. ID	LIB3083-006-Q1-L1-E8
Method	BLASTX
NCBI GI	g4455194
BLAST score	296
E value	8.0e-27
Match length	66
% identity	80
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	203262
Seq. ID	LIB3083-006-Q1-L1-F11
Method	BLASTX
NCBI GI	g3549667
BLAST score	490
E value	1.0e-49
Match length	117
% identity	79
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	203263
Seq. ID	LIB3083-006-Q1-L1-F12
Method	BLASTN
NCBI GI	g2980787
BLAST score	39
E value	1.0e-12
Match length	75
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	203264
Seq. ID	LIB3083-006-Q1-L1-F2
Method	BLASTX
NCBI GI	g3851636
BLAST score	458
E value	6.0e-46
Match length	107
% identity	81
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	203265
Seq. ID	LIB3083-006-Q1-L1-F3
Method	BLASTX
NCBI GI	g1172874
BLAST score	296
E value	3.0e-27
Match length	81
% identity	70
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	203266
Seq. ID	LIB3083-006-Q1-L1-F4
Method	BLASTX
NCBI GI	g2098709
BLAST score	378
E value	2.0e-46
Match length	111
% identity	85
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	203267
Seq. ID	LIB3083-006-Q1-L1-F6
Method	BLASTX
NCBI GI	g586076
BLAST score	419
E value	1.0e-41
Match length	80
% identity	95
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	203268
Seq. ID	LIB3083-006-Q1-L1-F8
Method	BLASTX
NCBI GI	g2829204
BLAST score	509
E value	9.0e-52
Match length	119
% identity	87
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No.	203269
Seq. ID	LIB3083-006-Q1-L1-F9
Method	BLASTX
NCBI GI	g3024121
BLAST score	373
E value	4.0e-36
Match length	89
% identity	83
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_1724104 (U79767) methionine adenosyltransferase [Mesembryanthemum crystallinum]

Seq. No.	203270
Seq. ID	LIB3083-006-Q1-L1-G1
Method	BLASTX
NCBI GI	g2270994
BLAST score	218
E value	3.0e-19
Match length	74
% identity	62
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	203271
Seq. ID	LIB3083-006-Q1-L1-G10
Method	BLASTX
NCBI GI	g3024028
BLAST score	578
E value	5.0e-60
Match length	116
% identity	93
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA)

Seq. No.	203272
Seq. ID	LIB3083-006-Q1-L1-G11
Method	BLASTX
NCBI GI	g3643593
BLAST score	214
E value	3.0e-17
Match length	88
% identity	57
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203273
Seq. ID	LIB3083-006-Q1-L1-G2
Method	BLASTN
NCBI GI	g1143223
BLAST score	222
E value	1.0e-122
Match length	396
% identity	96
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203274

09604400.1700000

Seq. ID	LIB3083-006-Q1-L1-G5
Method	BLASTX
NCBI GI	g4091008
BLAST score	328
E value	1.0e-30
Match length	128
% identity	55
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	203275
Seq. ID	LIB3083-006-Q1-L1-G7
Method	BLASTX
NCBI GI	g81816
BLAST score	332
E value	2.0e-31
Match length	78
% identity	82
NCBI Description	tubulin beta-1 chain - soybean

Seq. No.	203276
Seq. ID	LIB3083-006-Q1-L1-G8
Method	BLASTX
NCBI GI	g3786005
BLAST score	356
E value	3.0e-37
Match length	119
% identity	37
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	203277
Seq. ID	LIB3083-006-Q1-L1-H1
Method	BLASTX
NCBI GI	g3776005
BLAST score	374
E value	2.0e-43
Match length	98
% identity	93
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	203278
Seq. ID	LIB3083-006-Q1-L1-H10
Method	BLASTX
NCBI GI	g2811278
BLAST score	512
E value	4.0e-52
Match length	132
% identity	73
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	203279
Seq. ID	LIB3083-006-Q1-L1-H11
Method	BLASTX
NCBI GI	g4544412
BLAST score	236
E value	8.0e-20
Match length	117

% identity	41
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203280
Seq. ID	LIB3083-006-Q1-L1-H12
Method	BLASTX
NCBI GI	g1703108
BLAST score	619
E value	9.0e-65
Match length	119
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	203281
Seq. ID	LIB3083-006-Q1-L1-H2
Method	BLASTX
NCBI GI	g1076315
BLAST score	290
E value	4.0e-26
Match length	128
% identity	45
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	203282
Seq. ID	LIB3083-006-Q1-L1-H5
Method	BLASTX
NCBI GI	g2129473
BLAST score	288
E value	6.0e-26
Match length	105
% identity	55
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	203283
Seq. ID	LIB3083-006-Q1-L1-H6
Method	BLASTX
NCBI GI	g4539389
BLAST score	296
E value	5.0e-27
Match length	92
% identity	70
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203284
Seq. ID	LIB3083-006-Q1-L1-H7
Method	BLASTX
NCBI GI	g4063751
BLAST score	288
E value	8.0e-26

Match length	107
% identity	51
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	203285
Seq. ID	LIB3083-006-Q1-L1-H8
Method	BLASTX
NCBI GI	g3294467
BLAST score	196
E value	1.0e-15
Match length	57
% identity	67
NCBI Description	(U89341) phosphoglucomutase 1 [Zea mays]

Seq. No.	203286
Seq. ID	LIB3083-006-Q1-L1-H9
Method	BLASTX
NCBI GI	g2286153
BLAST score	383
E value	4.0e-37
Match length	80
% identity	97
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	203287
Seq. ID	LIB3083-007-Q1-L1-A10
Method	BLASTX
NCBI GI	g464849
BLAST score	335
E value	1.0e-31
Match length	100
% identity	70
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	203288
Seq. ID	LIB3083-007-Q1-L1-A11
Method	BLASTX
NCBI GI	g4217999
BLAST score	354
E value	8.0e-34
Match length	93
% identity	77
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.	203289
Seq. ID	LIB3083-007-Q1-L1-A5
Method	BLASTX
NCBI GI	g2642448
BLAST score	208
E value	1.0e-16
Match length	84
% identity	27

NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203290
Seq. ID	LIB3083-007-Q1-L1-A7
Method	BLASTN
NCBI GI	g2832611
BLAST score	37
E value	2.0e-11
Match length	132
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	203291
Seq. ID	LIB3083-007-Q1-L1-B10
Method	BLASTX
NCBI GI	g2245066
BLAST score	502
E value	5.0e-51
Match length	119
% identity	73
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	203292
Seq. ID	LIB3083-007-Q1-L1-B11
Method	BLASTX
NCBI GI	g1086249
BLAST score	346
E value	7.0e-33
Match length	99
% identity	67
NCBI Description	subtilisin-like protease - Alnus glutinosa >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease [Alnus glutinosa]

Seq. No.	203293
Seq. ID	LIB3083-007-Q1-L1-B2
Method	BLASTX
NCBI GI	g2244917
BLAST score	140
E value	1.0e-08
Match length	62
% identity	42
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203294
Seq. ID	LIB3083-007-Q1-L1-B3
Method	BLASTX
NCBI GI	g421929
BLAST score	471
E value	2.0e-47
Match length	98
% identity	14
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	203295
Seq. ID	LIB3083-007-Q1-L1-B5
Method	BLASTX
NCBI GI	g1841462
BLAST score	447
E value	7.0e-51
Match length	119
% identity	87
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No.	203296
Seq. ID	LIB3083-007-Q1-L1-B6
Method	BLASTX
NCBI GI	g586076
BLAST score	534
E value	8.0e-55
Match length	118
% identity	82
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	203297
Seq. ID	LIB3083-007-Q1-L1-B8
Method	BLASTN
NCBI GI	g1143223
BLAST score	137
E value	4.0e-71
Match length	312
% identity	40
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203298
Seq. ID	LIB3083-007-Q1-L1-C1
Method	BLASTX
NCBI GI	g1174448
BLAST score	160
E value	3.0e-11
Match length	79
% identity	44
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	203299
Seq. ID	LIB3083-007-Q1-L1-C11
Method	BLASTX
NCBI GI	g3175990
BLAST score	276
E value	6.0e-25
Match length	75
% identity	71
NCBI Description	(AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No.	203300

Seq. ID	LIB3083-007-Q1-L1-C5
Method	BLASTX
NCBI GI	g2642448
BLAST score	270
E value	7.0e-24
Match length	115
% identity	16
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203301
Seq. ID	LIB3083-007-Q1-L1-D1
Method	BLASTX
NCBI GI	g1632831
BLAST score	504
E value	3.0e-51
Match length	109
% identity	90
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	203302
Seq. ID	LIB3083-007-Q1-L1-D10
Method	BLASTX
NCBI GI	g1076627
BLAST score	331
E value	4.0e-31
Match length	100
% identity	69
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	203303
Seq. ID	LIB3083-007-Q1-L1-D11
Method	BLASTX
NCBI GI	g2129473
BLAST score	207
E value	1.0e-16
Match length	77
% identity	51
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	203304
Seq. ID	LIB3083-007-Q1-L1-D12
Method	BLASTX
NCBI GI	g3335359
BLAST score	356
E value	1.0e-36
Match length	100
% identity	80
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	203305
Seq. ID	LIB3083-007-Q1-L1-D4
Method	BLASTX

NCBI GI	g3482974
BLAST score	490
E value	1.0e-49
Match length	121
% identity	77
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	203306
Seq. ID	LIB3083-007-Q1-L1-D5
Method	BLASTX
NCBI GI	g322750
BLAST score	588
E value	4.0e-61
Match length	117
% identity	96
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	203307
Seq. ID	LIB3083-007-Q1-L1-D7
Method	BLASTX
NCBI GI	g4455234
BLAST score	177
E value	5.0e-13
Match length	73
% identity	52
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	203308
Seq. ID	LIB3083-007-Q1-L1-D8
Method	BLASTX
NCBI GI	g2642238
BLAST score	375
E value	4.0e-36
Match length	88
% identity	86
NCBI Description	(AF031241) endoplasmic reticulum HSC70-cognate binding protein precursor [Glycine max]

Seq. No.	203309
Seq. ID	LIB3083-007-Q1-L1-E10
Method	BLASTX
NCBI GI	g464840
BLAST score	507
E value	1.0e-51
Match length	122
% identity	85
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	203310
Seq. ID	LIB3083-007-Q1-L1-E11
Method	BLASTX

NCBI GI	g1666234
BLAST score	139
E value	9.0e-09
Match length	42
% identity	69
NCBI Description	(U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No.	203311
Seq. ID	LIB3083-007-Q1-L1-E3
Method	BLASTX
NCBI GI	g3175990
BLAST score	554
E value	4.0e-57
Match length	122
% identity	84
NCBI Description	(AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No.	203312
Seq. ID	LIB3083-007-Q1-L1-E5
Method	BLASTX
NCBI GI	g2642448
BLAST score	223
E value	2.0e-18
Match length	118
% identity	15
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203313
Seq. ID	LIB3083-007-Q1-L1-E6
Method	BLASTX
NCBI GI	g4164159
BLAST score	406
E value	8.0e-40
Match length	79
% identity	92
NCBI Description	(AB015496) ethylene receptor [Passiflora edulis]

Seq. No.	203314
Seq. ID	LIB3083-007-Q1-L1-E7
Method	BLASTX
NCBI GI	g3482929
BLAST score	288
E value	6.0e-26
Match length	122
% identity	50
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	203315
Seq. ID	LIB3083-007-Q1-L1-E8
Method	BLASTX
NCBI GI	g2702274
BLAST score	251
E value	1.0e-21

Match length	80
% identity	61
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	203316
Seq. ID	LIB3083-007-Q1-L1-F1
Method	BLASTX
NCBI GI	g2129597
BLAST score	477
E value	4.0e-48
Match length	97
% identity	93
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	203317
Seq. ID	LIB3083-007-Q1-L1-F12
Method	BLASTX
NCBI GI	g462137
BLAST score	396
E value	9.0e-39
Match length	101
% identity	75
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

Seq. No.	203318
Seq. ID	LIB3083-007-Q1-L1-F2
Method	BLASTX
NCBI GI	g3914394
BLAST score	444
E value	3.0e-44
Match length	120
% identity	73
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	203319
Seq. ID	LIB3083-007-Q1-L1-F3
Method	BLASTX
NCBI GI	g3511285
BLAST score	597
E value	3.0e-62
Match length	123
% identity	86
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	203320
Seq. ID	LIB3083-007-Q1-L1-F5
Method	BLASTX
NCBI GI	g1706958
BLAST score	379

E value	1.0e-36
Match length	120
% identity	68
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203321
Seq. ID	LIB3083-007-Q1-L1-F6
Method	BLASTX
NCBI GI	g3393062
BLAST score	407
E value	6.0e-40
Match length	107
% identity	68
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	203322
Seq. ID	LIB3083-007-Q1-L1-F7
Method	BLASTX
NCBI GI	g2435511
BLAST score	546
E value	3.0e-56
Match length	121
% identity	81
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	203323
Seq. ID	LIB3083-007-Q1-L1-F8
Method	BLASTX
NCBI GI	g2253384
BLAST score	578
E value	6.0e-60
Match length	120
% identity	92
NCBI Description	(AF007100) biotin carboxylase precursor [Glycine max]

Seq. No.	203324
Seq. ID	LIB3083-007-Q1-L1-F9
Method	BLASTX
NCBI GI	g3924596
BLAST score	493
E value	4.0e-50
Match length	104
% identity	89
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	203325
Seq. ID	LIB3083-007-Q1-L1-G1
Method	BLASTX
NCBI GI	g4325354
BLAST score	335
E value	2.0e-31
Match length	83
% identity	72
NCBI Description	(AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam:

09604096 - 060400

PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No.	203326
Seq. ID	LIB3083-007-Q1-L1-G10
Method	BLASTX
NCBI GI	g2961372
BLAST score	573
E value	5.0e-60
Match length	119
% identity	95
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	203327
Seq. ID	LIB3083-007-Q1-L1-G11
Method	BLASTX
NCBI GI	g1399450
BLAST score	380
E value	6.0e-37
Match length	92
% identity	82
NCBI Description	(U47660) beta-tubulin 2 [Lupinus albus]

Seq. No.	203328
Seq. ID	LIB3083-007-Q1-L1-G4
Method	BLASTX
NCBI GI	g3212116
BLAST score	177
E value	6.0e-13
Match length	71
% identity	46
NCBI Description	(Y17393) prefoldin subunit 2 [Mus musculus]

Seq. No.	203329
Seq. ID	LIB3083-007-Q1-L1-G6
Method	BLASTN
NCBI GI	g1143223
BLAST score	105
E value	5.0e-52
Match length	324
% identity	90
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203330
Seq. ID	LIB3083-007-Q1-L1-G9
Method	BLASTX
NCBI GI	g1619602
BLAST score	161
E value	2.0e-11
Match length	73
% identity	47
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	203331
Seq. ID	LIB3083-007-Q1-L1-H10
Method	BLASTX

NCBI GI	g1703168
BLAST score	180
E value	2.0e-13
Match length	92
% identity	46
NCBI Description	BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) >gi_482950_pir__B32105 clathrin-associated protein complex 2, beta chain minor component - rat >gi_203113 (M77245) beta'-chain clathrin associated protein complex AP-1 [Rattus norvegicus]

Seq. No.	203332
Seq. ID	LIB3083-007-Q1-L1-H11
Method	BLASTX
NCBI GI	g416758
BLAST score	227
E value	7.0e-19
Match length	79
% identity	57
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	203333
Seq. ID	LIB3083-007-Q1-L1-H12
Method	BLASTX
NCBI GI	g1370196
BLAST score	282
E value	3.0e-25
Match length	80
% identity	74
NCBI Description	(Z73947) RAB8D [Lotus japonicus]

Seq. No.	203334
Seq. ID	LIB3083-007-Q1-L1-H4
Method	BLASTN
NCBI GI	g1143223
BLAST score	125
E value	7.0e-64
Match length	317
% identity	88
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203335
Seq. ID	LIB3083-007-Q1-L1-H6
Method	BLASTX
NCBI GI	g2642443
BLAST score	200
E value	1.0e-15
Match length	88
% identity	47
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	203336
Seq. ID	LIB3083-008-Q1-L1-A10

Method	BLASTX
NCBI GI	g133872
BLAST score	294
E value	8.0e-27
Match length	93
% identity	70
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	203337
Seq. ID	LIB3083-008-Q1-L1-A11
Method	BLASTX
NCBI GI	g2341041
BLAST score	391
E value	5.0e-38
Match length	110
% identity	69
NCBI Description	(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb_AF047976). EST gb_W43451 comes from this gene. [Arabidopsis thaliana] >gi_3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No.	203338
Seq. ID	LIB3083-008-Q1-L1-A9
Method	BLASTX
NCBI GI	g2190547
BLAST score	238
E value	3.0e-20
Match length	86
% identity	59
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	203339
Seq. ID	LIB3083-008-Q1-L1-B10
Method	BLASTX
NCBI GI	g1706956
BLAST score	456
E value	1.0e-45
Match length	123
% identity	77
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203340
Seq. ID	LIB3083-008-Q1-L1-B11
Method	BLASTX
NCBI GI	g1272410
BLAST score	434
E value	3.0e-43
Match length	94
% identity	87

NCBI Description	(U52045) immunophilin precursor [Vicia faba]

Seq. No.	203341
Seq. ID	LIB3083-008-Q1-L1-B9
Method	BLASTX
NCBI GI	g1706956
BLAST score	580
E value	3.0e-60
Match length	114
% identity	98
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203342
Seq. ID	LIB3083-008-Q1-L1-C10
Method	BLASTX
NCBI GI	g4512671
BLAST score	467
E value	6.0e-47
Match length	123
% identity	72
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	203343
Seq. ID	LIB3083-008-Q1-L1-C11
Method	BLASTX
NCBI GI	g4234941
BLAST score	429
E value	1.0e-42
Match length	109
% identity	78
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	203344
Seq. ID	LIB3083-008-Q1-L1-C12
Method	BLASTN
NCBI GI	g451543
BLAST score	305
E value	1.0e-171
Match length	340
% identity	92
NCBI Description	Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi_1598725_gb_I18370_I18370 Sequence 25 from patent US

Seq. No.	203345
Seq. ID	LIB3083-008-Q1-L1-C9
Method	BLASTX
NCBI GI	g2827555
BLAST score	327
E value	2.0e-30
Match length	123
% identity	58
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	203346

Seq. ID	LIB3083-008-Q1-L1-D10
Method	BLASTX
NCBI GI	g2497753
BLAST score	286
E value	9.0e-26
Match length	106
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	203347
Seq. ID	LIB3083-008-Q1-L1-E10
Method	BLASTX
NCBI GI	g3204134
BLAST score	517
E value	8.0e-53
Match length	114
% identity	76
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	203348
Seq. ID	LIB3083-008-Q1-L1-E12
Method	BLASTX
NCBI GI	g4539386
BLAST score	325
E value	3.0e-30
Match length	85
% identity	71
NCBI Description	(AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No.	203349
Seq. ID	LIB3083-008-Q1-L1-E9
Method	BLASTX
NCBI GI	g3420239
BLAST score	323
E value	4.0e-30
Match length	62
% identity	98
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	203350
Seq. ID	LIB3083-008-Q1-L1-F10
Method	BLASTX
NCBI GI	g1171577
BLAST score	145
E value	4.0e-09
Match length	98
% identity	34
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	203351
Seq. ID	LIB3083-008-Q1-L1-F12
Method	BLASTX
NCBI GI	g4006848
BLAST score	272
E value	5.0e-24

Match length	124
% identity	48
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	203352
Seq. ID	LIB3083-008-Q1-L1-G10
Method	BLASTX
NCBI GI	g1657948
BLAST score	471
E value	2.0e-47
Match length	111
% identity	82
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	203353
Seq. ID	LIB3083-008-Q1-L1-G12
Method	BLASTX
NCBI GI	g1729980
BLAST score	476
E value	5.0e-48
Match length	107
% identity	78
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	203354
Seq. ID	LIB3083-008-Q1-L1-G9
Method	BLASTN
NCBI GI	g1143223
BLAST score	350
E value	0.0e+00
Match length	362
% identity	27
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203355
Seq. ID	LIB3083-008-Q1-L1-H10
Method	BLASTX
NCBI GI	g1076387
BLAST score	472
E value	2.0e-47
Match length	123
% identity	74
NCBI Description	protein kinase homolog - Arabidopsis thaliana >gi_717180_emb_CAA55866_ (X79279) protein kinase homologous to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]

Seq. No.	203356
Seq. ID	LIB3083-008-Q1-L1-H11
Method	BLASTX
NCBI GI	g4490727
BLAST score	141

E value	8.0e-09
Match length	108
% identity	8
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	203357
Seq. ID	LIB3083-008-Q1-L1-H12
Method	BLASTX
NCBI GI	g4417283
BLAST score	146
E value	3.0e-09
Match length	57
% identity	51
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	203358
Seq. ID	LIB3083-008-Q1-L1-H9
Method	BLASTX
NCBI GI	g3212854
BLAST score	435
E value	3.0e-43
Match length	114
% identity	77
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	203359
Seq. ID	LIB3083-009-Q1-L1-D12
Method	BLASTX
NCBI GI	g2499819
BLAST score	334
E value	2.0e-31
Match length	102
% identity	63
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	203360
Seq. ID	LIB3083-009-Q1-L1-D6
Method	BLASTX
NCBI GI	g3927831
BLAST score	244
E value	6.0e-21
Match length	99
% identity	58
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	203361
Seq. ID	LIB3083-009-Q1-L1-F6
Method	BLASTX
NCBI GI	g18734
BLAST score	551
E value	9.0e-57
Match length	119

% identity	88
NCBI Description	(X52493) DNA-directed RNA polymerase [Glycine max]

Seq. No.	203362
Seq. ID	LIB3083-009-Q1-L1-G11
Method	BLASTN
NCBI GI	g606941
BLAST score	52
E value	2.0e-20
Match length	233
% identity	79
NCBI Description	Gossypium hirsutum C312 clone Fb-B6 unidentified fiber mRNA, complete cds

Seq. No.	203363
Seq. ID	LIB3083-009-Q1-L1-G4
Method	BLASTX
NCBI GI	g3212870
BLAST score	266
E value	2.0e-23
Match length	73
% identity	74
NCBI Description	(AC004005) putative N-myristoyltransferase [Arabidopsis thaliana]

Seq. No.	203364
Seq. ID	LIB3083-009-Q1-L1-H11
Method	BLASTX
NCBI GI	g4235430
BLAST score	370
E value	1.0e-35
Match length	98
% identity	73
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	203365
Seq. ID	LIB3083-009-Q1-L1-H6
Method	BLASTX
NCBI GI	g3892045
BLAST score	164
E value	1.0e-11
Match length	67
% identity	61
NCBI Description	(AC002330) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	203366
Seq. ID	LIB3083-010-Q1-L1-A12
Method	BLASTX
NCBI GI	g3114901
BLAST score	283
E value	3.0e-26
Match length	111
% identity	64
NCBI Description	(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi_3114905_emb_CAA06709_ (AJ005806) pceberh [Populus balsamifera subsp. trichocarpa]

Seq. No.	203367
Seq. ID	LIB3083-010-Q1-L1-A3
Method	BLASTX
NCBI GI	g4417271
BLAST score	470
E value	3.0e-47
Match length	105
% identity	80
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	203368
Seq. ID	LIB3083-010-Q1-L1-A5
Method	BLASTX
NCBI GI	g3859606
BLAST score	461
E value	3.0e-46
Match length	121
% identity	71
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	203369
Seq. ID	LIB3083-010-Q1-L1-A7
Method	BLASTX
NCBI GI	g2842490
BLAST score	242
E value	9.0e-21
Match length	64
% identity	73
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	203370
Seq. ID	LIB3083-010-Q1-L1-B1
Method	BLASTX
NCBI GI	g1619297
BLAST score	367
E value	3.0e-35
Match length	87
% identity	82
NCBI Description	(Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No.	203371
Seq. ID	LIB3083-010-Q1-L1-B3
Method	BLASTX
NCBI GI	g1174592
BLAST score	219
E value	3.0e-22
Match length	81
% identity	74
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203372
Seq. ID	LIB3083-010-Q1-L1-B5

Method	BLASTX
NCBI GI	g1174592
BLAST score	649
E value	3.0e-68
Match length	129
% identity	95
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203373
Seq. ID	LIB3083-010-Q1-L1-B6
Method	BLASTX
NCBI GI	g3757514
BLAST score	376
E value	2.0e-36
Match length	98
% identity	74
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	203374
Seq. ID	LIB3083-010-Q1-L1-B7
Method	BLASTX
NCBI GI	g4204575
BLAST score	356
E value	5.0e-34
Match length	101
% identity	68
NCBI Description	(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No.	203375
Seq. ID	LIB3083-010-Q1-L1-C11
Method	BLASTX
NCBI GI	g2511590
BLAST score	240
E value	3.0e-23
Match length	95
% identity	68
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	203376
Seq. ID	LIB3083-010-Q1-L1-C3
Method	BLASTX
NCBI GI	g3881507
BLAST score	315
E value	5.0e-29
Match length	103
% identity	53
NCBI Description	(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	203377
Seq. ID	LIB3083-010-Q1-L1-C4

Method	BLASTX
NCBI GI	g4056469
BLAST score	375
E value	2.0e-41
Match length	121
% identity	76
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	203378
Seq. ID	LIB3083-010-Q1-L1-C5
Method	BLASTX
NCBI GI	g2961300
BLAST score	317
E value	3.0e-29
Match length	76
% identity	82
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	203379
Seq. ID	LIB3083-010-Q1-L1-C7
Method	BLASTX
NCBI GI	g1856971
BLAST score	199
E value	8.0e-16
Match length	80
% identity	57
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	203380
Seq. ID	LIB3083-010-Q1-L1-D1
Method	BLASTX
NCBI GI	g4406820
BLAST score	260
E value	6.0e-23
Match length	63
% identity	79
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No.	203381
Seq. ID	LIB3083-010-Q1-L1-D3
Method	BLASTX
NCBI GI	g4115377
BLAST score	296
E value	8.0e-27
Match length	123
% identity	53
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	203382
Seq. ID	LIB3083-010-Q1-L1-D6

Method	BLASTX
NCBI GI	g2632254
BLAST score	282
E value	4.0e-25
Match length	100
% identity	55
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	203383
Seq. ID	LIB3083-010-Q1-L1-E12
Method	BLASTX
NCBI GI	g3163946
BLAST score	407
E value	3.0e-40
Match length	84
% identity	94
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No.	203384
Seq. ID	LIB3083-010-Q1-L1-E4
Method	BLASTX
NCBI GI	g2267567
BLAST score	400
E value	3.0e-39
Match length	93
% identity	84
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	203385
Seq. ID	LIB3083-010-Q1-L1-E7
Method	BLASTX
NCBI GI	g4490301
BLAST score	184
E value	3.0e-14
Match length	70
% identity	49
NCBI Description	(AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203386
Seq. ID	LIB3083-010-Q1-L1-E8
Method	BLASTX
NCBI GI	g2285792
BLAST score	507
E value	2.0e-51
Match length	152
% identity	68
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	203387
Seq. ID	LIB3083-010-Q1-L1-F3
Method	BLASTX
NCBI GI	g4490342
BLAST score	452

E value	4.0e-45
Match length	138
% identity	70
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	203388
Seq. ID	LIB3083-010-Q1-L1-F5
Method	BLASTX
NCBI GI	g2642443
BLAST score	262
E value	9.0e-23
Match length	145
% identity	34
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	203389
Seq. ID	LIB3083-010-Q1-L1-F8
Method	BLASTX
NCBI GI	g974294
BLAST score	267
E value	2.0e-23
Match length	93
% identity	58
NCBI Description	(U31309) LP6 [Pinus taeda]

Seq. No.	203390
Seq. ID	LIB3083-010-Q1-L1-G10
Method	BLASTX
NCBI GI	g1449179
BLAST score	201
E value	1.0e-15
Match length	78
% identity	58
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	203391
Seq. ID	LIB3083-010-Q1-L1-G12
Method	BLASTX
NCBI GI	g1346172
BLAST score	349
E value	2.0e-33
Match length	90
% identity	80
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >gi_170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum]

Seq. No.	203392
Seq. ID	LIB3083-010-Q1-L1-G4
Method	BLASTX
NCBI GI	g3702332
BLAST score	169
E value	3.0e-14
Match length	83
% identity	54

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NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	203393
Seq. ID	LIB3083-010-Q1-L1-H5
Method	BLASTX
NCBI GI	g2500197
BLAST score	625
E value	2.0e-65
Match length	123
% identity	96
NCBI Description	RAC-LIKE GTP BINDING PROTEIN RAC13 >gi_1361976_pir__S57325 GTP-binding protein Rac 13 - upland cotton >gi_1087111_bbs_170156 (S79308) 21.8 kda GTP-binding protein=Rac13 [Gossypium hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, Peptide, 196 aa] [Gossypium hirsutum]
Seq. No.	203394
Seq. ID	LIB3083-010-Q1-L1-H7
Method	BLASTX
NCBI GI	g3367517
BLAST score	342
E value	3.0e-32
Match length	114
% identity	53
NCBI Description	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene. [Arabidopsis thaliana]
Seq. No.	203395
Seq. ID	LIB3083-011-Q1-L1-A1
Method	BLASTN
NCBI GI	g2501849
BLAST score	41
E value	7.0e-14
Match length	61
% identity	92
NCBI Description	Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, complete cds
Seq. No.	203396
Seq. ID	LIB3083-011-Q1-L1-A10
Method	BLASTX
NCBI GI	g2323344
BLAST score	365
E value	3.0e-35
Match length	81
% identity	80
NCBI Description	(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]
Seq. No.	203397
Seq. ID	LIB3083-011-Q1-L1-B1
Method	BLASTX
NCBI GI	g3123271
BLAST score	354
E value	6.0e-34
Match length	73

% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	203398
Seq. ID	LIB3083-011-Q1-L1-B10
Method	BLASTX
NCBI GI	g1052973
BLAST score	407
E value	4.0e-40
Match length	94
% identity	86
NCBI Description	(U37838) fructokinase [Beta vulgaris]

Seq. No.	203399
Seq. ID	LIB3083-011-Q1-L1-B11
Method	BLASTX
NCBI GI	g1915974
BLAST score	188
E value	1.0e-14
Match length	45
% identity	89
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	203400
Seq. ID	LIB3083-011-Q1-L1-B5
Method	BLASTX
NCBI GI	g1064826
BLAST score	221
E value	2.0e-18
Match length	57
% identity	82
NCBI Description	(D78206) Actin [Ipomoea nil]

Seq. No.	203401
Seq. ID	LIB3083-011-Q1-L1-C12
Method	BLASTN
NCBI GI	g1143223
BLAST score	180
E value	6.0e-97
Match length	228
% identity	24
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203402
Seq. ID	LIB3083-011-Q1-L1-C3
Method	BLASTX
NCBI GI	g940288
BLAST score	220
E value	7.0e-18
Match length	75
% identity	60
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	203403

Seq. ID	LIB3083-011-Q1-L1-D1
Method	BLASTX
NCBI GI	g2842490
BLAST score	263
E value	6.0e-23
Match length	70
% identity	76
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	203404
Seq. ID	LIB3083-011-Q1-L1-D10
Method	BLASTX
NCBI GI	g2052379
BLAST score	258
E value	2.0e-22
Match length	65
% identity	75
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	203405
Seq. ID	LIB3083-011-Q1-L1-E11
Method	BLASTX
NCBI GI	g4097579
BLAST score	128
E value	2.0e-09
Match length	59
% identity	57
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	203406
Seq. ID	LIB3083-011-Q1-L1-G10
Method	BLASTX
NCBI GI	g1708314
BLAST score	350
E value	4.0e-33
Match length	68
% identity	93
NCBI Description	HEAT SHOCK PROTEIN 83 >gi_169296 (M99431) heat shock protein 83 [Pharbitis nil] >gi_445625_prf__1909372A heat shock protein 83 [Ipomoea nil]

Seq. No.	203407
Seq. ID	LIB3083-011-Q1-L1-G2
Method	BLASTX
NCBI GI	g4558659
BLAST score	395
E value	2.0e-38
Match length	102
% identity	68
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	203408
Seq. ID	LIB3083-012-Q1-L1-A1
Method	BLASTX
NCBI GI	g136739
BLAST score	457
E value	6.0e-46

Match length	101
% identity	87
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	203409
Seq. ID	LIB3083-012-Q1-L1-A10
Method	BLASTN
NCBI GI	g2829203
BLAST score	63
E value	5.0e-27
Match length	127
% identity	87
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 lipid transfer protein precursor (LTP) mRNA, complete cds

Seq. No.	203410
Seq. ID	LIB3083-012-Q1-L1-A11
Method	BLASTX
NCBI GI	g3785987
BLAST score	156
E value	2.0e-10
Match length	87
% identity	39
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203411
Seq. ID	LIB3083-012-Q1-L1-A2
Method	BLASTX
NCBI GI	g1706956
BLAST score	681
E value	5.0e-72
Match length	129
% identity	98
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203412
Seq. ID	LIB3083-012-Q1-L1-A5
Method	BLASTX
NCBI GI	g2811278
BLAST score	204
E value	1.0e-16
Match length	62
% identity	65
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	203413
Seq. ID	LIB3083-012-Q1-L1-A6
Method	BLASTN
NCBI GI	g2829205
BLAST score	213
E value	1.0e-116
Match length	301
% identity	25

NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	203414
Seq. ID	LIB3083-012-Q1-L1-A8
Method	BLASTN
NCBI GI	g1000089
BLAST score	234
E value	1.0e-129
Match length	272
% identity	96
NCBI Description	Gossypium barbadense clone SIE6-3B E6 gene, complete cds

Seq. No.	203415
Seq. ID	LIB3083-012-Q1-L1-B10
Method	BLASTN
NCBI GI	g1143223
BLAST score	80
E value	4.0e-37
Match length	258
% identity	40
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203416
Seq. ID	LIB3083-012-Q1-L1-B12
Method	BLASTX
NCBI GI	g2454182
BLAST score	403
E value	2.0e-39
Match length	85
% identity	93
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	203417
Seq. ID	LIB3083-012-Q1-L1-B2
Method	BLASTX
NCBI GI	g3047117
BLAST score	315
E value	1.0e-29
Match length	64
% identity	92
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	203418
Seq. ID	LIB3083-012-Q1-L1-B3
Method	BLASTX
NCBI GI	g3643611
BLAST score	266
E value	8.0e-24
Match length	74
% identity	61
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	203419
Seq. ID	LIB3083-012-Q1-L1-B4

Method	BLASTN
NCBI GI	g1143223
BLAST score	120
E value	5.0e-61
Match length	314
% identity	42
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203420
Seq. ID	LIB3083-012-Q1-L1-B5
Method	BLASTX
NCBI GI	g3176098
BLAST score	370
E value	1.0e-35
Match length	110
% identity	68
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	203421
Seq. ID	LIB3083-012-Q1-L1-B7
Method	BLASTX
NCBI GI	g2244910
BLAST score	151
E value	4.0e-10
Match length	33
% identity	88
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	203422
Seq. ID	LIB3083-012-Q1-L1-B8
Method	BLASTX
NCBI GI	g3024126
BLAST score	627
E value	1.0e-65
Match length	128
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	203423
Seq. ID	LIB3083-012-Q1-L1-B9
Method	BLASTX
NCBI GI	g1170938
BLAST score	232
E value	1.0e-19
Match length	90
% identity	60
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_481566_pir__S38875 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429106_emb_CAA80866_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	203424

Seq. ID	LIB3083-012-Q1-L1-C1
Method	BLASTX
NCBI GI	g1706958
BLAST score	647
E value	5.0e-68
Match length	123
% identity	97
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203425
Seq. ID	LIB3083-012-Q1-L1-C6
Method	BLASTX
NCBI GI	g123548
BLAST score	235
E value	3.0e-20
Match length	55
% identity	82
NCBI Description	17.8 KD CLASS I HEAT SHOCK PROTEIN (CLONE DCHSP17.7) >gi_18353_emb_CAA37847_ (X53851) heat shock protein [Daucus carota]

Seq. No.	203426
Seq. ID	LIB3083-012-Q1-L1-C9
Method	BLASTX
NCBI GI	g2462745
BLAST score	168
E value	6.0e-12
Match length	62
% identity	45
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	203427
Seq. ID	LIB3083-012-Q1-L1-D10
Method	BLASTX
NCBI GI	g1706958
BLAST score	199
E value	9.0e-16
Match length	41
% identity	93
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203428
Seq. ID	LIB3083-012-Q1-L1-D12
Method	BLASTX
NCBI GI	g1321941
BLAST score	293
E value	1.0e-26
Match length	99
% identity	64
NCBI Description	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]

Seq. No.	203429
Seq. ID	LIB3083-012-Q1-L1-D3
Method	BLASTX
NCBI GI	g4490733
BLAST score	184

E value	5.0e-14
Match length	58
% identity	67
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	203430
Seq. ID	LIB3083-012-Q1-L1-D4
Method	BLASTX
NCBI GI	g2760345
BLAST score	607
E value	2.0e-63
Match length	127
% identity	24
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]

Seq. No.	203431
Seq. ID	LIB3083-012-Q1-L1-D5
Method	BLASTX
NCBI GI	g2828280
BLAST score	450
E value	5.0e-45
Match length	90
% identity	90
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	203432
Seq. ID	LIB3083-012-Q1-L1-D6
Method	BLASTX
NCBI GI	g3309243
BLAST score	472
E value	3.0e-50
Match length	114
% identity	91
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	203433
Seq. ID	LIB3083-012-Q1-L1-D7
Method	BLASTX
NCBI GI	g1706958
BLAST score	438
E value	1.0e-43
Match length	108
% identity	84
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203434
Seq. ID	LIB3083-012-Q1-L1-D8
Method	BLASTX
NCBI GI	g2129613
BLAST score	495
E value	3.0e-50
Match length	124
% identity	73
NCBI Description	homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No.	203435
Seq. ID	LIB3083-012-Q1-L1-D9
Method	BLASTX
NCBI GI	g1168480
BLAST score	141
E value	7.0e-09
Match length	81
% identity	38
NCBI Description	AQUAPORIN >gi_604477 (U18403) aquaporin [Atriplex canescens]

Seq. No.	203436
Seq. ID	LIB3083-012-Q1-L1-E1
Method	BLASTX
NCBI GI	g3421134
BLAST score	361
E value	1.0e-34
Match length	102
% identity	76
NCBI Description	(AF045666) arginine decarboxylase [Theobroma cacao]

Seq. No.	203437
Seq. ID	LIB3083-012-Q1-L1-E12
Method	BLASTX
NCBI GI	g2737973
BLAST score	251
E value	9.0e-22
Match length	85
% identity	58
NCBI Description	(U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No.	203438
Seq. ID	LIB3083-012-Q1-L1-E5
Method	BLASTX
NCBI GI	g4139264
BLAST score	233
E value	1.0e-19
Match length	43
% identity	100
NCBI Description	(AF111812) actin [Brassica napus]

Seq. No.	203439
Seq. ID	LIB3083-012-Q1-L1-E7
Method	BLASTX
NCBI GI	g169363
BLAST score	200
E value	9.0e-16
Match length	59
% identity	54
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	203440
Seq. ID	LIB3083-012-Q1-L1-F10
Method	BLASTX
NCBI GI	g2454182

BLAST score	219
E value	3.0e-18
Match length	42
% identity	98
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	203441
Seq. ID	LIB3083-012-Q1-L1-F2
Method	BLASTX
NCBI GI	g2583125
BLAST score	589
E value	3.0e-61
Match length	115
% identity	93
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	203442
Seq. ID	LIB3083-012-Q1-L1-F3
Method	BLASTX
NCBI GI	g2996096
BLAST score	465
E value	6.0e-47
Match length	87
% identity	99
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	203443
Seq. ID	LIB3083-012-Q1-L1-F6
Method	BLASTX
NCBI GI	g4138137
BLAST score	476
E value	5.0e-48
Match length	113
% identity	73
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	203444
Seq. ID	LIB3083-012-Q1-L1-F7
Method	BLASTX
NCBI GI	g267069
BLAST score	364
E value	2.0e-35
Match length	67
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	203445
Seq. ID	LIB3083-012-Q1-L1-F8
Method	BLASTX
NCBI GI	g4115377
BLAST score	436

E value	2.0e-43
Match length	112
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	203446
Seq. ID	LIB3083-012-Q1-L1-F9
Method	BLASTX
NCBI GI	g3033380
BLAST score	281
E value	9.0e-36
Match length	97
% identity	80
NCBI Description	(AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No.	203447
Seq. ID	LIB3083-012-Q1-L1-G11
Method	BLASTX
NCBI GI	g3850587
BLAST score	230
E value	1.0e-19
Match length	56
% identity	88
NCBI Description	(AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	203448
Seq. ID	LIB3083-012-Q1-L1-G3
Method	BLASTX
NCBI GI	g2104530
BLAST score	365
E value	3.0e-35
Match length	89
% identity	75
NCBI Description	(AF001308) PROLIFERA [Arabidopsis thaliana] >gi_2104548 (AF001535) AGAA.2, PROLIFERA [Arabidopsis thaliana]

Seq. No.	203449
Seq. ID	LIB3083-012-Q1-L1-G5
Method	BLASTX
NCBI GI	g2244861
BLAST score	149
E value	8.0e-10
Match length	54
% identity	57
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	203450
Seq. ID	LIB3083-012-Q1-L1-G8
Method	BLASTX
NCBI GI	g1173200
BLAST score	154
E value	4.0e-10
Match length	48
% identity	67

NCBI Description	40S RIBOSOMAL PROTEIN S14
Seq. No.	203451
Seq. ID	LIB3083-012-Q1-L1-G9
Method	BLASTN
NCBI GI	g2828187
BLAST score	32
E value	1.0e-08
Match length	48
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]
Seq. No.	203452
Seq. ID	LIB3083-012-Q1-L1-H11
Method	BLASTX
NCBI GI	g4490704
BLAST score	178
E value	3.0e-13
Match length	93
% identity	40
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]
Seq. No.	203453
Seq. ID	LIB3083-012-Q1-L1-H12
Method	BLASTX
NCBI GI	g135452
BLAST score	517
E value	6.0e-53
Match length	103
% identity	88
NCBI Description	TUBULIN BETA-1 CHAIN >gi_170060 (M21296) S-beta-1 tubulin [Glycine max]
Seq. No.	203454
Seq. ID	LIB3083-012-Q1-L1-H8
Method	BLASTX
NCBI GI	g2661840
BLAST score	339
E value	4.0e-32
Match length	100
% identity	63
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.	203455
Seq. ID	LIB3083-012-Q1-L1-H9
Method	BLASTX
NCBI GI	g2497486
BLAST score	362
E value	1.0e-34
Match length	97
% identity	77
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]
Seq. No.	203456

Seq. ID	LIB3083-013-Q1-L1-A6
Method	BLASTX
NCBI GI	g417154
BLAST score	237
E value	6.0e-20
Match length	47
% identity	91
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	203457
Seq. ID	LIB3083-013-Q1-L1-B6
Method	BLASTX
NCBI GI	g2911801
BLAST score	262
E value	7.0e-24
Match length	61
% identity	95
NCBI Description	(AF009565) alpha-tubulin [Gossypium hirsutum]

Seq. No.	203458
Seq. ID	LIB3083-013-Q1-L1-C7
Method	BLASTX
NCBI GI	g267146
BLAST score	318
E value	1.0e-29
Match length	91
% identity	70
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	203459
Seq. ID	LIB3083-013-Q1-L1-D5
Method	BLASTN
NCBI GI	g2811277
BLAST score	49
E value	8.0e-19
Match length	97
% identity	88
NCBI Description	Gossypium hirsutum expansin (GhEX1) mRNA, complete cds

Seq. No.	203460
Seq. ID	LIB3083-013-Q1-L1-E5
Method	BLASTX
NCBI GI	g4371292
BLAST score	174
E value	4.0e-13
Match length	59
% identity	57
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 203461

Seq. ID	LIB3083-013-Q1-L1-F3
Method	BLASTX
NCBI GI	g2497743
BLAST score	146
E value	3.0e-09
Match length	47
% identity	62
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	203462
Seq. ID	LIB3083-013-Q1-L1-H1
Method	BLASTX
NCBI GI	g4115377
BLAST score	162
E value	1.0e-11
Match length	42
% identity	79
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	203463
Seq. ID	LIB3083-014-Q1-L1-A1
Method	BLASTX
NCBI GI	g3522942
BLAST score	180
E value	1.0e-13
Match length	55
% identity	65
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203464
Seq. ID	LIB3083-014-Q1-L1-A11
Method	BLASTX
NCBI GI	g4056467
BLAST score	281
E value	3.0e-25
Match length	85
% identity	62
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	203465
Seq. ID	LIB3083-014-Q1-L1-A4
Method	BLASTN
NCBI GI	g166895
BLAST score	36
E value	6.0e-11
Match length	48
% identity	94
NCBI Description	A.thaliana alpha-1-tubulin gene, complete cds

Seq. No.	203466
Seq. ID	LIB3083-014-Q1-L1-A5

Method	BLASTN
NCBI GI	g451543
BLAST score	79
E value	2.0e-36
Match length	140
% identity	87
NCBI Description	Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi_1598725_gb_I18370_I18370 Sequence 25 from patent US

Seq. No.	203467
Seq. ID	LIB3083-014-Q1-L1-A6
Method	BLASTX
NCBI GI	g2827143
BLAST score	347
E value	5.0e-33
Match length	95
% identity	56
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	203468
Seq. ID	LIB3083-014-Q1-L1-B1
Method	BLASTX
NCBI GI	g3738208
BLAST score	248
E value	3.0e-21
Match length	84
% identity	58
NCBI Description	(AL031853) strong similarity to human Rev interacting protein Rip-1 [Schizosaccharomyces pombe]

Seq. No.	203469
Seq. ID	LIB3083-014-Q1-L1-B10
Method	BLASTX
NCBI GI	g2154609
BLAST score	264
E value	4.0e-23
Match length	97
% identity	58
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_ (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	203470
Seq. ID	LIB3083-014-Q1-L1-C1
Method	BLASTX
NCBI GI	g4115931
BLAST score	157
E value	1.0e-10
Match length	60
% identity	62
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	203471

Seq. ID	LIB3083-014-Q1-L1-C11
Method	BLASTX
NCBI GI	g464840
BLAST score	558
E value	1.0e-57
Match length	106
% identity	98
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	203472
Seq. ID	LIB3083-014-Q1-L1-C2
Method	BLASTX
NCBI GI	g2497753
BLAST score	167
E value	5.0e-12
Match length	82
% identity	39
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	203473
Seq. ID	LIB3083-014-Q1-L1-C3
Method	BLASTX
NCBI GI	g232024
BLAST score	534
E value	9.0e-55
Match length	115
% identity	87
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	203474
Seq. ID	LIB3083-014-Q1-L1-C4
Method	BLASTX
NCBI GI	g549060
BLAST score	163
E value	2.0e-11
Match length	53
% identity	60
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	203475
Seq. ID	LIB3083-014-Q1-L1-C6
Method	BLASTX
NCBI GI	g1694976
BLAST score	291
E value	1.0e-26

Match length	69
% identity	77
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	203476
Seq. ID	LIB3083-014-Q1-L1-C8
Method	BLASTX
NCBI GI	g3044212
BLAST score	359
E value	2.0e-34
Match length	90
% identity	74
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	203477
Seq. ID	LIB3083-014-Q1-L1-D11
Method	BLASTX
NCBI GI	g974782
BLAST score	276
E value	1.0e-24
Match length	57
% identity	96
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	203478
Seq. ID	LIB3083-014-Q1-L1-D2
Method	BLASTX
NCBI GI	g2829204
BLAST score	329
E value	7.0e-31
Match length	88
% identity	80
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	203479
Seq. ID	LIB3083-014-Q1-L1-D3
Method	BLASTX
NCBI GI	g3386600
BLAST score	325
E value	2.0e-30
Match length	70
% identity	94
NCBI Description	(AC004665) putative glycoprotein [Arabidopsis thaliana]

Seq. No.	203480
Seq. ID	LIB3083-014-Q1-L1-E10
Method	BLASTX
NCBI GI	g2995990
BLAST score	284
E value	1.0e-25
Match length	102
% identity	60
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis

thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	203481
Seq. ID	LIB3083-014-Q1-L1-E11
Method	BLASTX
NCBI GI	g4063760
BLAST score	139
E value	1.0e-08
Match length	67
% identity	42
NCBI Description	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No.	203482
Seq. ID	LIB3083-014-Q1-L1-E7
Method	BLASTX
NCBI GI	g2341034
BLAST score	204
E value	1.0e-16
Match length	43
% identity	95
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	203483
Seq. ID	LIB3083-014-Q1-L1-F11
Method	BLASTX
NCBI GI	g2129950
BLAST score	418
E value	2.0e-41
Match length	94
% identity	87
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco

Seq. No.	203484
Seq. ID	LIB3083-014-Q1-L1-G1
Method	BLASTX
NCBI GI	g3334261
BLAST score	191
E value	7.0e-15
Match length	58
% identity	50
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973) metallothionein-like protein [Malus domestica]

Seq. No.	203485
Seq. ID	LIB3083-014-Q1-L1-G10
Method	BLASTX
NCBI GI	g3851636
BLAST score	484
E value	5.0e-49
Match length	110
% identity	85
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 203486

Seq. ID	LIB3083-014-Q1-L1-G2
Method	BLASTN
NCBI GI	g606941
BLAST score	119
E value	9.0e-61
Match length	150
% identity	95
NCBI Description	Gossypium hirsutum C312 clone Fb-B6 unidentified fiber mRNA, complete cds

Seq. No.	203487
Seq. ID	LIB3083-014-Q1-L1-G6
Method	BLASTX
NCBI GI	g1871192
BLAST score	214
E value	2.0e-17
Match length	63
% identity	73
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	203488
Seq. ID	LIB3083-014-Q1-L1-G7
Method	BLASTN
NCBI GI	g2979540
BLAST score	34
E value	1.0e-09
Match length	50
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	203489
Seq. ID	LIB3083-014-Q1-L1-H6
Method	BLASTX
NCBI GI	g2564066
BLAST score	254
E value	3.0e-22
Match length	65
% identity	74
NCBI Description	(D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No.	203490
Seq. ID	LIB3083-015-Q1-L1-A1
Method	BLASTX
NCBI GI	g3309583
BLAST score	976
E value	1.0e-106
Match length	211
% identity	87
NCBI Description	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No.	203491
Seq. ID	LIB3083-015-Q1-L1-A10
Method	BLASTX
NCBI GI	g2098709

BLAST score	244
E value	6.0e-21
Match length	101
% identity	54
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	203492
Seq. ID	LIB3083-015-Q1-L1-A3
Method	BLASTX
NCBI GI	g1362046
BLAST score	483
E value	1.0e-48
Match length	124
% identity	76
NCBI Description	aspartate transaminase (EC 2.6.1.1) precursor - soybean >gi_710596 (L40579) mitochondrial aspartate aminotransferase [Glycine max]

Seq. No.	203493
Seq. ID	LIB3083-015-Q1-L1-A4
Method	BLASTX
NCBI GI	g4415936
BLAST score	159
E value	1.0e-10
Match length	142
% identity	37
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

Seq. No.	203494
Seq. ID	LIB3083-015-Q1-L1-A5
Method	BLASTX
NCBI GI	g2262170
BLAST score	530
E value	5.0e-54
Match length	186
% identity	58
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	203495
Seq. ID	LIB3083-015-Q1-L1-A8
Method	BLASTN
NCBI GI	g2865522
BLAST score	34
E value	2.0e-09
Match length	105
% identity	71
NCBI Description	Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA, complete cds

Seq. No.	203496
Seq. ID	LIB3083-015-Q1-L1-B1
Method	BLASTX
NCBI GI	g3650032
BLAST score	228
E value	6.0e-19
Match length	49

% identity	71
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	203497
Seq. ID	LIB3083-015-Q1-L1-B11
Method	BLASTX
NCBI GI	g4126473
BLAST score	430
E value	2.0e-42
Match length	137
% identity	67
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	203498
Seq. ID	LIB3083-015-Q1-L1-B2
Method	BLASTN
NCBI GI	g4165340
BLAST score	38
E value	7.0e-12
Match length	191
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	203499
Seq. ID	LIB3083-015-Q1-L1-B3
Method	BLASTX
NCBI GI	g4512659
BLAST score	332
E value	5.0e-31
Match length	142
% identity	54
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203500
Seq. ID	LIB3083-015-Q1-L1-B4
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	1.0e-19
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	203501
Seq. ID	LIB3083-015-Q1-L1-B9
Method	BLASTX
NCBI GI	g1174600
BLAST score	258
E value	1.0e-22
Match length	66
% identity	73

NCBI Description	TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717) beta-tubulin [Oryza sativa]
Seq. No.	203502
Seq. ID	LIB3083-015-Q1-L1-C12
Method	BLASTX
NCBI GI	g3927825
BLAST score	456
E value	5.0e-61
Match length	140
% identity	85
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	203503
Seq. ID	LIB3083-015-Q1-L1-C3
Method	BLASTX
NCBI GI	g4455158
BLAST score	435
E value	6.0e-43
Match length	97
% identity	82
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]
Seq. No.	203504
Seq. ID	LIB3083-015-Q1-L1-C4
Method	BLASTX
NCBI GI	g4490330
BLAST score	813
E value	3.0e-87
Match length	177
% identity	79
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]
Seq. No.	203505
Seq. ID	LIB3083-015-Q1-L1-C5
Method	BLASTX
NCBI GI	g2492636
BLAST score	481
E value	1.0e-48
Match length	104
% identity	91
NCBI Description	ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE) >gi_1084317_pir__S49849 aconitate hydratase (EC 4.2.1.3) - muskmelon (fragment) >gi_599723_emb_CAA58047_ (X82840) aconitase [Cucumis melo]
Seq. No.	203506
Seq. ID	LIB3083-015-Q1-L1-C7
Method	BLASTX
NCBI GI	g2129495
BLAST score	901
E value	2.0e-97
Match length	201
% identity	85
NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]

Seq. No.	203507
Seq. ID	LIB3083-015-Q1-L1-C8
Method	BLASTX
NCBI GI	g3618214
BLAST score	182
E value	3.0e-13
Match length	131
% identity	34
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	203508
Seq. ID	LIB3083-015-Q1-L1-C9
Method	BLASTX
NCBI GI	g170354
BLAST score	579
E value	5.0e-60
Match length	128
% identity	20
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	203509
Seq. ID	LIB3083-015-Q1-L1-D1
Method	BLASTX
NCBI GI	g421855
BLAST score	283
E value	2.0e-25
Match length	113
% identity	56
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No.	203510
Seq. ID	LIB3083-015-Q1-L1-D10
Method	BLASTX
NCBI GI	g114332
BLAST score	414
E value	2.0e-41
Match length	128
% identity	71
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35) LHA1 - tomato >gi_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum]

Seq. No.	203511
Seq. ID	LIB3083-015-Q1-L1-D11
Method	BLASTX
NCBI GI	g1563719
BLAST score	325
E value	3.0e-31
Match length	82
% identity	84

NCBI Description	(Y08320) cyclophylin [Digitalis lanata]

Seq. No.	203512
Seq. ID	LIB3083-015-Q1-L1-D12
Method	BLASTX
NCBI GI	g3287270
BLAST score	265
E value	2.0e-23
Match length	98
% identity	61
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	203513
Seq. ID	LIB3083-015-Q1-L1-D2
Method	BLASTX
NCBI GI	g3914430
BLAST score	658
E value	4.0e-69
Match length	149
% identity	86
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	203514
Seq. ID	LIB3083-015-Q1-L1-D4
Method	BLASTX
NCBI GI	g3851001
BLAST score	553
E value	7.0e-57
Match length	136
% identity	81
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No.	203515
Seq. ID	LIB3083-015-Q1-L1-D9
Method	BLASTX
NCBI GI	g267073
BLAST score	357
E value	8.0e-37
Match length	94
% identity	87
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	203516
Seq. ID	LIB3083-015-Q1-L1-E10
Method	BLASTX
NCBI GI	g4337195
BLAST score	619
E value	1.0e-64
Match length	136
% identity	88

NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	203517
Seq. ID	LIB3083-015-Q1-L1-E11
Method	BLASTX
NCBI GI	g1706958
BLAST score	500
E value	1.0e-50
Match length	123
% identity	76
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203518
Seq. ID	LIB3083-015-Q1-L1-E12
Method	BLASTX
NCBI GI	g1174592
BLAST score	537
E value	4.0e-55
Match length	108
% identity	91
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203519
Seq. ID	LIB3083-015-Q1-L1-E7
Method	BLASTX
NCBI GI	g4098129
BLAST score	305
E value	2.0e-28
Match length	68
% identity	85
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203520
Seq. ID	LIB3083-015-Q1-L1-F1
Method	BLASTX
NCBI GI	g4098129
BLAST score	845
E value	5.0e-91
Match length	168
% identity	95
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203521
Seq. ID	LIB3083-015-Q1-L1-F12
Method	BLASTX
NCBI GI	g2129825
BLAST score	497
E value	2.0e-50
Match length	115
% identity	85
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	203522
Seq. ID	LIB3083-015-Q1-L1-F2

Method	BLASTX
NCBI GI	g4098129
BLAST score	234
E value	6.0e-20
Match length	78
% identity	55
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203523
Seq. ID	LIB3083-015-Q1-L1-F5
Method	BLASTX
NCBI GI	g3135611
BLAST score	178
E value	9.0e-27
Match length	87
% identity	57
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	203524
Seq. ID	LIB3083-015-Q1-L1-F9
Method	BLASTX
NCBI GI	g477280
BLAST score	438
E value	2.0e-43
Match length	125
% identity	68
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	203525
Seq. ID	LIB3083-015-Q1-L1-G1
Method	BLASTX
NCBI GI	g1931640
BLAST score	437
E value	3.0e-43
Match length	124
% identity	63
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	203526
Seq. ID	LIB3083-015-Q1-L1-G10
Method	BLASTX
NCBI GI	g3023816
BLAST score	324
E value	5.0e-30
Match length	71
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	203527
Seq. ID	LIB3083-015-Q1-L1-G8

Method	BLASTX
NCBI GI	g3334138
BLAST score	208
E value	8.0e-17
Match length	84
% identity	51
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	203528
Seq. ID	LIB3083-015-Q1-L1-G9
Method	BLASTX
NCBI GI	g1915974
BLAST score	439
E value	1.0e-43
Match length	111
% identity	77
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	203529
Seq. ID	LIB3083-015-Q1-L1-H1
Method	BLASTX
NCBI GI	g1171577
BLAST score	307
E value	7.0e-28
Match length	170
% identity	36
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	203530
Seq. ID	LIB3083-015-Q1-L1-H10
Method	BLASTX
NCBI GI	g2267567
BLAST score	405
E value	1.0e-39
Match length	89
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	203531
Seq. ID	LIB3083-015-Q1-L1-H2
Method	BLASTX
NCBI GI	g3334138
BLAST score	214
E value	2.0e-17
Match length	75
% identity	56
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	203532
Seq. ID	LIB3083-015-Q1-L1-H3
Method	BLASTX
NCBI GI	g1706956

BLAST score	837
E value	4.0e-90
Match length	174
% identity	93
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203533
Seq. ID	LIB3083-015-Q1-L1-H4
Method	BLASTX
NCBI GI	g1332579
BLAST score	738
E value	2.0e-78
Match length	150
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	203534
Seq. ID	LIB3083-015-Q1-L1-H6
Method	BLASTX
NCBI GI	g2829204
BLAST score	505
E value	4.0e-51
Match length	120
% identity	85
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	203535
Seq. ID	LIB3083-015-Q1-L1-H9
Method	BLASTX
NCBI GI	g3023816
BLAST score	314
E value	6.0e-29
Match length	71
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	203536
Seq. ID	LIB3083-015-Q1-L2-A1
Method	BLASTX
NCBI GI	g3309583
BLAST score	791
E value	1.0e-84
Match length	169
% identity	88
NCBI Description	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No.	203537
Seq. ID	LIB3083-015-Q1-L2-A10
Method	BLASTX
NCBI GI	g2098709
BLAST score	498
E value	2.0e-50
Match length	135

% identity	72
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	203538
Seq. ID	LIB3083-015-Q1-L2-A11
Method	BLASTX
NCBI GI	g3096939
BLAST score	439
E value	1.0e-43
Match length	114
% identity	73
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	203539
Seq. ID	LIB3083-015-Q1-L2-A3
Method	BLASTX
NCBI GI	g1362046
BLAST score	519
E value	9.0e-53
Match length	130
% identity	78
NCBI Description	aspartate transaminase (EC 2.6.1.1) precursor - soybean >gi_710596 (L40579) mitochondrial aspartate aminotransferase [Glycine max]

Seq. No.	203540
Seq. ID	LIB3083-015-Q1-L2-A4
Method	BLASTX
NCBI GI	g4415936
BLAST score	222
E value	6.0e-18
Match length	95
% identity	54
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

Seq. No.	203541
Seq. ID	LIB3083-015-Q1-L2-A5
Method	BLASTX
NCBI GI	g2262170
BLAST score	536
E value	9.0e-55
Match length	187
% identity	58
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	203542
Seq. ID	LIB3083-015-Q1-L2-A6
Method	BLASTX
NCBI GI	g1310888
BLAST score	200
E value	2.0e-15
Match length	115
% identity	37
NCBI Description	Hordeum vulgare >gi_1310889_pdb_1CNS_B Hordeum vulgare

Seq. No.	203543

Seq. ID	LIB3083-015-Q1-L2-A7
Method	BLASTX
NCBI GI	g2833388
BLAST score	917
E value	2.0e-99
Match length	216
% identity	78
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	203544
Seq. ID	LIB3083-015-Q1-L2-B1
Method	BLASTX
NCBI GI	g2833388
BLAST score	474
E value	1.0e-47
Match length	124
% identity	69
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	203545
Seq. ID	LIB3083-015-Q1-L2-B11
Method	BLASTX
NCBI GI	g4126473
BLAST score	475
E value	9.0e-48
Match length	144
% identity	69
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	203546
Seq. ID	LIB3083-015-Q1-L2-B2
Method	BLASTX
NCBI GI	g3395439
BLAST score	176
E value	1.0e-12
Match length	95
% identity	43
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203547
Seq. ID	LIB3083-015-Q1-L2-B4
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	9.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No.	203548
Seq. ID	LIB3083-015-Q1-L2-B6
Method	BLASTX
NCBI GI	g132939
BLAST score	829
E value	5.0e-89
Match length	189
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	203549
Seq. ID	LIB3083-015-Q1-L2-B7
Method	BLASTX
NCBI GI	g4115377
BLAST score	491
E value	2.0e-49
Match length	197
% identity	48
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	203550
Seq. ID	LIB3083-015-Q1-L2-B8
Method	BLASTX
NCBI GI	g2104949
BLAST score	344
E value	3.0e-32
Match length	79
% identity	81
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	203551
Seq. ID	LIB3083-015-Q1-L2-B9
Method	BLASTX
NCBI GI	g1076738
BLAST score	223
E value	1.0e-18
Match length	66
% identity	68
NCBI Description	beta-tubulin R2242 - rice

Seq. No.	203552
Seq. ID	LIB3083-015-Q1-L2-C10
Method	BLASTX
NCBI GI	g1658197
BLAST score	638
E value	7.0e-67
Match length	144
% identity	83
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	203553
Seq. ID	LIB3083-015-Q1-L2-C11

Method	BLASTX
NCBI GI	g123620
BLAST score	703
E value	2.0e-74
Match length	138
% identity	98
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950 heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]

Seq. No.	203554
Seq. ID	LIB3083-015-Q1-L2-C12
Method	BLASTX
NCBI GI	g3927825
BLAST score	665
E value	5.0e-70
Match length	137
% identity	91
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	203555
Seq. ID	LIB3083-015-Q1-L2-C3
Method	BLASTX
NCBI GI	g4455158
BLAST score	453
E value	5.0e-45
Match length	98
% identity	85
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	203556
Seq. ID	LIB3083-015-Q1-L2-C4
Method	BLASTX
NCBI GI	g4490330
BLAST score	798
E value	2.0e-85
Match length	165
% identity	83
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	203557
Seq. ID	LIB3083-015-Q1-L2-C5
Method	BLASTX
NCBI GI	g1351856
BLAST score	818
E value	8.0e-88
Match length	188
% identity	84
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	203558
Seq. ID	LIB3083-015-Q1-L2-C7

Method	BLASTX
NCBI GI	g2129495
BLAST score	898
E value	4.0e-97
Match length	214
% identity	79
NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]

Seq. No.	203559
Seq. ID	LIB3083-015-Q1-L2-C8
Method	BLASTX
NCBI GI	g3618214
BLAST score	168
E value	1.0e-11
Match length	154
% identity	32
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	203560
Seq. ID	LIB3083-015-Q1-L2-C9
Method	BLASTX
NCBI GI	g100490
BLAST score	476
E value	6.0e-48
Match length	130
% identity	22
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	203561
Seq. ID	LIB3083-015-Q1-L2-D1
Method	BLASTX
NCBI GI	g2065021
BLAST score	482
E value	2.0e-48
Match length	176
% identity	57
NCBI Description	(Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana]

Seq. No.	203562
Seq. ID	LIB3083-015-Q1-L2-D11
Method	BLASTX
NCBI GI	g1563719
BLAST score	295
E value	1.0e-26
Match length	67
% identity	82
NCBI Description	(Y08320) cyclophylin [Digitalis lanata]

Seq. No.	203563
Seq. ID	LIB3083-015-Q1-L2-D12
Method	BLASTX
NCBI GI	g3287270

BLAST score	504
E value	3.0e-51
Match length	145
% identity	74
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	203564
Seq. ID	LIB3083-015-Q1-L2-D2
Method	BLASTX
NCBI GI	g3914430
BLAST score	738
E value	2.0e-78
Match length	166
% identity	87
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	203565
Seq. ID	LIB3083-015-Q1-L2-D4
Method	BLASTX
NCBI GI	g3851001
BLAST score	562
E value	6.0e-58
Match length	136
% identity	82
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No.	203566
Seq. ID	LIB3083-015-Q1-L2-D6
Method	BLASTX
NCBI GI	g3850999
BLAST score	258
E value	2.0e-22
Match length	88
% identity	60
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No.	203567
Seq. ID	LIB3083-015-Q1-L2-D7
Method	BLASTX
NCBI GI	g1173027
BLAST score	433
E value	1.0e-42
Match length	114
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	203568
Seq. ID	LIB3083-015-Q1-L2-D9
Method	BLASTX
NCBI GI	g135449
BLAST score	560

E value	9.0e-58
Match length	132
% identity	83
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]

Seq. No.	203569
Seq. ID	LIB3083-015-Q1-L2-E11
Method	BLASTX
NCBI GI	g1706958
BLAST score	527
E value	7.0e-54
Match length	136
% identity	71
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203570
Seq. ID	LIB3083-015-Q1-L2-E12
Method	BLASTX
NCBI GI	g1174592
BLAST score	680
E value	8.0e-72
Match length	130
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203571
Seq. ID	LIB3083-015-Q1-L2-E3
Method	BLASTX
NCBI GI	g4098129
BLAST score	828
E value	6.0e-89
Match length	155
% identity	99
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203572
Seq. ID	LIB3083-015-Q1-L2-E8
Method	BLASTX
NCBI GI	g2244736
BLAST score	676
E value	3.0e-71
Match length	124
% identity	100
NCBI Description	(D88415) expansin [Gossypium hirsutum]

Seq. No.	203573
Seq. ID	LIB3083-015-Q1-L2-F1
Method	BLASTX
NCBI GI	g4098129
BLAST score	952
E value	1.0e-103
Match length	190
% identity	96

NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203574
Seq. ID	LIB3083-015-Q1-L2-F11
Method	BLASTX
NCBI GI	g1173187
BLAST score	590
E value	3.0e-61
Match length	118
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	203575
Seq. ID	LIB3083-015-Q1-L2-F12
Method	BLASTX
NCBI GI	g2129825
BLAST score	141
E value	7.0e-09
Match length	71
% identity	55
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	203576
Seq. ID	LIB3083-015-Q1-L2-F2
Method	BLASTN
NCBI GI	g1143223
BLAST score	285
E value	1.0e-159
Match length	555
% identity	39
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203577
Seq. ID	LIB3083-015-Q1-L2-F3
Method	BLASTX
NCBI GI	g806310
BLAST score	192
E value	2.0e-14
Match length	166
% identity	24
NCBI Description	(J02746) proline-rich protein [Glycine max]

Seq. No.	203578
Seq. ID	LIB3083-015-Q1-L2-F5
Method	BLASTX
NCBI GI	g2827141
BLAST score	335
E value	4.0e-31
Match length	132
% identity	55
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	203579
Seq. ID	LIB3083-015-Q1-L2-F6
Method	BLASTN
NCBI GI	g1143223
BLAST score	62
E value	2.0e-26
Match length	171
% identity	24
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203580
Seq. ID	LIB3083-015-Q1-L2-F9
Method	BLASTX
NCBI GI	g2995380
BLAST score	324
E value	4.0e-30
Match length	80
% identity	76
NCBI Description	(AJ001903) thioredoxin H [Triticum durum]

Seq. No.	203581
Seq. ID	LIB3083-015-Q1-L2-G10
Method	BLASTX
NCBI GI	g3023816
BLAST score	324
E value	5.0e-30
Match length	71
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	203582
Seq. ID	LIB3083-015-Q1-L2-G11
Method	BLASTX
NCBI GI	g4406816
BLAST score	154
E value	2.0e-10
Match length	30
% identity	93
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	203583
Seq. ID	LIB3083-015-Q1-L2-G12
Method	BLASTX
NCBI GI	g3256066
BLAST score	577
E value	8.0e-60
Match length	128
% identity	88
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No.	203584
Seq. ID	LIB3083-015-Q1-L2-G3
Method	BLASTX
NCBI GI	g1912286
BLAST score	378

E value	2.0e-36
Match length	73
% identity	93
NCBI Description	(U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No.	203585
Seq. ID	LIB3083-015-Q1-L2-G8
Method	BLASTX
NCBI GI	g728777
BLAST score	328
E value	1.0e-30
Match length	124
% identity	52
NCBI Description	ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36) >gi_1498257 (L07540) replication factor C, 36-kDa subunit [Homo sapiens]

Seq. No.	203586
Seq. ID	LIB3083-015-Q1-L2-H1
Method	BLASTX
NCBI GI	g1171577
BLAST score	301
E value	3.0e-27
Match length	170
% identity	36
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	203587
Seq. ID	LIB3083-015-Q1-L2-H10
Method	BLASTX
NCBI GI	g2267567
BLAST score	394
E value	3.0e-38
Match length	85
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	203588
Seq. ID	LIB3083-015-Q1-L2-H12
Method	BLASTX
NCBI GI	g2864609
BLAST score	375
E value	4.0e-36
Match length	130
% identity	55
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	203589
Seq. ID	LIB3083-015-Q1-L2-H2

Method	BLASTX
NCBI GI	g3334138
BLAST score	242
E value	3.0e-20
Match length	85
% identity	55
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	203590
Seq. ID	LIB3083-015-Q1-L2-H3
Method	BLASTX
NCBI GI	g1706956
BLAST score	841
E value	1.0e-90
Match length	175
% identity	93
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203591
Seq. ID	LIB3083-015-Q1-L2-H4
Method	BLASTX
NCBI GI	g1332579
BLAST score	885
E value	1.0e-95
Match length	183
% identity	11
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	203592
Seq. ID	LIB3083-015-Q1-L2-H6
Method	BLASTX
NCBI GI	g2829204
BLAST score	520
E value	7.0e-53
Match length	120
% identity	88
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	203593
Seq. ID	LIB3083-015-Q1-L2-H7
Method	BLASTX
NCBI GI	g4098128
BLAST score	829
E value	4.0e-89
Match length	192
% identity	83
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203594
Seq. ID	LIB3083-015-Q1-L2-H9
Method	BLASTX
NCBI GI	g3023816
BLAST score	195
E value	7.0e-17
Match length	67

% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	203595
Seq. ID	LIB3083-016-Q1-L1-A1
Method	BLASTX
NCBI GI	g135460
BLAST score	498
E value	1.0e-50
Match length	107
% identity	90
NCBI Description	TUBULIN BETA-2 CHAIN >gi_100933_pir__S14702 tubulin beta-2 chain - maize >gi_22184_emb_CAA37061_ (X52879) beta 2 tubulin (AA 1-444) [Zea mays]

Seq. No.	203596
Seq. ID	LIB3083-016-Q1-L1-A7
Method	BLASTX
NCBI GI	g3831440
BLAST score	178
E value	4.0e-13
Match length	88
% identity	41
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	203597
Seq. ID	LIB3083-016-Q1-L1-A8
Method	BLASTX
NCBI GI	g2088662
BLAST score	162
E value	3.0e-11
Match length	64
% identity	55
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	203598
Seq. ID	LIB3083-016-Q1-L1-B1
Method	BLASTX
NCBI GI	g2924520
BLAST score	456
E value	1.0e-45
Match length	95
% identity	88
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	203599
Seq. ID	LIB3083-016-Q1-L1-B2
Method	BLASTX
NCBI GI	g3757517
BLAST score	144
E value	4.0e-09
Match length	120

% identity	7
NCBI Description	(AC005167) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No.	203600
Seq. ID	LIB3083-017-Q1-L1-A1
Method	BLASTX
NCBI GI	g3386621
BLAST score	186
E value	3.0e-14
Match length	82
% identity	28
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	203601
Seq. ID	LIB3083-017-Q1-L1-A2
Method	BLASTX
NCBI GI	g3386621
BLAST score	494
E value	5.0e-50
Match length	136
% identity	73
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	203602
Seq. ID	LIB3083-017-Q1-L1-A5
Method	BLASTX
NCBI GI	g2760347
BLAST score	457
E value	7.0e-46
Match length	92
% identity	17
NCBI Description	(U84968) ubiquitin [Arabidopsis thaliana]

Seq. No.	203603
Seq. ID	LIB3083-017-Q1-L1-A7
Method	BLASTX
NCBI GI	g3513727
BLAST score	620
E value	9.0e-65
Match length	146
% identity	85
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	203604
Seq. ID	LIB3083-017-Q1-L1-B2
Method	BLASTX
NCBI GI	g4324967
BLAST score	379
E value	4.0e-37
Match length	74
% identity	99
NCBI Description	(AF114796) ADP-ribosylation factor [Glycine max]

Seq. No.	203605
Seq. ID	LIB3083-017-Q1-L1-B4
Method	BLASTX
NCBI GI	g3193284
BLAST score	406
E value	7.0e-40
Match length	116
% identity	67
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	203606
Seq. ID	LIB3083-017-Q1-L1-C1
Method	BLASTX
NCBI GI	g2760349
BLAST score	490
E value	1.0e-49
Match length	107
% identity	19
NCBI Description	(U84969) ubiquitin [Arabidopsis thaliana]

Seq. No.	203607
Seq. ID	LIB3083-017-Q1-L1-C2
Method	BLASTX
NCBI GI	g1346194
BLAST score	283
E value	2.0e-25
Match length	85
% identity	72
NCBI Description	GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) >gi_1022797 (U37697) glutathione reductase [Arabidopsis thaliana]

Seq. No.	203608
Seq. ID	LIB3083-017-Q1-L1-C4
Method	BLASTX
NCBI GI	g3128192
BLAST score	450
E value	5.0e-45
Match length	110
% identity	76
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	203609
Seq. ID	LIB3083-017-Q1-L1-D3
Method	BLASTX
NCBI GI	g135460
BLAST score	331
E value	3.0e-31
Match length	88
% identity	74
NCBI Description	TUBULIN BETA-2 CHAIN >gi_100933_pir__S14702 tubulin beta-2 chain - maize >gi_22184_emb_CAA37061_ (X52879) beta 2 tubulin (AA 1-444) [Zea mays]

Seq. No.	203610
Seq. ID	LIB3083-017-Q1-L1-D5

Method	BLASTX
NCBI GI	g3551131
BLAST score	233
E value	1.0e-19
Match length	108
% identity	50
NCBI Description	(AB012044) plasma membrane aquaporin (PAQ1) [Raphanus sativus]

Seq. No.	203611
Seq. ID	LIB3083-017-Q1-L1-E2
Method	BLASTX
NCBI GI	g462264
BLAST score	200
E value	5.0e-16
Match length	62
% identity	65
NCBI Description	GTP-BINDING PROTEIN HFLX >gi_1361024_pir__S56398 GTPase homolog protein hflX - Escherichia coli >gi_436156 (U00005) putative GTPase required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] >gi_537014 (U14003) putative GTPase required for high frequency lysogenization by bacteriophage lambda; TTG start codon [Escherichia coli] >gi_1790615 (AE000489) GTP - binding subunit of protease specific for phage lambda cII repressor [Escherichia coli]

Seq. No.	203612
Seq. ID	LIB3083-017-Q1-L1-E5
Method	BLASTX
NCBI GI	g2065531
BLAST score	277
E value	8.0e-25
Match length	87
% identity	61
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	203613
Seq. ID	LIB3083-017-Q1-L1-E6
Method	BLASTX
NCBI GI	g4544399
BLAST score	141
E value	6.0e-09
Match length	90
% identity	37
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	203614
Seq. ID	LIB3083-017-Q1-L1-E7
Method	BLASTX
NCBI GI	g3128168
BLAST score	472
E value	2.0e-47
Match length	132
% identity	60
NCBI Description	(AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No.	203615
Seq. ID	LIB3083-017-Q1-L1-F3
Method	BLASTX
NCBI GI	g2352998
BLAST score	191
E value	2.0e-14
Match length	132
% identity	31
NCBI Description	(AF014461) EXO70 protein [Mus musculus]

Seq. No.	203616
Seq. ID	LIB3083-017-Q1-L1-F5
Method	BLASTN
NCBI GI	g2935297
BLAST score	50
E value	3.0e-19
Match length	98
% identity	89
NCBI Description	Gossypium hirsutum 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (hmg1) gene, complete cds

Seq. No.	203617
Seq. ID	LIB3083-017-Q1-L1-F7
Method	BLASTX
NCBI GI	g464734
BLAST score	236
E value	7.0e-20
Match length	55
% identity	85
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No.	203618
Seq. ID	LIB3083-017-Q1-L1-G1
Method	BLASTX
NCBI GI	g2244799
BLAST score	390
E value	8.0e-38
Match length	122
% identity	60
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	203619
Seq. ID	LIB3083-017-Q1-L1-G5
Method	BLASTX
NCBI GI	g3668084
BLAST score	330
E value	3.0e-31
Match length	78
% identity	78
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	203620
Seq. ID	LIB3083-017-Q1-L1-H3
Method	BLASTX
NCBI GI	g4220476
BLAST score	513
E value	3.0e-52
Match length	135
% identity	70
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	203621
Seq. ID	LIB3083-017-Q1-L1-H5
Method	BLASTX
NCBI GI	g3023187
BLAST score	634
E value	2.0e-66
Match length	140
% identity	89
NCBI Description	14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi_1773328 (U80070) 14-3-3-like protein [Mesembryanthemum crystallinum]

Seq. No.	203622
Seq. ID	LIB3083-017-Q1-L1-H7
Method	BLASTX
NCBI GI	g267069
BLAST score	683
E value	4.0e-72
Match length	128
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	203623
Seq. ID	LIB3083-018-Q1-L1-A1
Method	BLASTX
NCBI GI	g3386621
BLAST score	391
E value	4.0e-38
Match length	95
% identity	80
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	203624
Seq. ID	LIB3083-018-Q1-L1-A3
Method	BLASTX
NCBI GI	g3386621
BLAST score	277
E value	6.0e-25
Match length	85
% identity	69
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	203625
Seq. ID	LIB3083-018-Q1-L1-A6

Method	BLASTX
NCBI GI	g3513727
BLAST score	236
E value	6.0e-20
Match length	95
% identity	60
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	203626
Seq. ID	LIB3083-018-Q1-L1-C1
Method	BLASTX
NCBI GI	g3128192
BLAST score	493
E value	6.0e-50
Match length	122
% identity	76
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	203627
Seq. ID	LIB3083-018-Q1-L1-C6
Method	BLASTX
NCBI GI	g3128192
BLAST score	257
E value	2.0e-22
Match length	89
% identity	58
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	203628
Seq. ID	LIB3083-018-Q1-L1-E1
Method	BLASTX
NCBI GI	g1743277
BLAST score	543
E value	9.0e-56
Match length	108
% identity	94
NCBI Description	(Y09741) beta-tubulin 1 [Hordeum vulgare]

Seq. No.	203629
Seq. ID	LIB3083-018-Q1-L1-E3
Method	BLASTX
NCBI GI	g1729846
BLAST score	213
E value	8.0e-23
Match length	115
% identity	52
NCBI Description	TUBULIN BETA CHAIN 3 >gi_1155203_emb_CAA91941_ (Z67993) beta-tubulin [Porphyra purpurea]

Seq. No.	203630
Seq. ID	LIB3083-018-Q1-L1-E6
Method	BLASTX
NCBI GI	g267072

BLAST score	177
E value	4.0e-13
Match length	81
% identity	43
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100072_pir__S20868 tubulin beta-1 chain - garden pea >gi_20758_emb_CAA38613_ (X54844) beta-tubulin 1 [Pisum sativum]

Seq. No.	203631
Seq. ID	LIB3083-020-Q1-L1-A6
Method	BLASTX
NCBI GI	g3738291
BLAST score	205
E value	3.0e-16
Match length	75
% identity	49
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	203632
Seq. ID	LIB3083-020-Q1-L1-A8
Method	BLASTX
NCBI GI	g3650032
BLAST score	233
E value	2.0e-19
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	203633
Seq. ID	LIB3083-020-Q1-L1-B10
Method	BLASTX
NCBI GI	g115492
BLAST score	631
E value	3.0e-66
Match length	123
% identity	57
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	203634
Seq. ID	LIB3083-020-Q1-L1-B11
Method	BLASTX
NCBI GI	g4510400
BLAST score	503
E value	4.0e-51
Match length	132
% identity	72
NCBI Description	(AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No.	203635
Seq. ID	LIB3083-020-Q1-L1-B12
Method	BLASTX
NCBI GI	g3395431
BLAST score	170
E value	5.0e-12

Match length	80
% identity	42
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	203636
Seq. ID	LIB3083-020-Q1-L1-B2
Method	BLASTX
NCBI GI	g3153906
BLAST score	492
E value	9.0e-50
Match length	144
% identity	72
NCBI Description	(AF066078) S-adenosylmethionine decarboxylase [Helianthus annuus]

Seq. No.	203637
Seq. ID	LIB3083-020-Q1-L1-B3
Method	BLASTX
NCBI GI	g1174592
BLAST score	591
E value	2.0e-61
Match length	138
% identity	86
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	203638
Seq. ID	LIB3083-020-Q1-L1-B4
Method	BLASTX
NCBI GI	g4415994
BLAST score	394
E value	2.0e-38
Match length	80
% identity	94
NCBI Description	(AF059289) beta-tubulin 3 [Eleusine indica]

Seq. No.	203639
Seq. ID	LIB3083-020-Q1-L1-B5
Method	BLASTX
NCBI GI	g3377797
BLAST score	439
E value	1.0e-43
Match length	117
% identity	73
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	203640
Seq. ID	LIB3083-020-Q1-L1-B6
Method	BLASTX
NCBI GI	g4158219
BLAST score	383
E value	4.0e-37

Match length	114
% identity	65
NCBI Description	(Y18623) amylogenin [Oryza sativa]

Seq. No.	203641
Seq. ID	LIB3083-020-Q1-L1-B8
Method	BLASTX
NCBI GI	g4204300
BLAST score	208
E value	2.0e-16
Match length	79
% identity	52
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	203642
Seq. ID	LIB3083-020-Q1-L1-C1
Method	BLASTX
NCBI GI	g832876
BLAST score	498
E value	1.0e-50
Match length	113
% identity	84
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	203643
Seq. ID	LIB3083-020-Q1-L1-C2
Method	BLASTX
NCBI GI	g1086250
BLAST score	251
E value	2.0e-21
Match length	114
% identity	46
NCBI Description	SUC1-sucrose proton symporter - Plantago major >gi_667047_emb_CAA59113_ (X84379) SUC1-sucrose proton symporter [Plantago major]

Seq. No.	203644
Seq. ID	LIB3083-020-Q1-L1-C7
Method	BLASTX
NCBI GI	g1174613
BLAST score	662
E value	1.0e-69
Match length	136
% identity	96
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	203645
Seq. ID	LIB3083-020-Q1-L1-D1
Method	BLASTX
NCBI GI	g2244860
BLAST score	244
E value	9.0e-21

Match length	127
% identity	46
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	203646
Seq. ID	LIB3083-020-Q1-L1-D3
Method	BLASTX
NCBI GI	g3882211
BLAST score	304
E value	1.0e-27
Match length	130
% identity	47
NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]

Seq. No.	203647
Seq. ID	LIB3083-020-Q1-L1-D4
Method	BLASTX
NCBI GI	g3243234
BLAST score	523
E value	2.0e-53
Match length	132
% identity	77
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	203648
Seq. ID	LIB3083-020-Q1-L1-D5
Method	BLASTX
NCBI GI	g881625
BLAST score	342
E value	2.0e-32
Match length	68
% identity	94
NCBI Description	(U29432) 22.8 kDa protein [Ipomoea trifida]

Seq. No.	203649
Seq. ID	LIB3083-020-Q1-L1-D6
Method	BLASTX
NCBI GI	g3318611
BLAST score	467
E value	7.0e-47
Match length	128
% identity	73
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	203650
Seq. ID	LIB3083-020-Q1-L1-D7
Method	BLASTX
NCBI GI	g2388580
BLAST score	376
E value	8.0e-39
Match length	117
% identity	68
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	203651
Seq. ID	LIB3083-020-Q1-L1-E11
Method	BLASTN
NCBI GI	g2829205
BLAST score	323
E value	0.0e+00
Match length	371
% identity	18
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	203652
Seq. ID	LIB3083-020-Q1-L1-E12
Method	BLASTX
NCBI GI	g3377850
BLAST score	239
E value	3.0e-20
Match length	66
% identity	76
NCBI Description	(AF076274) contains simlarity to Canis familiaris signal peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis thaliana]

Seq. No.	203653
Seq. ID	LIB3083-020-Q1-L1-E4
Method	BLASTX
NCBI GI	g2306917
BLAST score	380
E value	1.0e-36
Match length	90
% identity	83
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	203654
Seq. ID	LIB3083-020-Q1-L1-E5
Method	BLASTX
NCBI GI	g4185143
BLAST score	212
E value	4.0e-17
Match length	70
% identity	60
NCBI Description	(AC005724) putative signal recognition particle receptor beta subunit [Arabidopsis thaliana]

Seq. No.	203655
Seq. ID	LIB3083-020-Q1-L1-E8
Method	BLASTX
NCBI GI	g2829204
BLAST score	494
E value	5.0e-50
Match length	116
% identity	85
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No. 203656

Seq. ID	LIB3083-020-Q1-L1-F10
Method	BLASTX
NCBI GI	g4220482
BLAST score	362
E value	1.0e-34
Match length	119
% identity	36
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203657
Seq. ID	LIB3083-020-Q1-L1-F12
Method	BLASTX
NCBI GI	g4467111
BLAST score	305
E value	5.0e-28
Match length	101
% identity	56
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	203658
Seq. ID	LIB3083-020-Q1-L1-F2
Method	BLASTX
NCBI GI	g320558
BLAST score	297
E value	5.0e-27
Match length	99
% identity	63
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	203659
Seq. ID	LIB3083-020-Q1-L1-F3
Method	BLASTX
NCBI GI	g4455234
BLAST score	198
E value	2.0e-15
Match length	54
% identity	67
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	203660
Seq. ID	LIB3083-020-Q1-L1-F4
Method	BLASTX
NCBI GI	g3297823
BLAST score	247
E value	4.0e-21
Match length	73
% identity	71
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	203661
Seq. ID	LIB3083-020-Q1-L1-F6
Method	BLASTX
NCBI GI	g4468812
BLAST score	395
E value	2.0e-38
Match length	97

% identity	46
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	203662
Seq. ID	LIB3083-020-Q1-L1-G3
Method	BLASTN
NCBI GI	g19212
BLAST score	64
E value	1.0e-27
Match length	238
% identity	25
NCBI Description	Tomato extensin mRNA (clone w17-1)

Seq. No.	203663
Seq. ID	LIB3083-020-Q1-L1-G8
Method	BLASTX
NCBI GI	g2982453
BLAST score	532
E value	1.0e-54
Match length	124
% identity	82
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	203664
Seq. ID	LIB3083-020-Q1-L1-H11
Method	BLASTX
NCBI GI	g2288887
BLAST score	466
E value	6.0e-47
Match length	107
% identity	85
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	203665
Seq. ID	LIB3083-020-Q1-L1-H4
Method	BLASTX
NCBI GI	g462141
BLAST score	244
E value	8.0e-21
Match length	49
% identity	90
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH) >gi_1085816_pir__S38570 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Atriplex nummularia >gi_409575 (U02886) glyceraldehyde-3-phosphate dehydrogenase [Atriplex nummularia] >gi_414607_emb_CAA53269_ (X75597) glyceraldehyde-3-phosphate dehydrogenase [Atriplex nummularia]

Seq. No.	203666
Seq. ID	LIB3083-020-Q1-L1-H8

Method	BLASTX
NCBI GI	g2118017
BLAST score	592
E value	2.0e-61
Match length	133
% identity	74
NCBI Description	non-S-RNase (EC 3.1.-.-) - Japanese pear >gi_1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus pyrifolia]

Seq. No.	203667
Seq. ID	LIB3083-021-Q1-L1-A1
Method	BLASTX
NCBI GI	g3136336
BLAST score	495
E value	2.0e-50
Match length	107
% identity	54
NCBI Description	(AF064552) calmodulin; Cam [Apium graveolens]

Seq. No.	203668
Seq. ID	LIB3083-021-Q1-L1-A10
Method	BLASTX
NCBI GI	g3643607
BLAST score	581
E value	3.0e-60
Match length	129
% identity	43
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	203669
Seq. ID	LIB3083-021-Q1-L1-A12
Method	BLASTN
NCBI GI	g18502
BLAST score	33
E value	5.0e-09
Match length	81
% identity	85
NCBI Description	G.hirsutum Lea5 gene for late embryogenesis abundant protein

Seq. No.	203670
Seq. ID	LIB3083-021-Q1-L1-A2
Method	BLASTX
NCBI GI	g2245108
BLAST score	443
E value	4.0e-44
Match length	128
% identity	62
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	203671
Seq. ID	LIB3083-021-Q1-L1-A3
Method	BLASTX
NCBI GI	g465820
BLAST score	300
E value	2.0e-27

Match length	88
% identity	60
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi_280536_pir__S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154) C40H1.6 [Caenorhabditis elegans]

Seq. No.	203672
Seq. ID	LIB3083-021-Q1-L1-A4
Method	BLASTX
NCBI GI	g2290780
BLAST score	441
E value	8.0e-44
Match length	140
% identity	70
NCBI Description	(AF002667) heat shock cognate protein [Solanum commersonii]

Seq. No.	203673
Seq. ID	LIB3083-021-Q1-L1-A5
Method	BLASTX
NCBI GI	g3695388
BLAST score	207
E value	2.0e-16
Match length	86
% identity	43
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	203674
Seq. ID	LIB3083-021-Q1-L1-A6
Method	BLASTX
NCBI GI	g2253583
BLAST score	257
E value	3.0e-22
Match length	102
% identity	62
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203675
Seq. ID	LIB3083-021-Q1-L1-A9
Method	BLASTX
NCBI GI	g2129770
BLAST score	298
E value	4.0e-27
Match length	71
% identity	72
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	203676
Seq. ID	LIB3083-021-Q1-L1-B10
Method	BLASTX
NCBI GI	g1762945
BLAST score	240
E value	3.0e-20

Match length	57
% identity	81
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	203677
Seq. ID	LIB3083-021-Q1-L1-B11
Method	BLASTX
NCBI GI	g2811278
BLAST score	457
E value	1.0e-45
Match length	118
% identity	73
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	203678
Seq. ID	LIB3083-021-Q1-L1-B2
Method	BLASTX
NCBI GI	g584794
BLAST score	300
E value	3.0e-27
Match length	86
% identity	67
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170289 (M80489) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]

Seq. No.	203679
Seq. ID	LIB3083-021-Q1-L1-B4
Method	BLASTX
NCBI GI	g4210330
BLAST score	553
E value	6.0e-57
Match length	128
% identity	81
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	203680
Seq. ID	LIB3083-021-Q1-L1-B5
Method	BLASTN
NCBI GI	g1143223
BLAST score	196
E value	1.0e-106
Match length	423
% identity	33
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203681
Seq. ID	LIB3083-021-Q1-L1-B7
Method	BLASTX
NCBI GI	g3283220
BLAST score	524
E value	2.0e-53
Match length	143
% identity	34

NCBI Description	(AF061241) splicing factor hPRP17 [Homo sapiens]

Seq. No.	203682
Seq. ID	LIB3083-021-Q1-L1-B9
Method	BLASTX
NCBI GI	g3925703
BLAST score	552
E value	6.0e-57
Match length	125
% identity	87
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	203683
Seq. ID	LIB3083-021-Q1-L1-C12
Method	BLASTX
NCBI GI	g2706450
BLAST score	218
E value	1.0e-17
Match length	48
% identity	85
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	203684
Seq. ID	LIB3083-021-Q1-L1-C3
Method	BLASTX
NCBI GI	g4325370
BLAST score	307
E value	4.0e-28
Match length	91
% identity	63
NCBI Description	(AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]

Seq. No.	203685
Seq. ID	LIB3083-021-Q1-L1-C4
Method	BLASTX
NCBI GI	g267069
BLAST score	599
E value	2.0e-62
Match length	112
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	203686
Seq. ID	LIB3083-021-Q1-L1-C6
Method	BLASTX
NCBI GI	g3513727
BLAST score	581
E value	3.0e-60
Match length	138
% identity	44
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:

kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	203687
Seq. ID	LIB3083-021-Q1-L1-C9
Method	BLASTX
NCBI GI	g4406814
BLAST score	322
E value	7.0e-30
Match length	90
% identity	70
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	203688
Seq. ID	LIB3083-021-Q1-L1-D12
Method	BLASTX
NCBI GI	g1174749
BLAST score	545
E value	5.0e-56
Match length	129
% identity	83
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_1362177_pir__S53760 triose-phosphate isomerase (EC 5.3.1.1), cytosolic - rye >gi_407525_emb_CAA81487_ (Z26875) triosephosphate isomerase [Secale cereale] >gi_1095493_prf__2109226A triosephosphate isomerase [Secale cereale]

Seq. No.	203689
Seq. ID	LIB3083-021-Q1-L1-D2
Method	BLASTX
NCBI GI	g2661840
BLAST score	235
E value	9.0e-20
Match length	64
% identity	72
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	203690
Seq. ID	LIB3083-021-Q1-L1-E2
Method	BLASTX
NCBI GI	g2435518
BLAST score	334
E value	2.0e-31
Match length	103
% identity	67
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	203691
Seq. ID	LIB3083-021-Q1-L1-E3
Method	BLASTX
NCBI GI	g1769895
BLAST score	420
E value	1.0e-41

Match length	117
% identity	76
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	203692
Seq. ID	LIB3083-021-Q1-L1-E5
Method	BLASTX
NCBI GI	g1769895
BLAST score	491
E value	1.0e-49
Match length	130
% identity	73
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	203693
Seq. ID	LIB3083-021-Q1-L1-E6
Method	BLASTX
NCBI GI	g4454468
BLAST score	590
E value	3.0e-61
Match length	143
% identity	76
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	203694
Seq. ID	LIB3083-021-Q1-L1-F1
Method	BLASTX
NCBI GI	g485742
BLAST score	539
E value	2.0e-55
Match length	117
% identity	91
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	203695
Seq. ID	LIB3083-021-Q1-L1-F11
Method	BLASTX
NCBI GI	g100525
BLAST score	509
E value	7.0e-52
Match length	103
% identity	23
NCBI Description	ubiquitin precursor UbB2 - common sunflower (fragment) >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein [Helianthus annuus]

Seq. No.	203696
Seq. ID	LIB3083-021-Q1-L1-F2
Method	BLASTX
NCBI GI	g2661840
BLAST score	468
E value	6.0e-47
Match length	139
% identity	63
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	203697
Seq. ID	LIB3083-021-Q1-L1-F3
Method	BLASTX
NCBI GI	g2909783
BLAST score	516
E value	1.0e-52
Match length	129
% identity	41
NCBI Description	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	203698
Seq. ID	LIB3083-021-Q1-L1-F4
Method	BLASTX
NCBI GI	g2564237
BLAST score	272
E value	3.0e-24
Match length	67
% identity	78
NCBI Description	(Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	203699
Seq. ID	LIB3083-021-Q1-L1-F6
Method	BLASTX
NCBI GI	g1694976
BLAST score	387
E value	2.0e-37
Match length	85
% identity	84
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	203700
Seq. ID	LIB3083-021-Q1-L1-F7
Method	BLASTX
NCBI GI	g3511285
BLAST score	216
E value	2.0e-28
Match length	104
% identity	63
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	203701
Seq. ID	LIB3083-021-Q1-L1-F8
Method	BLASTX
NCBI GI	g1706956
BLAST score	748
E value	9.0e-80
Match length	142
% identity	99
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	203702
Seq. ID	LIB3083-021-Q1-L1-F9
Method	BLASTX

NCBI GI	g3128176
BLAST score	182
E value	2.0e-13
Match length	119
% identity	34
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	203703
Seq. ID	LIB3083-021-Q1-L1-G1
Method	BLASTX
NCBI GI	g485742
BLAST score	432
E value	8.0e-43
Match length	114
% identity	80
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	203704
Seq. ID	LIB3083-021-Q1-L1-G11
Method	BLASTX
NCBI GI	g2129840
BLAST score	453
E value	3.0e-45
Match length	130
% identity	68
NCBI Description	nucleosome assembly protein 1 - soybean >gi_1161252 (L38856) nucleosome assembly protein 1 [Glycine max]

Seq. No.	203705
Seq. ID	LIB3083-021-Q1-L1-G12
Method	BLASTX
NCBI GI	g461498
BLAST score	464
E value	1.0e-46
Match length	130
% identity	70
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	203706
Seq. ID	LIB3083-021-Q1-L1-G2
Method	BLASTN
NCBI GI	g1143223
BLAST score	35
E value	3.0e-10
Match length	127
% identity	83
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203707
Seq. ID	LIB3083-021-Q1-L1-G3
Method	BLASTX
NCBI GI	g2979562
BLAST score	179

E value	2.0e-13
Match length	86
% identity	50
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	203708
Seq. ID	LIB3083-021-Q1-L1-G5
Method	BLASTX
NCBI GI	g1360141
BLAST score	169
E value	6.0e-12
Match length	109
% identity	43
NCBI Description	(X97980) protein kinase [Solanum berthaultii]

Seq. No.	203709
Seq. ID	LIB3083-021-Q1-L1-G6
Method	BLASTX
NCBI GI	g2829204
BLAST score	505
E value	3.0e-51
Match length	120
% identity	85
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	203710
Seq. ID	LIB3083-021-Q1-L1-G7
Method	BLASTX
NCBI GI	g1345501
BLAST score	618
E value	1.0e-64
Match length	137
% identity	89
NCBI Description	(X59517) glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]

Seq. No.	203711
Seq. ID	LIB3083-021-Q1-L1-G8
Method	BLASTX
NCBI GI	g2497743
BLAST score	164
E value	2.0e-11
Match length	57
% identity	58
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	203712
Seq. ID	LIB3083-021-Q1-L1-H1
Method	BLASTX
NCBI GI	g4455206
BLAST score	503

E value	4.0e-51
Match length	138
% identity	75
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	203713
Seq. ID	LIB3083-021-Q1-L1-H10
Method	BLASTX
NCBI GI	g125887
BLAST score	189
E value	3.0e-14
Match length	95
% identity	46
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	203714
Seq. ID	LIB3083-021-Q1-L1-H11
Method	BLASTX
NCBI GI	g1854386
BLAST score	404
E value	2.0e-39
Match length	100
% identity	77
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	203715
Seq. ID	LIB3083-021-Q1-L1-H3
Method	BLASTX
NCBI GI	g3176669
BLAST score	335
E value	2.0e-31
Match length	135
% identity	54
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	203716
Seq. ID	LIB3083-021-Q1-L1-H5
Method	BLASTX
NCBI GI	g4105772
BLAST score	242
E value	4.0e-21
Match length	54
% identity	40
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	203717
Seq. ID	LIB3083-021-Q1-L1-H6
Method	BLASTX
NCBI GI	g2833311
BLAST score	249
E value	3.0e-21
Match length	64

% identity	69
NCBI Description	HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi_630728_pir__S43605 R07E5.13 protein (clone R07E5) - Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683) R07E5.13 [Caenorhabditis elegans]

Seq. No.	203718
Seq. ID	LIB3083-021-Q1-L1-H7
Method	BLASTX
NCBI GI	g2935416
BLAST score	427
E value	3.0e-42
Match length	111
% identity	78
NCBI Description	(AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No.	203719
Seq. ID	LIB3083-022-Q1-L1-A12
Method	BLASTX
NCBI GI	g464850
BLAST score	214
E value	3.0e-17
Match length	55
% identity	76
NCBI Description	TUBULIN BETA-1 CHAIN >gi_421783_pir__S32668 tubulin beta-1 chain - fern (Anemia phyllitidis) >gi_296498_emb_CAA48929_ (X69185) beta tubulin 1 [Anemia phyllitidis]

Seq. No.	203720
Seq. ID	LIB3083-022-Q1-L1-A3
Method	BLASTX
NCBI GI	g1706958
BLAST score	298
E value	4.0e-27
Match length	67
% identity	87
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	203721
Seq. ID	LIB3083-022-Q1-L1-A4
Method	BLASTX
NCBI GI	g3298474
BLAST score	566
E value	2.0e-58
Match length	137
% identity	82
NCBI Description	(AB012765) ovp1 [Oryza sativa]

Seq. No.	203722
Seq. ID	LIB3083-022-Q1-L1-A5
Method	BLASTX
NCBI GI	g1710551
BLAST score	253
E value	9.0e-22
Match length	49
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_

(X95458) ribosomal protein L39 [Zea mays]

Seq. No.	203723
Seq. ID	LIB3083-022-Q1-L1-A9
Method	BLASTX
NCBI GI	g2275196
BLAST score	439
E value	1.0e-43
Match length	90
% identity	93
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No.	203724
Seq. ID	LIB3083-022-Q1-L1-B10
Method	BLASTX
NCBI GI	g3273828
BLAST score	171
E value	3.0e-12
Match length	95
% identity	45
NCBI Description	(AF068686) nodule-enhanced malate dehydrogenase [Glycine max]

Seq. No.	203725
Seq. ID	LIB3083-022-Q1-L1-B11
Method	BLASTN
NCBI GI	g3873174
BLAST score	40
E value	4.0e-13
Match length	98
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	203726
Seq. ID	LIB3083-022-Q1-L1-B3
Method	BLASTX
NCBI GI	g2275210
BLAST score	284
E value	2.0e-25
Match length	111
% identity	51
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	203727
Seq. ID	LIB3083-022-Q1-L1-B4
Method	BLASTX
NCBI GI	g4006890
BLAST score	407
E value	8.0e-40
Match length	81
% identity	89
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	203728
Seq. ID	LIB3083-022-Q1-L1-B5
Method	BLASTX
NCBI GI	g1657948
BLAST score	511
E value	5.0e-52
Match length	126
% identity	79
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	203729
Seq. ID	LIB3083-022-Q1-L1-B7
Method	BLASTX
NCBI GI	g116923
BLAST score	301
E value	2.0e-27
Match length	134
% identity	47
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	203730
Seq. ID	LIB3083-022-Q1-L1-B8
Method	BLASTX
NCBI GI	g2130139
BLAST score	245
E value	7.0e-21
Match length	105
% identity	49
NCBI Description	hypothetical protein - maize >gi_949980_emb_CAA61258_ (X88779) orf [Zea mays]

Seq. No.	203731
Seq. ID	LIB3083-022-Q1-L1-B9
Method	BLASTX
NCBI GI	g585876
BLAST score	426
E value	5.0e-42
Match length	123
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026 ribosomal protein L25 - common tobacco >gi_310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No.	203732
Seq. ID	LIB3083-022-Q1-L1-C1
Method	BLASTX
NCBI GI	g1703375
BLAST score	525
E value	1.0e-53
Match length	102
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	203733
Seq. ID	LIB3083-022-Q1-L1-C10
Method	BLASTX
NCBI GI	g3212877
BLAST score	424
E value	8.0e-42
Match length	127
% identity	66
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	203734
Seq. ID	LIB3083-022-Q1-L1-C2
Method	BLASTX
NCBI GI	g3114901
BLAST score	233
E value	2.0e-19
Match length	69
% identity	68
NCBI Description	(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi_3114905_emb_CAA06709_ (AJ005806) pceberh [Populus balsamifera subsp. trichocarpa]

Seq. No.	203735
Seq. ID	LIB3083-022-Q1-L1-C3
Method	BLASTX
NCBI GI	g2827700
BLAST score	414
E value	1.0e-40
Match length	106
% identity	75
NCBI Description	(AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No.	203736
Seq. ID	LIB3083-022-Q1-L1-C4
Method	BLASTX
NCBI GI	g1172811
BLAST score	645
E value	9.0e-68
Match length	125
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor suppresser [Oryza sativa]

Seq. No.	203737
Seq. ID	LIB3083-022-Q1-L1-C7
Method	BLASTX
NCBI GI	g3386619
BLAST score	226
E value	1.0e-18
Match length	95
% identity	49
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203738

Seq. ID	LIB3083-022-Q1-L1-C9
Method	BLASTX
NCBI GI	g1709970
BLAST score	457
E value	1.0e-45
Match length	125
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	203739
Seq. ID	LIB3083-022-Q1-L1-D1
Method	BLASTX
NCBI GI	g3337361
BLAST score	523
E value	2.0e-53
Match length	135
% identity	69
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	203740
Seq. ID	LIB3083-022-Q1-L1-D2
Method	BLASTX
NCBI GI	g1881585
BLAST score	283
E value	3.0e-25
Match length	94
% identity	69
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	203741
Seq. ID	LIB3083-022-Q1-L1-D3
Method	BLASTX
NCBI GI	g3236238
BLAST score	446
E value	2.0e-44
Match length	140
% identity	68
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	203742
Seq. ID	LIB3083-022-Q1-L1-D6
Method	BLASTX
NCBI GI	g3334138
BLAST score	523
E value	2.0e-53
Match length	114
% identity	81
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	203743
Seq. ID	LIB3083-022-Q1-L1-D9
Method	BLASTX
NCBI GI	g4033424
BLAST score	596

E value	4.0e-62
Match length	121
% identity	89
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No.	203744
Seq. ID	LIB3083-022-Q1-L1-E10
Method	BLASTX
NCBI GI	g1170508
BLAST score	350
E value	4.0e-33
Match length	99
% identity	71
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir__S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No.	203745
Seq. ID	LIB3083-022-Q1-L1-E12
Method	BLASTX
NCBI GI	g3450889
BLAST score	187
E value	1.0e-14
Match length	58
% identity	64
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	203746
Seq. ID	LIB3083-022-Q1-L1-E2
Method	BLASTX
NCBI GI	g4539383
BLAST score	374
E value	4.0e-36
Match length	95
% identity	69
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	203747
Seq. ID	LIB3083-022-Q1-L1-E3
Method	BLASTX
NCBI GI	g3935181
BLAST score	644
E value	1.0e-67
Match length	138
% identity	84
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	203748
Seq. ID	LIB3083-022-Q1-L1-E4
Method	BLASTX

NCBI GI	g1717854
BLAST score	155
E value	3.0e-10
Match length	48
% identity	52
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1072368_emb_CAA63351_ (X92663) ubiquitin-conjugating enzyme UbcD2 [Drosophila melanogaster]

Seq. No.	203749
Seq. ID	LIB3083-022-Q1-L1-E5
Method	BLASTX
NCBI GI	g1732511
BLAST score	445
E value	3.0e-44
Match length	109
% identity	76
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	203750
Seq. ID	LIB3083-022-Q1-L1-E6
Method	BLASTX
NCBI GI	g2570047
BLAST score	173
E value	2.0e-12
Match length	118
% identity	30
NCBI Description	(Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No.	203751
Seq. ID	LIB3083-022-Q1-L1-E7
Method	BLASTX
NCBI GI	g584928
BLAST score	326
E value	2.0e-30
Match length	121
% identity	46
NCBI Description	ENDOCHITINASE CH25 PRECURSOR >gi_2118034_pir__S59953 chitinase (EC 3.2.1.14) class I precursor - rape >gi_167130 (M95835) endochitinase [Brassica napus]

Seq. No.	203752
Seq. ID	LIB3083-022-Q1-L1-E8
Method	BLASTX
NCBI GI	g2811278
BLAST score	532
E value	2.0e-54
Match length	133
% identity	74
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	203753
Seq. ID	LIB3083-022-Q1-L1-F1
Method	BLASTN
NCBI GI	g1143223

BLAST score	148
E value	1.0e-77
Match length	386
% identity	49
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.	203754
Seq. ID	LIB3083-022-Q1-L1-F11
Method	BLASTX
NCBI GI	g4204300
BLAST score	200
E value	7.0e-16
Match length	74
% identity	59
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	203755
Seq. ID	LIB3083-022-Q1-L1-F3
Method	BLASTX
NCBI GI	g1839188
BLAST score	244
E value	1.0e-36
Match length	117
% identity	72
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	203756
Seq. ID	LIB3083-022-Q1-L1-F5
Method	BLASTX
NCBI GI	g71498
BLAST score	294
E value	8.0e-27
Match length	95
% identity	63
NCBI Description	heat shock protein 17.7 - garden pea

Seq. No.	203757
Seq. ID	LIB3083-022-Q1-L1-F7
Method	BLASTX
NCBI GI	g3176709
BLAST score	199
E value	2.0e-15
Match length	68
% identity	47
NCBI Description	(AC002392) putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana]

Seq. No.	203758
Seq. ID	LIB3083-022-Q1-L1-F8
Method	BLASTX
NCBI GI	g1825645
BLAST score	276
E value	2.0e-24
Match length	72
% identity	68
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana

ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No.	203759
Seq. ID	LIB3083-022-Q1-L1-F9
Method	BLASTX
NCBI GI	g3935145
BLAST score	294
E value	1.0e-26
Match length	84
% identity	64
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	203760
Seq. ID	LIB3083-022-Q1-L1-G1
Method	BLASTX
NCBI GI	g4105561
BLAST score	692
E value	3.0e-73
Match length	140
% identity	96
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	203761
Seq. ID	LIB3083-022-Q1-L1-G2
Method	BLASTX
NCBI GI	g4063751
BLAST score	201
E value	1.0e-15
Match length	124
% identity	30
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	203762
Seq. ID	LIB3083-022-Q1-L1-G4
Method	BLASTX
NCBI GI	g3980406
BLAST score	447
E value	2.0e-44
Match length	135
% identity	67
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	203763
Seq. ID	LIB3083-022-Q1-L1-G7
Method	BLASTX
NCBI GI	g2623297
BLAST score	174
E value	2.0e-12
Match length	99
% identity	40
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	203764
Seq. ID	LIB3083-022-Q1-L1-G9
Method	BLASTX
NCBI GI	g135452
BLAST score	417
E value	2.0e-41
Match length	82
% identity	96
NCBI Description	TUBULIN BETA-1 CHAIN >gi_170060 (M21296) S-beta-1 tubulin [Glycine max]

Seq. No.	203765
Seq. ID	LIB3083-022-Q1-L1-H1
Method	BLASTX
NCBI GI	g3135264
BLAST score	181
E value	2.0e-13
Match length	43
% identity	79
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	203766
Seq. ID	LIB3083-022-Q1-L1-H2
Method	BLASTX
NCBI GI	g584794
BLAST score	435
E value	4.0e-43
Match length	133
% identity	68
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170289 (M80489) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]

Seq. No.	203767
Seq. ID	LIB3083-022-Q1-L1-H6
Method	BLASTX
NCBI GI	g3738257
BLAST score	396
E value	1.0e-38
Match length	90
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	203768
Seq. ID	LIB3083-022-Q1-L1-H7
Method	BLASTN
NCBI GI	g2980787
BLAST score	38
E value	5.0e-12
Match length	74
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	203769

Seq. ID	LIB3083-022-Q1-L1-H8
Method	BLASTX
NCBI GI	g3811007
BLAST score	587
E value	6.0e-61
Match length	122
% identity	91
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	203770
Seq. ID	LIB3083-022-Q1-L1-H9
Method	BLASTX
NCBI GI	g2695711
BLAST score	399
E value	6.0e-39
Match length	116
% identity	69
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	203771
Seq. ID	LIB3083-023-Q1-L1-A1
Method	BLASTX
NCBI GI	g1783305
BLAST score	213
E value	3.0e-17
Match length	80
% identity	55
NCBI Description	(D78609) bZIP protein [Oryza sativa]

Seq. No.	203772
Seq. ID	LIB3083-023-Q1-L1-A3
Method	BLASTX
NCBI GI	g2494299
BLAST score	364
E value	8.0e-35
Match length	130
% identity	59
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	203773
Seq. ID	LIB3083-023-Q1-L1-A7
Method	BLASTX
NCBI GI	g1854386
BLAST score	418
E value	3.0e-41
Match length	117
% identity	68
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	203774
Seq. ID	LIB3083-023-Q1-L1-B10
Method	BLASTX
NCBI GI	g1854386

BLAST score	160
E value	7.0e-18
Match length	101
% identity	51
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	203775
Seq. ID	LIB3083-023-Q1-L1-B11
Method	BLASTX
NCBI GI	g2497742
BLAST score	329
E value	1.0e-30
Match length	73
% identity	88
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	203776
Seq. ID	LIB3083-023-Q1-L1-B2
Method	BLASTX
NCBI GI	g1568480
BLAST score	146
E value	4.0e-14
Match length	76
% identity	58
NCBI Description	(Z71703) cdc2-like protein kinase [Beta vulgaris]

Seq. No.	203777
Seq. ID	LIB3083-023-Q1-L1-B3
Method	BLASTX
NCBI GI	g2146731
BLAST score	401
E value	3.0e-39
Match length	121
% identity	33
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	203778
Seq. ID	LIB3083-023-Q1-L1-B4
Method	BLASTX
NCBI GI	g2244833
BLAST score	145
E value	3.0e-09
Match length	104
% identity	20
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	203779
Seq. ID	LIB3083-023-Q1-L1-B5
Method	BLASTX
NCBI GI	g2160322
BLAST score	385
E value	2.0e-37
Match length	94

% identity	77
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	203780
Seq. ID	LIB3083-023-Q1-L1-B9
Method	BLASTX
NCBI GI	g1518540
BLAST score	147
E value	1.0e-09
Match length	51
% identity	61
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	203781
Seq. ID	LIB3083-023-Q1-L1-C1
Method	BLASTX
NCBI GI	g4406780
BLAST score	257
E value	7.0e-32
Match length	99
% identity	72
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	203782
Seq. ID	LIB3083-023-Q1-L1-C2
Method	BLASTX
NCBI GI	g4098128
BLAST score	540
E value	2.0e-55
Match length	132
% identity	81
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	203783
Seq. ID	LIB3083-023-Q1-L1-C4
Method	BLASTX
NCBI GI	g3953478
BLAST score	455
E value	4.0e-49
Match length	135
% identity	81
NCBI Description	(AC002328) F22O2.23 [Arabidopsis thaliana]

Seq. No.	203784
Seq. ID	LIB3083-023-Q1-L1-C7
Method	BLASTX
NCBI GI	g4103635
BLAST score	194
E value	8.0e-15
Match length	129
% identity	40
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	203785
Seq. ID	LIB3083-023-Q1-L1-C8

Method	BLASTX
NCBI GI	g2497486
BLAST score	192
E value	1.0e-14
Match length	54
% identity	69
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	203786
Seq. ID	LIB3083-023-Q1-L1-D1
Method	BLASTX
NCBI GI	g2129473
BLAST score	357
E value	6.0e-34
Match length	140
% identity	49
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	203787
Seq. ID	LIB3083-023-Q1-L1-D10
Method	BLASTX
NCBI GI	g2497743
BLAST score	177
E value	8.0e-13
Match length	57
% identity	61
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	203788
Seq. ID	LIB3083-023-Q1-L1-D12
Method	BLASTX
NCBI GI	g2695861
BLAST score	277
E value	6.0e-25
Match length	73
% identity	74
NCBI Description	(Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]

Seq. No.	203789
Seq. ID	LIB3083-023-Q1-L1-D5
Method	BLASTX
NCBI GI	g4417283
BLAST score	259
E value	2.0e-22
Match length	133
% identity	38
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	203790
Seq. ID	LIB3083-023-Q1-L1-D6
Method	BLASTX
NCBI GI	g1129145
BLAST score	500
E value	1.0e-50
Match length	137
% identity	72
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	203791
Seq. ID	LIB3083-023-Q1-L1-D7
Method	BLASTX
NCBI GI	g3236242
BLAST score	292
E value	1.0e-26
Match length	85
% identity	72
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	203792
Seq. ID	LIB3083-023-Q1-L1-D8
Method	BLASTX
NCBI GI	g4115377
BLAST score	393
E value	3.0e-38
Match length	118
% identity	58
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	203793
Seq. ID	LIB3083-023-Q1-L1-E1
Method	BLASTX
NCBI GI	g3738302
BLAST score	487
E value	3.0e-49
Match length	110
% identity	85
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	203794
Seq. ID	LIB3083-023-Q1-L1-E10
Method	BLASTX
NCBI GI	g2129559
BLAST score	253
E value	4.0e-22
Match length	74
% identity	74
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	203795
Seq. ID	LIB3083-023-Q1-L1-E11
Method	BLASTX
NCBI GI	g2997615
BLAST score	496
E value	3.0e-50
Match length	106
% identity	91
NCBI Description	(AF035439) CUM10 [Cucumis sativus]

Seq. No.	203796
Seq. ID	LIB3083-023-Q1-L1-E12
Method	BLASTX
NCBI GI	g2129499
BLAST score	555
E value	3.0e-57
Match length	132
% identity	79
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	203797
Seq. ID	LIB3083-023-Q1-L1-E2
Method	BLASTX
NCBI GI	g2739366
BLAST score	200
E value	1.0e-15
Match length	73
% identity	48
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	203798
Seq. ID	LIB3083-023-Q1-L1-E3
Method	BLASTX
NCBI GI	g4455171
BLAST score	213
E value	3.0e-17
Match length	66
% identity	58
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203799
Seq. ID	LIB3083-023-Q1-L1-E4
Method	BLASTX
NCBI GI	g4538929
BLAST score	204
E value	5.0e-16
Match length	116
% identity	41
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	203800
Seq. ID	LIB3083-023-Q1-L1-E5
Method	BLASTX
NCBI GI	g3892055

BLAST score	520
E value	3.0e-53
Match length	114
% identity	84
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	203801
Seq. ID	LIB3083-023-Q1-L1-E8
Method	BLASTX
NCBI GI	g227774
BLAST score	153
E value	5.0e-10
Match length	134
% identity	34
NCBI Description	basic chitinase [Arabidopsis thaliana]

Seq. No.	203802
Seq. ID	LIB3083-023-Q1-L1-F5
Method	BLASTX
NCBI GI	g2789434
BLAST score	307
E value	1.0e-28
Match length	72
% identity	83
NCBI Description	(AB001389) CLB1 [Lycopersicon esculentum]

Seq. No.	203803
Seq. ID	LIB3083-023-Q1-L1-F6
Method	BLASTX
NCBI GI	g4138209
BLAST score	180
E value	3.0e-13
Match length	112
% identity	29
NCBI Description	(AJ223071) serine/threonine kinase protein MSTK2L,long-form [Mus musculus]

Seq. No.	203804
Seq. ID	LIB3083-023-Q1-L1-F7
Method	BLASTX
NCBI GI	g4417283
BLAST score	238
E value	6.0e-20
Match length	117
% identity	42
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	203805
Seq. ID	LIB3083-023-Q1-L1-F8
Method	BLASTX
NCBI GI	g3885343
BLAST score	195
E value	5.0e-15
Match length	75
% identity	44
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203806
Seq. ID	LIB3083-023-Q1-L1-G1
Method	BLASTX
NCBI GI	g3641837
BLAST score	405
E value	1.0e-39
Match length	121
% identity	71
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	203807
Seq. ID	LIB3083-023-Q1-L1-G10
Method	BLASTX
NCBI GI	g2245021
BLAST score	175
E value	1.0e-12
Match length	60
% identity	57
NCBI Description	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No.	203808
Seq. ID	LIB3083-023-Q1-L1-G2
Method	BLASTX
NCBI GI	g3522942
BLAST score	246
E value	6.0e-21
Match length	113
% identity	49
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	203809
Seq. ID	LIB3083-023-Q1-L1-G3
Method	BLASTX
NCBI GI	g1332579
BLAST score	139
E value	4.0e-12
Match length	92
% identity	5
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	203810
Seq. ID	LIB3083-023-Q1-L1-G4
Method	BLASTX
NCBI GI	g1488052
BLAST score	437
E value	2.0e-43
Match length	108
% identity	79
NCBI Description	(U63927) beta-tubulin 2 [Daucus carota]

Seq. No.	203811
Seq. ID	LIB3083-023-Q1-L1-G6
Method	BLASTX
NCBI GI	g81952